

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:30:56 ; Search time 801.32 Seconds
(without alignments)
21.265 Million cell updates/sec

Title: US-09-016-061-6

Perfect score: 612

Sequence: 1 EVQLVESGGGLVQPKRSRL.....RHNGSFAYWGQGLTVTSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main: *
1: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
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20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
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22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	612	100.0	117	11 US-08-790-540A-6	Sequence 6, Appli
3	612	100.0	117	11 US-08-791-391A-6	Sequence 6, Appli
4	612	100.0	117	11 US-08-791-391A-6	Sequence 6, Appli
5	612	100.0	117	14 US-09-016-061-6	Sequence 6, Appli
6	612	100.0	117	17 US-09-339-922A-6	Sequence 6, Appli
7	596	97.4	117	1 PCT-US98-25828-56	Sequence 56, Appl
8	596	97.4	117	13 PCT-US98-016-56	Sequence 56, Appl
9	582	95.1	130	1 PCT-US98-25828-44	Sequence 44, Appl
10	582	95.1	130	13 US-08-986-016-44	Sequence 44, Appl
11	552	90.2	117	11 US-08-790-540-2	Sequence 2, Appli

552	90.2	117	11	US-08-790-540A-2	Sequence 2, Appli
552	90.2	117	11	US-08-791-391A-2	Sequence 2, Appli
552	90.2	117	11	US-08-791-391A-2	Sequence 2, Appli
552	90.2	117	14	US-09-016-061-2	Sequence 2, Appli
552	90.2	117	17	US-09-339-922A-2	Sequence 2, Appli
535	87.4	123	17	US-09-381-497-2	Sequence 2, Appli
501	81.9	117	11	US-08-752-693A-3	Sequence 3, Appli
501	81.9	117	18	US-09-438-136-248	Sequence 248, App
501	81.9	136	6	US-08-256-375-31	Sequence 31, Appl
501	81.9	136	6	US-08-256-375-32	Sequence 32, Appl
501	81.9	136	6	US-08-256-375-33	Sequence 33, Appl
501	81.9	136	6	US-08-256-375A-31	Sequence 31, Appl
501	81.9	136	6	US-08-256-375A-32	Sequence 32, Appl
501	81.9	136	6	US-08-256-375A-33	Sequence 33, Appl
501	81.9	136	6	US-08-256-375A-34	Sequence 34, Appl
501	81.9	136	9	US-08-595-848-31	Sequence 31, Appl
501	81.9	136	9	US-08-595-848-32	Sequence 32, Appl
501	81.9	136	9	US-08-595-848-33	Sequence 33, Appl
501	81.9	136	9	US-08-595-848-34	Sequence 34, Appl
501	81.9	136	13	US-08-976-183-31	Sequence 31, Appl
501	81.9	136	13	US-08-976-183-32	Sequence 32, Appl
501	81.9	136	13	US-08-976-183-33	Sequence 33, Appl
501	81.9	136	13	US-08-976-183-34	Sequence 34, Appl
501	81.9	136	13	US-08-976-183A-31	Sequence 31, Appl
501	81.9	136	13	US-08-976-183A-32	Sequence 32, Appl
501	81.9	136	13	US-08-976-183A-33	Sequence 33, Appl
501	81.9	136	13	US-08-976-183A-34	Sequence 34, Appl
501	81.9	136	12	US-08-815-030-1	Sequence 1, Appli
497	81.2	245	1	PCT-US98-08662-5	Sequence 5, Appli
497	81.2	245	14	US-09-069-821-5	Sequence 5, Appli
497	81.2	265	18	US-09-420-592A-5	Sequence 5, Appli
496	81.0	136	8	US-08-465-785A-57	Sequence 57, Appl
494.5	80.8	120	16	US-09-232-290-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-790-540-6
; Sequence 6, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids

;
; type: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-2

Query Match 90.2%; Score 552; DB 11; Length 117;
Best Local Similarity 88.0%; Pred. No. 2.5e-53;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPKRSRLRLSCAASGFAFSSYDMSWVRQIPEKRLWEWAKVSSGGGSTYY 60
Db 1 QVQLVESGGGVVQPKRSRLRLSCAASGFTFSYDMSWVRQAPKGLWEWAKVSSGGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYICARHNYGSPAYWGQGLTVTVSA 117
Db 61 LDTVQGRFTISRDNKNTLYLQMSLSRAEDTAVYYCARHNYGSPAYWGQGLTVTVSS 117

RESULT 12

US-08-790-540A-2
; Sequence 2, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-2

Query Match 90.2%; Score 552; DB 11; Length 117;
Best Local Similarity 88.0%; Pred. No. 2.5e-53;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPKRSRLRLSCAASGFAFSSYDMSWVRQIPEKRLWEWAKVSSGGGSTYY 60
Db 1 QVQLVESGGGVVQPKRSRLRLSCAASGFTFSYDMSWVRQAPKGLWEWAKVSSGGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYICARHNYGSPAYWGQGLTVTVSA 117
Db 61 LDTVQGRFTISRDNKNTLYLQMSLSRAEDTAVYYCARHNYGSPAYWGQGLTVTVSS 117

RESULT 13

US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391-2

Query Match 90.2%; Score 552; DB 11; Length 117;
Best Local Similarity 88.0%; Pred. No. 2.5e-53;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPKRSRLRLSCAASGFAFSSYDMSWVRQIPEKRLWEWAKVSSGGGSTYY 60
Db 1 QVQLVESGGGVVQPKRSRLRLSCAASGFTFSYDMSWVRQAPKGLWEWAKVSSGGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYICARHNYGSPAYWGQGLTVTVSA 117
Db 61 LDTVQGRFTISRDNKNTLYLQMSLSRAEDTAVYYCARHNYGSPAYWGQGLTVTVSS 117

RESULT 14

US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/791.391A
;; FILING DATE: 30-JAN-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IX 1482
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.2%; Score 552; DB 11; Length 117;
Best Local Similarity 88.0%; Pred. No. 2.5e-53;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVKPGRSLRLSCLCAASGFATSSYDMSWVRQIPEKRLKLEWAKVSSGGGTTY 60
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DB 1 QVQLVESGGGVQPGKSLRLSCLCAASGFATSSYDMSWVRQAPGKGLWAKVSSGGGTTY 60
QY 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDATMYTCARHNYGSPAYWGQGLTVTVSA 117
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DB 61 LDTVGRTTISRDNKNTLYLQMSLSRAEDTAVYYCARHNYGSPAYWGQGLTVTVSS 117

RESULT 15
US-09-016-061-2
;; Sequence 2, Application US/09016061
;; GENERAL INFORMATION:
;; APPLICANT: Huse, William D.
;; APPLICANT: Glaser, Scott M.
;; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
;; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
;; NUMBER OF SEQUENCES: 100
;; CORRESPONDENCE ADDRESS:
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016.061
;; FILING DATE: 30-JAN-1998
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/791.391
;; FILING DATE: 30-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IX 2965
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid

;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-016-061-2
Query Match 90.2%; Score 552; DB 14; Length 117;
Best Local Similarity 88.0%; Pred. No. 2.5e-53;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
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DB 1 QVQLVESGGGVQPGKSLRLSCLCAASGFATSSYDMSWVRQAPGKGLWAKVSSGGGTTY 60
QY 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDATMYTCARHNYGSPAYWGQGLTVTVSA 117
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DB 61 LDTVGRTTISRDNKNTLYLQMSLSRAEDTAVYYCARHNYGSPAYWGQGLTVTVSS 117
Search completed: March 28, 2001, 06:55:25
Job time: 1469 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:31:11 ; Search time 79.56 Seconds
(without alignments)
19.378 Million cell updates/sec

Title: US-09-016-061-6
Perfect score: 612
Sequence: 1 EVQLVESGGGLVKGKPSRLRL.....RHNYGSFAYWGQGLTVTVSA 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*

1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	465	76.0	120	5	US-09-530-237-1
3	463.5	75.7	116	1	PCT-US01-03537-80
4	458	74.8	117	5	US-09-385-673-15
5	457.5	74.8	124	1	PCT-US01-03537-81
6	456	74.5	121	1	PCT-US01-03537-92
7	455	74.3	119	4	US-08-478-684G-11
8	454.5	74.3	118	5	US-09-780-035-67
9	453.5	74.1	130	5	US-09-726-258-19
10	453.5	74.1	251	5	US-09-726-258-27
11	453	74.0	130	5	US-09-341-711-54
12	452	73.9	121	5	US-09-194-356A-9
13	450.5	73.6	120	1	PCT-US01-03537-85
14	450.5	73.6	128	1	PCT-US01-03537-77
15	450.5	73.6	128	1	PCT-US01-03537-79
16	448	73.2	113	5	US-09-194-356A-8
17	448	73.2	123	1	PCT-US01-03537-82
18	448	73.2	130	5	US-09-341-711-53
19	445	72.7	125	1	PCT-US01-03537-76
20	445	72.7	238	5	US-09-430-048-24
21	444	72.5	117	1	PCT-US01-03537-83
22	443	72.4	130	5	US-09-341-711-52
23	441.5	72.1	255	5	US-09-618-869-8
24	441	72.1	112	5	US-09-430-048-15
25	441	72.1	127	1	PCT-US01-03537-87
26	440	71.9	125	1	PCT-US01-03537-84
27	439	71.7	130	5	US-09-341-711-51

28	438.5	71.7	248	5	US-09-315-926A-80	Sequence 80, Appl
29	436	71.2	98	1	PCT-US01-03537-44	Sequence 44, Appl
30	436	71.2	112	5	US-09-430-048-14	Sequence 14, Appl
31	431.5	70.5	124	1	PCT-US01-03537-89	Sequence 89, Appl
32	431	70.4	98	1	PCT-US01-03537-38	Sequence 38, Appl
33	429	70.1	98	1	PCT-US01-03537-39	Sequence 39, Appl
34	429	70.1	138	5	US-09-403-107-144	Sequence 144, App
35	426	69.6	138	5	US-09-403-107-150	Sequence 150, App
36	423	69.1	98	1	PCT-US01-03537-41	Sequence 41, Appl
37	423	69.1	119	1	PCT-US01-03537-88	Sequence 88, Appl
38	422.5	69.0	128	1	PCT-US01-03537-78	Sequence 78, Appl
39	421	68.8	238	5	US-09-430-048-22	Sequence 22, Appl
40	420.5	68.7	300	5	US-09-188-082-4	Sequence 4, Appl
41	420	68.6	98	1	PCT-US01-03537-45	Sequence 45, Appl
42	417.5	68.2	120	1	PCT-US00-26619-17	Sequence 17, Appl
43	416.5	68.1	301	5	US-09-188-082-14	Sequence 14, Appl
44	416.5	68.1	553	5	US-09-188-082-16	Sequence 16, Appl
45	416	68.0	113	5	US-09-430-048-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-518-737-2
; Sequence 2, Application US/09518737
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2

Query Match	79.3%	Score 485.5;	DB 5;	Length 124;
Best Local Similarity	79.3%	Pred. No. 2.4e-46;		
Matches	96;	Conservative	7;	Mismatches 13;
				Indels 5;
				Gaps 2;
Qy	1	EVQLVESGGGLVKGKPSRLRLSCAASGFAFSSYDMSVMWRQIPKRLLEWAKVSSGGSTYY	60	
Db	1	EVQLVESGGGLVKGKPSRLRLSCAASGFTFSYDMSVMWRQIPKRLLEWAKVSSGGSTYY	60	
Qy	61	LDTVQGRFTISRDNAKNTLYLQMSSLNSEDYAMYYCARH----	NYGSFAYWGQGLTVTVS	116
Db	61	PDSVKGRTISRDNAKNTLYLQMSSLKSEDTAMYYCARQGVYVNFQ-TAYWGQGLTVTVS	119	
Qy	117	A 117		
Db	120	A 120		

RESULT 2
US-09-530-237-1
; Sequence 1, Application US/09530237
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD
; TITLE OF INVENTION: Inducer for production of antigen-specific antibody, expression
; TITLE OF INVENTION: containing gene therefor, and method for inducing production
; TITLE OF INVENTION: antibody
; FILE REFERENCE: SEI 98-30 PCT

RESULT 4
US-09-385-673-15
; Sequence 15, Application US/09385673
; GENERAL INFORMATION:

[illegible]


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-726-258-19

Query Match 74.1%; Score 453.5; DB 5; Length 130;
Best Local Similarity 76.7%; Pred. No. 8.1e-43;
Matches 92; Conservative 7; Mismatches 18; Indels 3; Gaps 1;

Qy 1 EVLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60
Db 1 EVLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60

Qy 61 LDTVGRTISRDNKNTLYLQMSLSNSEDYAMFYCARALISSATWFGYWGQGLTVTVA 117
Db 61 PDSVKGRTISRDNKNTLYLQMSLSNSEDYAMFYCARALISSATWFGYWGQGLTVTVA 120

RESULT 10
US-09-726-258-27
; Sequence 27, Application US/09726258
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-726-258-27

Query Match 74.1%; Score 453.5; DB 5; Length 251;
Best Local Similarity 76.7%; Pred. No. 1.8e-42;
Matches 92; Conservative 7; Mismatches 18; Indels 3; Gaps 1;

Qy 1 EVLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60
Db 24 EVLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWYAKVSSGGSTYY 83

Qy 61 LDTVGRTISRDNKNTLYLQMSLSNSEDYAMFYCARALISSATWFGYWGQGLTVTVA 117
Db 84 PDSVKGRTISRDNKNTLYLQMSLSNSEDYAMFYCARALISSATWFGYWGQGLTVTVA 143

RESULT 11
US-09-341-711-54
; Sequence 54, Application US/09341711
; GENERAL INFORMATION:
; APPLICANT: BioInvent International AB
; APPLICANT: Soderlind, Ulf
; APPLICANT: Borrebaeck, Carl
; TITLE OF INVENTION: A Method For In Vitro Molecular
; TITLE OF INVENTION: Evolution of Protein Function
; FILE REFERENCE: Mewburn 341711
; CURRENT APPLICATION NUMBER: US/09/341,711
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: PCT/GB98/00219
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB9701425.2
; PRIOR FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: scFv-B11 Antibody Fragment
; US-09-341-711-54

Query Match 74.0%; Score 453; DB 5; Length 130;
Best Local Similarity 76.1%; Pred. No. 9.2e-43;
Matches 89; Conservative 11; Mismatches 13; Indels 4; Gaps 2;

Qy 1 EVLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWYAKVSSGGSTYY 60
Db 9 EVLVESGGGLVPGKSLRLSCAASGFAFSYDMSWVRQIPEKRLWYAKVSSGGSTYY 68

Qy 61 LDTVGRTISRDNKNTLYLQMSLSNSEDYAMFYCARALISSATWFGYWGQGLTVTVA 117
Db 69 ADSVKGRTISRDNKNTLYLQMSLSNSEDYAMFYCARALISSATWFGYWGQGLTVTVA 121
```


PCT-US01-03537-79
; Sequence 79, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: xaa = Any Amino Acid
PCT-US01-03537-79

Query Match 73.6%; Score 450.5; DB 1; Length 128;
Best Local Similarity 70.3%; Pred. NO. 1.7e-42;
Matches 90; Conservative 12; Mismatches 15; Indels 11; Gaps 3;
Qy 1 EVQLVESGGGLVQPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFAFSSYDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
Qy 61 LDTVQGRFTISRDNKNTLYLQMSSLNSEDYAMYYCA--RHNY----GSFAY----WGQ 109
Db 61 ADSVKGRFTISRDNKNTLYLQMSSLNSEDYAMYYCA--RHNY----GSFAY----WGQ 120
Qy 110 GTLVTVSA 117
Db 121 GTTVTVSS 128

Search completed: March 28, 2001, 06:56:57
Job time: 1546 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:35 ; Search time 141.45 Seconds
(without alignments)
51.364 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDSVS.....CQSGSWPHTFGGTTKLEIK 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: piri:*
2: piri2:*
3: piri3:*
4: piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	94.3	107	2 A45722	anti-glycoprotein
2	528	94.1	107	2 B45722	anti-glycoprotein
3	523	93.2	123	2 S35479	Ig kappa chain pre
4	513	91.4	106	2 PL0267	Ig kappa chain v r
5	507	90.4	138	2 A26471	Ig kappa chain pre
6	499	88.9	102	2 S26346	Ig kappa chain v r
7	497	88.6	104	2 B43413	Ig kappa chain v r
8	482	85.9	107	2 C45722	anti-glycoprotein
9	434	77.4	108	2 C30502	Ig kappa chain v r
10	424	75.6	103	2 SL19975	Ig kappa chain v r
11	420	74.9	128	2 PN0445	Ig kappa chain pre
12	402	71.7	96	2 G33730	Ig kappa chain v r
13	379	67.6	115	1 KVM517	Ig kappa chain pre
14	378	67.4	144	2 PL0106	Ig kappa chain pre
15	374	66.7	111	2 S23628	Ig kappa chain v r
16	374	66.7	117	2 S40362	Ig kappa chain - h
17	374	66.7	128	2 S40379	Ig kappa chain v-j
18	373.5	66.6	114	2 S54905	Ig kappa chain v r
19	372	66.3	108	2 SL9674	Ig kappa chain v r
20	372	66.3	128	2 A56701	Ig kappa chain v r
21	368	65.6	106	2 PC4282	Ig kappa chain (an
22	368	65.6	108	2 G44151	Ig kappa chain v r
23	367	65.4	107	2 S34005	Ig kappa chain v r
24	365.5	65.2	215	2 JE0244	Ig kappa chain NIG
25	365	65.1	128	2 S40343	Ig kappa chain v-j
26	364	64.9	128	1 K3HU41	Ig kappa chain pre
27	360.5	64.3	109	2 A30608	Ig kappa chain v-i
28	360.5	64.3	129	2 A32274	Ig kappa chain pre
29	359	64.0	111	2 S09963	Ig kappa chain v-j

30	359	64.0	128	2 S40345	Ig kappa chain v-j
31	358.5	63.9	109	2 G30607	Ig kappa chain v-i
32	357.5	63.7	108	2 B30608	Ig kappa chain v-i
33	356.5	63.5	109	1 K3HUPM	Ig kappa chain v-i
34	355.5	63.4	116	2 B26555	Ig kappa chain v-i
35	355	63.3	108	2 S36279	Ig lambda chain v
36	354.5	63.2	109	2 H30601	Ig kappa chain v-i
37	354	63.1	125	2 S40344	Ig kappa chain v-j
38	354	63.1	129	2 S29627	Ig kappa chain v r
39	353	62.9	108	2 B49047	Ig kappa chain v r
40	352.5	62.8	109	2 G30601	Ig kappa chain v-i
41	352	62.7	107	2 S36264	Ig lambda chain v
42	351	62.6	107	2 S57444	Ig kappa chain v-j
43	350.5	62.5	108	2 C30608	Ig kappa chain v-i
44	350.5	62.5	109	1 K3HUTI	Ig kappa chain v-i
45	349.5	62.3	109	2 D30601	Ig kappa chain v-i

ALIGNMENTS

RESULT 1
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C:Species: Mus musculus (house mouse))
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 94.3%; Score 529; DB 2; Length 107;
Best Local Similarity 93.5%; Pred. No. 2.1e-41;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWQOKSHESPRLLIKYRSQISGIPS 60
DB 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWQOKSHESPRLLIKYRSQISGIPS 60
QY 61 RFGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
DB 61 RFGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107

RESULT 2
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (C:Species: Mus musculus (house mouse))
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A:Reference number: A45722; MUID:93100833
A:Accession: B45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

QY 3 VLTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSRF 62
 DB 1 VLTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSRF 60

QY 63 SGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEK 104
 DB 61 SGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEK 102

RESULT 7
 B43413
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 497; DB 2; Length 104;
 Best Local Similarity 91.3%; Pred. No. 1.6e-38;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSRFS 63
 DB 1 LTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSRFS 60

QY 64 GSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107
 DB 61 GSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 104

RESULT 8
 C45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (f
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: C45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
 A:Reference number: A45722; MUID:93100833
 A:Accession: C45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 482; DB 2; Length 107;
 Best Local Similarity 85.8%; Pred. No. 3.8e-37;
 Matches 9; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 IVLTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSR 61
 DB 2 VLTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSR 61

QY 62 FSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107
 DB 62 FSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107

RESULT 9

C30502
 Ig kappa chain V region (D444) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
 C:Accession: C30502
 R:Eilat, D.; Webster, D.M.; Rees, A.R.
 J. Immunol. 141, 1745-1753, 1988
 A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1
 A:Reference number: A30502; MUID:88315787
 A:Accession: C30502
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <EIL>
 A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 434; DB 2; Length 108;
 Best Local Similarity 76.6%; Pred. No. 8.6e-33;
 Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPS 60

DB 1 DILLTQSPAILSVSPGERVSFSCRASQISGTSLSHWYQORTNGSPRLLIKYASESISGIPS 60

QY 61 FSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107

DB 61 FSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107

RESULT 10

S19975
 Ig kappa chain V region (M-T408) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S19975
 R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
 submitted to the EMBL Data Library, March 1992
 A:Description: Structural characterization of CD4 mAb.
 A:Reference number: S19963
 A:Accession: S19975
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-103 <WEI>
 A:Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 75.6%; Score 424; DB 2; Length 103;
 Best Local Similarity 77.5%; Pred. No. 6.6e-32;
 Matches 79; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 6 QSPATLSVTPGDSVSLSCQASQISINHLHWYQOKSHSPRLLIKYRSQISGIPSRFS 65

DB 1 QSPATLSLSPGERATLSCRASQISIDYLSHWYQOKSHSPRLLIKYRSQISGIPSRFS 60

QY 66 GSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107

DB 61 GSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 102

RESULT 11

PN0445
 Ig kappa chain precursor V-I region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PN0445
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction
A;Reference number: PN0444; MUID:93138402

A;Accession: PN0445
A;Molecule type: mRNA
A;Residues: 1-128 <RNA>
A;Cross-references: GB:L02347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 420; DB 2; Length 128;
Best Local Similarity 72.9%; Pred. No. 1.9e-31;
Matches 78; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60
DB 11 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 70

QY 61 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWPHTFGGKLEIK 107
DB 71 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWPHTFGGKLEIK 117

RESULT 12

Ig kappa chain V region (23.32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: G33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unpaired with lambda-chains
A;Reference number: A33730; MUID:89367325
A;Accession: G33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <LAW>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 402; DB 2; Length 96;
Best Local Similarity 81.1%; Pred. No. 6e-30;
Matches 77; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60
DB 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60

QY 61 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWP 95
DB 61 SPRGSGSGTDFALSIINSVETEDGVVYQNGHSEFP 95

RESULT 13

Ig kappa chain precursor V region (L7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999
C;Accession: A01925
R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A;Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences
A;Reference number: A93259; MUID:81220975
A;Accession: A01925
A;Molecule type: DNA

A;Residues: 1-115 <PEC>
A;Cross-references: GB:V01564; GB:J00574; NID:951718; PID:CAA24884.1; PID:g758153
A;Note: the sequence was determined from the germline gene
A;Note: there appear to be two possible splice junctions at the 3' end of the intron;
C;Genetics:
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a higher order structure.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
F;43-108/Disulfide bonds: #status predicted

Query Match 67.6%; Score 379; DB 1; Length 115;
Best Local Similarity 74.7%; Pred. No. 8.9e-28;
Matches 71; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60
DB 21 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 80

QY 61 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWP 95
DB 81 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWP 115

RESULT 14

Ig kappa chain precursor V-J-C region (LSI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma to the lambda chain of immunoglobulin
A;Reference number: PL0106; MUID:89235583
A;Accession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region <JRG>
F;128-144/Domain: C region (fragment) <CRE>

Query Match 67.4%; Score 378; DB 2; Length 144;
Best Local Similarity 64.5%; Pred. No. 1.4e-27;
Matches 69; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60
DB 21 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 80

QY 61 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWPHTFGGKLEIK 107
DB 81 RFGSGSGTDFALSIINSVETEDFGMYCQSGSWPHTFGGKLEIK 127

RESULT 15

Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23628

Query Match	56.7%	Score 374	DB 2	Length 111
Best Local Similarity	64.5%	Pred. No. 2.4e-27		
Matches	69	Conservative	20	Mismatches 18
			Indels	0
			Gaps	0
QY	1	DIVLTQSPATLSVTPGDVSVLSCAQSISNHLHWYQOKSHESPLLIIKYRSQISGIPS	60	
	:			
	:			
Db	1	EIVLTQSPATLSLSPGERATLSCRASVSYSLLAWYQKPGQAPRLIYDASNRATGIPA	60	
	:			
	:			
QY	61	RFSGSGSGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK	107	
	:			
	:			
Db	61	RFSGSGSGTFTLTISLEPEDFAVYTCQRRSNWPFFGQGTKEYIK	107	
	:			
	:			

Search completed: March 28, 2001, 06:41:35
Job time: 858 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:24 ; Search time 124.69 Seconds

(without alignments)

27.415 Million cell updates/sec

Title: US-09-016-061-8

Perfect score: 561

Sequence: 1 DIVLTQSPATLSVTPGDSVS.....COQSGSWPHTFGGKTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	379	67.6	115	1 KV5L_MOUSE	P01642 mus musculus
2	364	64.9	128	1 KV3B_HUMAN	P06311 homo sapien
3	356.5	63.5	109	1 KV3F_HUMAN	P01624 homo sapien
4	351.5	62.7	129	1 KV3H_HUMAN	P04207 homo sapien
5	350.5	62.5	109	1 KV3D_HUMAN	P01622 homo sapien
6	347.5	61.9	109	1 KV3B_HUMAN	P01620 homo sapien
7	346.5	61.8	129	1 KV3L_HUMAN	P18135 homo sapien
8	344	61.3	108	1 KV5L_MOUSE	P01644 mus musculus
9	342	61.0	108	1 KV5O_MOUSE	P01648 mus musculus
10	341.5	60.9	109	1 KV3E_HUMAN	P01623 homo sapien
11	341.5	60.9	129	1 KV3M_HUMAN	P18136 homo sapien
12	339	60.4	108	1 KV5L_MOUSE	P01645 mus musculus
13	339	60.4	108	1 KV5M_MOUSE	P01646 mus musculus
14	336.5	60.0	108	1 KV3A_HUMAN	P01619 homo sapien
15	336	59.9	108	1 KV5N_MOUSE	P01647 mus musculus
16	334	59.5	108	1 KV1_CANFA	P01618 canis famil
17	334	59.5	111	1 KV3D_MOUSE	P03977 mus musculus
18	334	59.5	111	1 KV3B_MOUSE	P01660 mus musculus
19	333	59.4	111	1 KV3L_MOUSE	P01664 mus musculus
20	333	59.4	111	1 KV3R_MOUSE	P01670 mus musculus
21	332	59.2	108	1 KV1M_HUMAN	P01605 homo sapien
22	330	58.8	108	1 KV1C_HUMAN	P01595 homo sapien
23	330	58.8	111	1 KV3A_MOUSE	P01654 mus musculus
24	330	58.8	115	1 KV3L_HUMAN	P04433 homo sapien
25	329	58.6	108	1 KV5E_MOUSE	P01649 mus musculus
26	328	58.5	108	1 KV1S_HUMAN	P01611 homo sapien
27	328	58.5	111	1 KV3T_MOUSE	P01672 mus musculus
28	327	58.3	108	1 KV5J_MOUSE	P01643 mus musculus
29	327	58.3	111	1 KV3C_MOUSE	P01656 mus musculus
30	326.5	58.2	113	1 KV2G_MOUSE	P01631 mus musculus
31	326.5	58.2	117	1 KV2E_HUMAN	P06309 homo sapien
32	324	57.8	108	1 KV1H_HUMAN	P01600 homo sapien
33	324	57.8	111	1 KV3M_MOUSE	P01665 mus musculus

ALIGNMENTS

RESULT 1

```
KV5L_MOUSE
ID   KV5L_MOUSE  STANDARD;          PRT;   115 AA.
AC   P01642;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81220975.
RA   Pech M., Hochli J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
CC   -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
CC   THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC   LACKING RESIDUES 17-19.
DR   PIR; A01925; KVM5L7.
DR   INTERPRO; IPR003006;
KW   Immunoglobulin V region; Signal.
FT   SIGNAL    1..20
FT   CHAIN     21..>115  IG KAPPA CHAIN V-V REGION L7.
FT   DOMAIN    21..43    FRAMEWORK 1.
FT   DOMAIN    44..54    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN    55..69    FRAMEWORK 2.
FT   DOMAIN    70..76    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN    77..108   FRAMEWORK 3.
FT   DOMAIN    109..>115 COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID  43..108   BY SIMILARITY.
FT   NON_TER   115..115
SQ   SEQUENCE 115 AA; 12615 MW;  C17BEC758C577E00 CRC64;
P04431 homo sapien
P01655 mus musculo
P01667 mus musculo
P01673 mus musculo
P01674 mus musculo
P01671 mus musculo
P04206 homo sapien
P01604 homo sapien
P04430 homo sapien
P01633 mus musculo
P01666 mus musculo
P01662 mus musculo
```

Query Match

Best Local Similarity 67.6%; Score 379; DB 1; Length 115;
Matches 71; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

```
Qy 1 DIVLTQSPATLSVTPGDSVSLSCQASQSTSNHLHWYQQKSHSPRLLIKYRSISGIPS 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWTYQRTNGSPRLLIKYVASEISGIPS 80
```

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Qy 61 RFSGSGSGTDFALSNVETEDFGMYFCQSGSWP 95
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 RFSGSGSGTDFTLINSVSEDIADYICQGSNSWP 115
```

RESULT 2

```
KV3K_HUMAN
ID   KV3K_HUMAN  STANDARD;          PRT;   128 AA.
AC   P06311;
DT   01-JAN-1988 (Rel. 06, Created)
```

```
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041852.
RA Klobeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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DR EMBL; Z00021; CAA77316.1; -
DR PIR; A01899; K3H041.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 54 FRAMEWORK 2.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 64.9%; Score 364; DB 1; Length 128;
Best Local Similarity 64.5%; Pred. No. 5e-31;
Matches 69; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQOKSHSPRLIKYRSQISGIP 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 EIVLTQSPGTLSPGESATLSQASQSSNLAQYQKRGQSPRLIRDSRRANGIPD 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RFSGSGGTDFALSIQSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 RFSGSGGTDFTLISRLPEDEFAVYCYQYSPYTFGGGKLEIK 127
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN V-III REGION POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE. 76276460.
RX MEDLINE; 76276460.
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IgM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
```

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CC GLOBULIN ACTIVITY.
DR PIR; A01897; K3H0PM.
DR HSSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 63.5%; Score 356.5; DB 1; Length 109;
Best Local Similarity 63.0%; Pred. No. 2.5e-30;
Matches 68; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQOKSHSPRLIKYRSQISGIP 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVMTQSPGTVLSVSGERATLSQASQISNSYLAQYQKRGQSPRLIYGASTRATGIP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 SRFSGSGGTDFALSIQSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ARFSGSGGTFTLTISSQSEDFAVYCYQYNNWPTFGGTRVEIK 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86177570.
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
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CC -----
DR EMBL; M12740; AAA58992.1; -
DR PIR; A01898; K3HUC1.
DR HSSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 62.7%; Score 351.5; DB 1; Length 129;
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Best Local Similarity 61.18; Pred. No. 1e-29;
Matches 66; Conservative 22; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTFGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYRSQISGIPS 60
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
Db 21 EIVMTQSPATLSVSPGERATLSRASQSVSNLAWYQKPGQPPRLIIYGASTRATGIPA 80
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
QY 61 RFSGSGSGTDFALSINSVETEDFGMYFCQSGSW-PHTFGGKTLEIK 107
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
Db 81 RFSGSGSGTDFLTISRQSEDFAVYCYQYNNPPWTFGGQTRVEIK 128
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:

RESULT 5
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 72188439.
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT T1). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PTR; A01895; K3HUTI.
DR HSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 62.5%; Score 350.5; DB 1; Length 109;
Best Local Similarity 63.08; Pred. No. 1e-29;
Matches 68; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTFGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYRSQISGIP 59
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
Db 1 EIVLTQSPGTLSPGERATLSRASQSVSNFLAWYQKPGQAPRLIIYVASSRATGIP 60
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
QY 60 SRFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
Db 61 DRFSGSGSGTDFLTISRLEPDDFAVYCYQYSGSPFTGGQTKVELK 108
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:

RESULT 6
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82046598.
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two

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```

RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
DR HSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FEB4 CRC64;

Query Match 61.9%; Score 347.5; DB 1; Length 109;
Best Local Similarity 62.0%; Pred. No. 2.1e-29;
Matches 67; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTFGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYRSQISGIP 59
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
Db 1 EIVLTQSPGTLSPGERATLSRASQSVSNFLAWYQKPGQAPRLIIYGCSSSRATGIP 60
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
QY 60 SRFSGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKTLEIK 107
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:
Db 61 DRFSGSGSGTDFLTISRLEPDDFAVYCYQYSGSPFTGGQSKVEIK 108
   :|||||:|||||: :|||||:|||||: :|||||: :|||||: :|||||: :|||||:

RESULT 7
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88171307.
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P10022; K3HUHA.
DR HSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JKI SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 61.8%; Score 346.5; DB 1; Length 129;
Best Local Similarity 62.0%; Pred. No. 3.3e-29;
Matches 67; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

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QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQISGIP 59
DB 21 EIVLTQSPGTLSPGERATLSCRASQSSSYSLAYLQKPGQAPRLLIYGYSSRATGIP 80
QY 60 SRFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 81 DRFSGSGGTDFLTSLRLEPEDFAVYCYQYGTSPRTFGGKVEIK 128

RESULT 8
KV5K_MOUSE STANDARD; PRT; 108 AA.
ID KV5K_MOUSE 1 23 FRAMEWORK 1.
AC P01644; 24 34 COMPLEMENTARITY-DETERMINING 1.
DT 21-JUL-1986 (Rel. 01, Created) 35 49 FRAMEWORK 2.
DT 21-JUL-1986 (Rel. 01, Last sequence update) 50 56 COMPLEMENTARITY-DETERMINING 2.
DT 15-JUL-1999 (Rel. 38, Last annotation update) 57 88 FRAMEWORK 3.
DE IG KAPPA CHAIN V-V REGION HP R16.7. 89 97 FRAMEWORK 4.
OS Mus musculus (Mouse). 98 108 BY SIMILARITY.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP STRAIN=A/J;
RC STRAIN=A/J;
RX MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsionate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
DR Immunoglobulin V region; Antiarsonate antibody.
KW DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DOMAIN 98 108 BY SIMILARITY.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 61.3%; Score 344; DB 1; Length 108;
Best Local Similarity 60.7%; Pred. No. 4.8e-29;
Matches 65; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQISGIP 60
DB 1 DIQMTQTSSLSASGLDRVTISCRASQDISNLYNWKQKPDGTVKLLIYYTSLRLHSGVPS 60
QY 61 RFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 RFSGSGGTDFLTSLISNLEQEDISTYFCQGNLPRTFGGGKLEIK 107

RESULT 9
KV5O_MOUSE STANDARD; PRT; 108 AA.
ID KV5O_MOUSE 1 23 FRAMEWORK 1.
AC P01648; 24 34 COMPLEMENTARITY-DETERMINING 1.
DT 21-JUL-1986 (Rel. 01, Created) 35 49 FRAMEWORK 2.
DT 21-JUL-1986 (Rel. 01, Last sequence update) 50 56 COMPLEMENTARITY-DETERMINING 2.
DT 15-JUL-1999 (Rel. 38, Last annotation update) 57 88 FRAMEWORK 3.
DE IG KAPPA CHAIN V-V REGION HP 91A3. 89 97 FRAMEWORK 4.
OS Mus musculus (Mouse). 98 108 BY SIMILARITY.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP STRAIN=A/J;
RC STRAIN=A/J;
RX MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsionate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
DR Immunoglobulin V region; Antiarsonate antibody.
KW DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DOMAIN 98 108 BY SIMILARITY.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 61.3%; Score 344; DB 1; Length 108;
Best Local Similarity 60.7%; Pred. No. 4.8e-29;
Matches 65; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQISGIP 60
DB 1 DIQMTQTSSLSASGLDRVTISCRASQDISNLYNWKQKPDGTVKLLIYYTSLRLHSGVPS 60
QY 61 RFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 RFSGSGGTDFLTSLISNLEQEDISTYFCQGNLPRTFGGGKLEIK 107

RESULT 9
KV5O_MOUSE STANDARD; PRT; 108 AA.
ID KV5O_MOUSE 1 23 FRAMEWORK 1.
AC P01648; 24 34 COMPLEMENTARITY-DETERMINING 1.
DT 21-JUL-1986 (Rel. 01, Created) 35 49 FRAMEWORK 2.
DT 21-JUL-1986 (Rel. 01, Last sequence update) 50 56 COMPLEMENTARITY-DETERMINING 2.
DT 15-JUL-1999 (Rel. 38, Last annotation update) 57 88 FRAMEWORK 3.
DE IG KAPPA CHAIN V-V REGION HP 91A3. 89 97 FRAMEWORK 4.
OS Mus musculus (Mouse). 98 108 BY SIMILARITY.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP STRAIN=A/J;
RC STRAIN=A/J;
RX MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsionate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
DR Immunoglobulin V region; Antiarsonate antibody.
KW DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DOMAIN 98 108 BY SIMILARITY.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 61.0%; Score 342; DB 1; Length 108;
Best Local Similarity 58.9%; Pred. No. 7.8e-29;
Matches 63; Conservative 23; Mismatches 21; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQISGIP 60
DB 1 DIQMTQTSSLSASGLDRVTISCRASQDISNLYNWKQKPDGTVKLLIYYTSLRLHSGVPS 60
QY 61 RFSGSGGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 RFSGSGGTDFLTSLISNLEQEDISTYFCQGNLPRTFGGGKLEIK 107

RESULT 10
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID KV3E_HUMAN 1 23 FRAMEWORK 1.
AC P01623; 24 34 COMPLEMENTARITY-DETERMINING 1.
DT 21-JUL-1986 (Rel. 01, Created) 35 49 FRAMEWORK 2.
DT 21-JUL-1986 (Rel. 01, Last sequence update) 50 56 COMPLEMENTARITY-DETERMINING 2.
DT 15-JUL-1999 (Rel. 38, Last annotation update) 57 88 FRAMEWORK 3.
DE IG KAPPA CHAIN V-III REGION WOL. 89 97 FRAMEWORK 4.
OS Homo sapiens (Human). 98 108 BY SIMILARITY.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82046598.
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HWL.
DR HSSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
DR Immunoglobulin V region. 98 108 BY SIMILARITY.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 60.9%; Score 341.5; DB 1; Length 109;
Best Local Similarity 62.0%; Pred. No. 8.9e-29;
Matches 67; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQISGIP 59
DB 1 DIQMTQTSSLSASGLDRVTISCRASQDISNLYNWKQKPDGTVKLLIYYTSLRLHSGVPS 59

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Query Match 60.4%; Score 339; DB 1; Length 108;
Best Local Similarity 60.7%; Pred. No. 1.6e-28;
Matches 65; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-NHLHWYQOKSHSPRLLIKYSQSISSIP 60
DB 1 DIQMTQSTSLASGLDRVTISCRASQDISNLYLNWYQOKPDGTVKLLIYVTSRLHSGVPS 60

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 RFGSGSGTDSLTSISNLEQEDATYFCQGYMLPRTFEGGKLEIK 107

RESULT 14
KV3A_HUMAN STANDARD; PRT; 108 AA.

AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE.

RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3HUB6.
DR HSSP: P01789; 2MCP.
DR INTERPRO: IPR003006; .
DR PFAM: PF00047; ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 60.0%; Score 336.5; DB 1; Length 108;
Best Local Similarity 60.2%; Pred. No. 2.9e-28;
Matches 65; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-NHLHWYQOKSHSPRLLIKYSQSISSIP 59
DB 1 ZIVLTZSPGTLSPGZRAALSQASQSLSGNVLAWYQOKPGQAPRLMYGVSSRATGIP 60

QY 60 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 DRPFGSGSGADFTLTISRLZPEDFAVYVYCOQYGGSPPTFGGKLEIK 108

RESULT 15
KV5N_MOUSE STANDARD; PRT; 108 AA.

AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Completed amino acid sequence of light chain variable regions derived

from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVM5AR.
DR INTERPRO: IPR003006; .
DR PFAM: PF00047; ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match 59.9%; Score 336; DB 1; Length 108;
Best Local Similarity 58.9%; Pred. No. 3.3e-28;
Matches 63; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-NHLHWYQOKSHSPRLLIKYSQSISSIP 60
DB 1 DIQMTQSTSLASGLDRVTISCRASQDISNLYLNWYQOKPDGTVKLLIYVTSRLHSGVPS 60

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 61 RFGSGSGTDSLTSISNLEQEDATYFCQGYMLPRTFEGGKLEIK 107

Search completed: March 28, 2001, 07:29:25
Job time: 1632 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:26:53 ; Search time 263.81 Seconds
(without alignments)
47.539 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDSVS.....CQSGSWPHTFGGTKLEIK 107

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_invertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361.5	64.4	109	4 Q9UL85	Q9ul85 homo sapien
2	358	63.8	108	4 Q9UL83	Q9ul83 homo sapien
3	346.5	61.8	109	4 Q9UL78	Q9ul78 homo sapien
4	336	59.9	108	4 Q9UL77	Q9ul77 homo sapien
5	336	59.9	298	11 Q9QIF0	Q9qif0 mus musculu
6	333	59.4	108	4 Q9UL79	Q9ul79 homo sapien
7	324.5	57.8	109	4 Q9UL86	Q9ul86 homo sapien
8	324	57.8	108	4 Q9UL70	Q9ul70 homo sapien
9	322.5	57.5	107	4 Q9UL81	Q9ul81 homo sapien
10	312	55.6	107	11 Q9JL84	Q9jl84 mus musculu
11	311	55.4	99	11 Q9JL74	Q9jl74 mus musculu
12	310	55.3	214	11 Q9JL85	Q9jl85 mus musculu
13	303.5	54.1	104	11 Q9JL82	Q9jl82 mus musculu
14	303.5	54.1	106	5 Q9U410	Q9u410 schistosoma
15	299	53.3	101	11 Q9JL78	Q9jl78 mus musculu
16	293	52.2	114	4 Q9UL80	Q9ul80 homo sapien
17	290	51.7	103	11 Q9JL76	Q9jl76 mus musculu
18	279	49.7	97	11 Q9JL76	Q9jl76 mus musculu
19	258	46.0	109	6 Q9N0W5	Q9n0w5 oryctolagus

20	199.5	35.5	107	4 Q9UL82	Q9ul82 homo sapien
21	197.5	35.2	107	4 Q9NSD6	Q9nsd6 homo sapien
22	144	25.7	93	4 Q9UL76	Q9ul76 homo sapien
23	142	25.3	130	4 Q9NP29	Q9np29 homo sapien
24	140	25.0	168	4 Q9UQ56	Q9uq56 homo sapien
25	140	25.0	246	4 Q9UQ55	Q9uq55 homo sapien
26	129.5	23.1	209	6 Q9XSM7	Q9xsm7 salmtri sci
27	127	22.6	210	6 P79336	P79336 felis silve
28	123	21.9	100	13 Q9YH19	Q9yh19 ginglymosto
29	121	21.6	152	13 Q9YH11	Q9yh11 ginglymosto
30	121	21.6	342	13 Q9IB00	Q9ib00 sphoeroides
31	120.5	21.5	123	4 Q9UKI3	Q9uk13 homo sapien
32	119	21.2	136	13 Q9YHL6	Q9yh16 ginglymosto
33	118	21.0	123	11 Q61243	Q61243 mus musculu
34	118	21.0	136	13 Q9YHP2	Q9ynp2 ginglymosto
35	118	21.0	142	13 Q9YHQ2	Q9yhn2 ginglymosto
36	116	20.7	136	13 Q9YHR9	Q9yhr9 ginglymosto
37	115.5	20.6	509	11 Q08907	Q08907 mus musculu
38	113.5	20.2	134	13 Q9YHG7	Q9yhg7 ginglymosto
39	111	19.8	136	13 Q9YHP4	Q9yhp4 ginglymosto
40	109.5	19.5	340	13 Q9IA26	Q9iaz6 sphoeroides
41	109.5	19.5	509	11 Q9WTN4	Q9wtcn4 mus musculu
42	109	19.4	136	13 Q9YHP3	Q9yhp3 ginglymosto
43	109	19.4	186	11 Q62861	Q62861 rattus norv
44	108.5	19.3	340	13 Q9IA20	Q9iaz0 sphoeroides
45	108.5	19.3	509	11 Q9QX57	Q9qx57 mus musculu

ALIGNMENTS

RESULT 1
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN-VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035029; AAD56265.1; -;
DR HSP; P01607; IREX.
DR INTERPRO: IPR003006; -;
DR PFAM: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 64.4%; Score 361.5; DB 4; Length 109;
Best Local Similarity 64.8%; Pred. No. 1.2e-32;
Matches 70; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSTNSILHWYQKSHSPRLIKYRSSISIPS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPATLSVTPGDSVSLSCQASQSTNSILHWYQKSHSPRLIKYRSSISIPS 60
QY 61 RSGSGSGTDFALINSVETEDFGMYFCQSGSNPH-TFGGGTKLEIK 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFGSGSGTFTLTLSQSEDFAIYHCQYNSMPPLTTFGGGTVKEIK 108

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RESULT 2
Q9UL83 ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -
DR HSSP: P01607; IREI
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; ig: 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9FC5A92EBA96EEA CRC64;

Query Match 63.8%; Score 358; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 2.8e-32;
Matches 65; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-SNHLHWYQKSHESPRLLIKYRSQISGIPS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVYTSPTATLSVSPGERATLSQASQSI-SNHLHWYQKSHESPRLLIKYRSQISGIPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q9UL78 ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -
DR HSSP: P01789; IMCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; ig: 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 61.8%; Score 346.5; DB 4; Length 109;
Best Local Similarity 63.0%; Pred. No. 5.3e-31;

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Matches 68; Conservative 18; Mismatches 21; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-SNHLHWYQKSHESPRLLIKYRSQISGIPS 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPGTLSLSPGERATLSQASQSI-SNHLHWYQKSHESPRLLIKYRSQISGIPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 60 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DRFGSGSGTDFTLTISRLEPEDCAVYCCQYVSSGSSPLTGGGKVEIK 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q9UL77 ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -
DR HSSP: P01607; IREI
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; ig: 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 59.9%; Score 336; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 7.6e-30;
Matches 65; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVLSQASQSI-SNHLHWYQKSHESPRLLIKYRSQISGIPS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQTSFSSLSASVGDRTVITCRASQSI-SNHLHWYQKSHESPRLLIKYRSQISGIPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISRLEPEDCAVYCCQYVSSGSSPLTGGGKVEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q9QYF0 ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BA1B/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinozaki N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB036341; BAA88633.1; -
DR HSP; P01607; IREI.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 59.98; Score 336; DB 11; Length 298;
Best Local Similarity 58.34; Pred. No. 2.4e-29;
Matches 63; Conservative 26; Mismatches 17; Indels 2; Gaps 2;

Qy 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQSIS-GIP 59
Db 173 DIETQSPASLASVGETVITTCRASGNIHNYLAWYQOKSPQLLV-YNAKTLADGVP 231

Qy 60 SRFSGSGGTDFALNSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 232 SRFSGSGGTQYSLKINSQPEDFGSYCYQHFWTPYTFGGGKLEIK 279

RESULT 6
Qy 9QUL79 PRELIMINARY; PRT; 108 AA.
AC 9QUL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035035; AAD56271.1; -
DR HSP; P01607; IREI.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 59.48; Score 333; DB 4; Length 108;
Best Local Similarity 59.88; Pred. No. 1.6e-29;
Matches 64; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

Qy 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQSISGIPS 60
Db 1 DIVMTQSPSLASGDRVTITSCRSQSISSVLAQYQOKPGKAPPELLIYAASSTLQSGVPS 60

Qy 61 RFSGSGGTDFALNSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGGTDFLTITSCIQSEDFATYCYQYSPFPTEGQGTKEIK 107

RESULT 7
Qy 9QUL86 PRELIMINARY; PRT; 109 AA.
AC 9QUL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -
DR HSP; P01789; IMCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 24325F72C7DAC83 CRC64;

Query Match 57.88; Score 324.5; DB 4; Length 109;
Best Local Similarity 60.2%; Pred. No. 1.4e-28;
Matches 65; Conservative 18; Mismatches 24; Indels 1; Gaps 1;

Qy 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQSISGIP 59
Db 1 EIVLTQSPGTLSTLPPGERATLSCRSQSVSSVLAQYQOKPGAPRLLIYGTSSRATGIP 60

Qy 60 SRFSGSGGTDFALNSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 DRFSGSGSETDFTLTISRLEPEDFAVYCYQYSSITFCGPGTKVDIK 108

RESULT 8
Qy 9QUL70 PRELIMINARY; PRT; 108 AA.
AC 9QUL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -
DR HSP; P01607; IREI.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 57.88; Score 324; DB 4; Length 108;
Best Local Similarity 58.9%; Pred. No. 1.6e-28;
Matches 63; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 DIVLTQSPATLSVTPGDSVSLSCQASQSI-SNHLHWYQOKSHSPRLLIKYRSQSISGIPS 60
Db 1 DIQMTQSPSLASVGDRTVITTCRASQSISSVLAQYQOKPGKVPKSLIYAASSTLQSGVPS 60

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QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTGGTKLEIK 107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 RFGSGSGTDFLTISLQPEDVATYCYQKYNAPRTFGPTKLEIK 107

RESULT 9
Q9JL81
ID Q9JL81 PRELIMINARY; PRT; 107 AA.
AC Q9JL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1;
DR HSSP; P80362; 1WTL
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 070549FDE0754748 CRC64;

Query Match 57.5%; Score 322.5; DB 4; Length 107;
Best Local Similarity 58.9%; Pred. No. 2.3e-28;
Matches 63; Conservative 21; Mismatches 22; Indels 1; Gaps 1;

QY 1 DIVLTOSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIQMTQSTSSLSASGDRVTVTKASQSVSNLYNWYQKPGKAPNLLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTGGTKLEIK 107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 RFGSGSGTDFLTISLQPEDVATYCYQKYNAPRTFGPTKVDIR 106

RESULT 10
Q9JL84
ID Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
  acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206022; AAF69320.1;
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACALIE5D CRC64;

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Query Match 55.6%; Score 312; DB 11; Length 107;
Best Local Similarity 56.1%; Pred. No. 3.4e-27;
Matches 60; Conservative 16; Mismatches 31; Indels 0; Gaps 0;

QY 1 DIVLTOSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIQMTQSTSSLSASGDRVTVTKASQSVSNLYNWYQKPGKAPNLLIYTSSLXSGVPS 60

QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTGGTKLEIK 107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 RFGSGSGTDFLTISLQPEDVATYCYQKYNAPRTFGPTKLEIK 107

RESULT 11
Q9JL74
ID Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
  acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206032; AAF69330.1;
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match 55.4%; Score 311; DB 11; Length 99;
Best Local Similarity 58.8%; Pred. No. 4e-27;
Matches 57; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 11 LSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLTIKYRSQISGIPSRSFGSGGTD 70
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 LLVSAGDRVTITCKASQSVSNLVYQKPGSPKLLIYASNRVTGVPDRFTGSGYCTD 62

QY 71 FALSINSVETEDFGMYFCQSGSWPHFTGGTKLEIK 107
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 FTFTISTVQAEALAVYFCQDYSSPRTFGGTTKLEIK 99

RESULT 12
Q9RIA5
ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
  antibody (Mab 7, its light and heavy chains) and construction of a
  single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1;
DR HSSP; P01789; 1MCP.
DR INTERPRO; IPR003006;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:20 ; Search time 183.85 Seconds
(without alignments)
19.901 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLQSPATLSVTPGDSVS.....COQSGSWPHTFGGKLEIK 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36:*

- 1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT:*
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- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT:*
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- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	561	100.0	107	19 W76004	LM609 antibody lig
2	530	94.5	109	20 Y06380	Murine monoclonal
3	526	93.8	127	15 R54093	Sequence of mouse
4	519	92.5	108	12 R15438	Light chain variab
5	519	92.5	109	15 R52033	Light chain variab
6	519	92.5	240	12 R15443	Single chain Fv fr
7	516	92.0	107	14 R38601	HYH light chain.
8	516	92.0	107	19 W58482	Murine HYH antibod
9	501	89.3	108	20 W84094	Murine vitronectin
10	498	88.8	108	17 W00241	EGF receptor chime
11	490	87.3	127	21 Y32405	Mouse anti-verotox
12	486.5	86.7	109	20 W89176	Anti-p53 monoclonal

13	470	83.8	107	19 W76002	Vitaxin antibody 1
14	465	82.9	128	20 Y30199	Light chain variab
15	465	82.9	214	20 Y30202	Light chain sequen
16	464	82.7	107	19 W76006	LM609 grafted anti
17	459	81.8	108	17 W04333	Light chain of mon
18	438	78.1	107	20 W84098	Humanised anti- alp
19	438	78.1	112	20 W84100	Vitronectin alpha-
20	432	77.0	107	13 R25729	Humanised VL regio
21	426	75.9	107	15 R50190	Light chain variab
22	426	75.9	107	20 Y26979	Light chain variab
23	422	75.2	244	20 Y31610	Mucin Tn antigen-b
24	421	75.0	127	21 Y32407	Mouse anti-verotox
25	420	74.9	107	14 R32129	Anti-IL2R beta ant
26	419	74.7	240	14 R34510	Fv(TU27). Homo sa
27	418	74.5	107	14 R37610	B-B10 Mab L chain
28	418	74.5	127	18 W08945	Kappa light chain
29	418	74.5	127	18 W08941	Kappa light chain
30	418	74.5	127	18 W08943	Kappa light chain
31	417	74.3	127	19 W44176	Monoclonal antibod
32	417	74.3	651	17 W05135	scFv(225)-ETA fusl
33	417	74.3	892	17 W05139	scFv2(FRP5/225)-ET
34	417	74.3	892	17 W05140	scFv2(225/FRP5)-ET
35	417	74.3	1020	17 W05141	scFv2(FRP5/225)-ET
36	416	74.2	126	10 P30479	Chimeric monoclonal
37	416	74.2	127	18 W08946	Kappa light chain
38	416	74.2	240	19 W26799	Anti-gp54 Mab 48-1
39	415	74.0	106	19 W71241	Light chain variab
40	415	74.0	107	21 Y70604	Vkappa region of h
41	415	74.0	127	15 R50187	Light chain variab
42	415	74.0	127	20 Y26980	Light chain variab
43	415	74.0	240	19 W71243	scFv comprising he
44	415	74.0	245	21 Y70605	scFv fragment of h
45	414	73.8	127	15 R50192	Light chain variab

ALIGNMENTS

RESULT 1

ID W76004 standard; Protein; 107 AA.

AC W76004;

DT 02-NOV-1998 (first entry)

DE LM609 antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX OS

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; W76004.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX
 PS Claim 46; Fig 2b; 129pp; English.

XX
 CC This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 561; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.6e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQKSHSPRLLIKYSQSIGIPS 60
 Db 1 divltqspatlsvtpgdsvslscqasqisnhlhwqkshesprllikyrsgisgips 60

QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107

Db 61 rfgsgsgtdfalsinsvtedfgmyfcqsgswphtfgggtkleik 107

RESULT 2

Y06380
 ID Y06380 standard; Protein; 109 AA.

XX
 AC Y06380;

XX
 DT 06-SEP-1999 (first entry)

DE Murine monoclonal antibody LM609 V lambda.

XX
 DE Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX
 OS Mus musculus.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..2 /note= "vector-encoded residues"
 FT Region 24..34 /note= "CDR1"
 FT Region 50..56 /note= "CDR2"
 FT Region 89..97 /note= "CDR3"

XX
 PN W09929888-A1.

XX
 PD 17-JUN-1999.

XX
 PF 04-DEC-1998; 98WO-0525828.

XX
 PR 05-DEC-1997; 97US-0986016.

XX
 PA (SCRI) SCRIPPS RES INST.

XX
 PI Barbas CF, Rader C;

XX
 XN WPI; 1999-394979/33.

XX
 PT Production of humanized mouse monoclonal antibodies

XX
 PS Disclosure; Page 49-50; 55pp; English.

XX
 CC This sequence represents the light chain V lambda region of
 CC murine monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX
 SQ Sequence 109 AA;

Query Match 94.5%; Score 530; DB 20; Length 109;
 Best Local Similarity 92.5%; Pred. No. 8.1e-34;
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQKSHSPRLLIKYSQSIGIPS 60
 Db 1 elvmqtatlsvtpgdsvslscqasqisnhlhwqkshesprllikyrsgisgips 60

QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107

Db 61 rfgsgsgtdfalsinsvtedfgmyfcqsgswphtfgggtkleik 107

RESULT 3

R54093
 ID R54093 standard; Protein; 127 AA.

XX
 AC R54093;

XX
 DT 29-DEC-1994 (first entry)

XX
 DE Sequence of mouse V-kappa showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.

XX
 KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;
 KW complementarity determining region.

XX
 OS Mus musculus.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..20 /label= leader
 FT Region 21..43 /label= FR1
 FT Region 44..54 /label= CDR1
 FT Region 55..70 /label= FR2
 FT Region 71..76 /label= CDR2
 FT Region 77..108 /label= FR3
 FT Region 109..117 /label= CDR3
 FT Region 118..127 /label= FR4

XX
 PN W09412661-A.

XX
 PD 09-JUN-1994.

XX

DR WPI; 1994-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 XX
 PS Example 1; Fig 3A; 230pp; English.
 CC The present sequence is that of the light chain variable (LC VR) region
 CC of murine antibody 3Hm. This sequence was aligned with 11 other known
 CC antibody LC VRs and a set of framework positions of surface exposed amino
 CC acid residues was determined. This information can be used in a method to
 CC determine how to modify a rodent antibody or fragment by resurfacing in
 CC order to produce a humanised rodent antibody. Residues (determined from
 CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
 CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
 CC combinations of surface residues in the murine sequences were found in
 CC the human sequences and vice versa. However the residues in individual
 CC positions appear to be conserved.
 XX
 SQ Sequence 109 AA;
 Query Match 92.5%; Score 519; DB 15; Length 109;
 Best Local Similarity 92.5%; Pred. No. 5.5e-33;
 Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
 Db 1 divltqspatlsvtpgdsvlsqasqisnlnhwyqkshesprllikyasqisgips 60
 QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
 Db 61 rfssgsggtdfalinsvtedfmgfycqsgswnpytfgggkkleik 107
 RESULT 6
 R15443
 ID R15443 standard; Protein; 240 AA.
 XX
 AC R15443;
 XX
 DT 25-FEB-1992 (first entry)
 DE Single chain Fv from pSCV1 for blocking HRV binding to ICAM-1.
 XX antigen-binding fragment; inflammation; auto-immune disease.
 KW Homo sapiens.
 OS
 XX
 PN EP459577-A.
 XX
 PD 04-DEC-1991.
 XX
 PF 25-MAY-1991; 91EP-0201243.
 XX
 PR 01-JUN-1990; 90US-0532001.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
 XX WPI; 1991-355850/49.
 XX Microbially expressed portions of monoclonal antibody - can block
 PT attachment of rhinovirus ligands to inter-cellular adhesion
 PT molecule (ICAM-1)
 XX
 PS Claim 5; Page 21; 28pp; English.
 CC The Fv fragment encoded by pSCV1 was able to protect cells against
 CC infection by HRV-14. It was less active than modified Fv fragments
 CC which included a Gly-Gly-Gly-Gly-Ser flexible linker between the L

CC and H chains as either a monomer or a dimer.
 CC See also R15437-R15442.
 SQ Sequence 240 AA;
 Query Match 92.5%; Score 519; DB 12; Length 240;
 Best Local Similarity 92.5%; Pred. No. 1.2e-32;
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIVLTQSPATLSVTPGDVSVLSQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
 Db 1 divltqspatlsvtpgdsvlsqasqisnlnhwyqkshesprllikhasqisgips 60
 QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
 Db 61 rfssgsggtdfalinsvtedfmgfycqsgswnpytfgggkkleik 107
 RESULT 7
 R38601
 ID R38601 standard; peptide; 107 AA.
 XX
 AC R38601;
 XX
 DT 28-OCT-1993 (first entry)
 XX
 DE HHV light chain.
 XX
 KW Antibody; variable domain; light; L; heavy; H; consensus;
 KW affinity; antigen; immunogenicity; humanisation; framework.
 OS Homo sapiens.
 XX
 PN WO9311794-A.
 XX
 PD 24-JUN-1993.
 XX
 PF 14-DEC-1992; 92WO-US10906.
 XX
 PR 13-DEC-1991; 91US-0808464.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 XX WPI; 1993-213827/26.
 DR
 XX
 PT Antibodies prepn. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.
 XX
 PS Disclosure; Page 84; 160pp; English.
 XX
 CC The amino acid sequences of the light and heavy chains of the
 CC variable domains from antibodies HHV [HHV-10 Fab-lysosyme complex]
 CC (R38601 and R38608, respectively), MCPC [IgA Fab MCP603-phosphocholine
 CC complex] (R38602-03 and R38609-10, respectively), NEWM [Ig Fab' NEW]
 CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
 CC R38612, respectively) may be used to determine an alignment from which
 CC appropriate changes may be made.
 CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.
 XX
 SQ Sequence 107 AA;
 Query Match 92.0%; Score 516; DB 14; Length 107;
 Best Local Similarity 91.6%; Pred. No. 9.2e-33;

Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0

QY 1 DIVLTQSPTATLSVTPGDSVSLSCQASQISNHLHWYOQKSHSPRLTIKYRSQISGPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 divltqspatlsvtpgnsvslscraqsqignnlhwyyqkshesprllikyvasqsigps 60

QY 61 RFGSGSGTDFALINSINVTEDFGMYFCQQSGSWPHTFGGGTKEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 rfgsgsgtftlinsinvetedfgyfcqqsgsnwpytfgggtkdik 107

RESULT 8
W58482 ID W58482 standard; protein; 107 AA.
XX AC AC AC AC AC AC AC AC AC AC AC AC AC AC AC AC AC AC AC
W58482;
XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX
DT 18-AUG-1998 (first entry)
XX Murine HYH antibody light chain variable domain.
XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
XX OS Mus sp.
PN US5770196-A.
XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX
PD 23-JUN-1998.
PF 07-JUN-1995; 95US-0472788.
XX 23-JUN-1993; 93US-0082842.
PR 13-DEC-1991; 91US-0808464.
PR 14-DEC-1992; 92WO-US10906.
PR 07-JUN-1995; 95US-0472788.
XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX
PA (XOMA) XOMA CORP.
PI Studnicka GM;
DR WPI; 1998-376744/32.
XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX
PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT with humanised variable regions
PS Disclosure; Column 43-44; 77pp; English.
XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX XX
A method has been developed of depleting CD5+ cells in an animal. The method comprises administering a cytotoxic protein containing a modified immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig molecule or an immunoconjugate or fusion protein containing an anti-CD5 Ig molecule, and where the modified Ig variable domain comprises at least one of (a) a modified light chain variable region (see W58478 or W58480), and (b) a modified heavy chain variable region (see W58479 or W58481), where W58478 and W58479 are humanised forms of the H65 light and heavy chain variable domains with low risk amino acid substitutions (i.e. low risk of reducing antigen-binding specificity.) and W58480 and W58481 are humanised forms of the H65 light and heavy chain variable domains with moderate risk amino acid substitutions and are present in humanised H65 antibody he3 (ATCC HB 11206). The method is useful for treating autoimmune diseases, especially systemic lupus erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The present sequence represents the murine HYH antibody light chain variable domain.

Query Match 92.0%; Score 516; DB 19; Length 107;
Best Local Similarity 91.6%; Pred. No. 9.2e-33;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy	1	DIVLTQSPATLSVTPGDVSLSVCASQGISNHLHWYQOKSHESPLLIIKYRSQSIGIPSS	60
Db	1	divltqspatlsvtpgnsavslscrasqignhlhwYgqkshesprllikyasqsiglps	60
Qy	61	RFSGSGSGCTDPAI LSTNSVETDFGMYFCQSGSQSWPHTFGGCTKLEIK	107
Db	61	rfsqsgsgcdftlslnsvetdfgmyfcqsgsqswpytfggckldlk	107
RESULT	9		
ID	W84094		
XX	W84094 standard; Protein; 108 AA.		
XX	W84094;		
XX			
XX			
DT	15-MAR-1999	(first entry)	
XX			
DE	Murine vitronectin alpha-v beta-3 receptor MAB VL region.		
XX			
KW	Humanised antibody; monoclonal antibody; MAB; antibody engineering;		
KW	mouser; vitronectin; alpha-v beta-3; receptor; restenosis;		
KW	cancer; metastasis; rheumatoid arthritis; atherosclerosis;		
KW	angiogenesis; diabetic retinopathy; inflammation;		
KW	macular degeneration; hyperosteoros; Paget's disease;		
KW	hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.		
XX			
OS	Mus sp.		
XX			
XX			
FH	Key	Location/Qualifiers	
FT	Region	24..34	
FT		/label= CDR1	
FT	Region	50..56	
FT		/label= CDR2	
FT	Region	89..97	
FT		/label= CDR3	
XX			
PN	WO9840488-A1.		
XX			
PD	17-SEP-1998.		
XX			
PF	12-MAR-1998;	98WO-US04987.	
XX			
PR	12-MAR-1997;	97US-0039609.	
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
XX			
PI	Johanson KO, Jonak ZL, Taylor AH;		
XX			
DR	WPI; 1999-034590/03.		
XX	N-PSDB; V71798.		
XX			
PT	New anti alpha_v beta_3 vitronectin receptor antibodies - used for		
PT	immunotherapeutic treatment of e.g. diabetic retinopathy,		
PT	inflammatory disorders, atherosclerosis, restenosis, cancers or		
PT	osteoporosis		
XX			
PS	Example 13; Page 59-60; 97pp; English.		
XX			
CC	This is the amino acid sequence of the light chain variable region		
CC	(VL) of the anti-human alpha-v beta-3 vitronectin receptor murine		
CC	monoclonal antibody D12, as deduced from isolated cDNA (see		
CC	W71798). D12 VH (see W84093) and VL show sequence similarity to		
CC	Kabat VH subgroup I (see W84095) and Kabat VK subgroup III (see		
CC	W84096), respectively. Humanised VH (see W84097) and VL (see		
CC	W84098) were constructed by combining the framework regions of the		
CC	human V region consensus sequences with complementarity determining		
CC	regions of D12 (keeping some preferred murine framework residues).		
CC	The humanised antibodies are specifically reactive with the human		
CC	alpha-v beta-3 protein receptor and capable of neutralising the		
CC	receptor. They can be used for passive immunotherapy of a disorder		
CC	mediated by the alpha-v beta-3 receptor, e.g. cardiovascular		
CC	disorders or angiogenic-related disorders, such as angiogenesis		
CC	associated with diabetic retinopathy, atherosclerosis and		

CC restenosis, chronic inflammatory disorders, macular degeneration,
CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC diseases where bone resorption is associated with pathology such as
CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
CC of malignancy, osteolytic lesions produced by bone metastasis, bone
CC loss due to immobilisation or sex hormone deficiency. They can also
CC be used for targeted drug therapy, and for detection and diagnosis.
XX
XX
SQ Sequence 108 AA;

Query Match 89.3%; Score 501; DB 20; Length 108;
Best Local Similarity 88.8%; Pred. No. 1.3e-31;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHESPRLLIKYRSQSISGIPS 60
DB 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHESPRLLIKYRSQSISGIPS 60
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTFGGKLEIK 107
DB 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTFGGKLEIK 107

RESULT 10
W00241
ID W00241 standard; Protein; 108 AA.
XX
AC W00241;

XX 22-NOV-1996 (first entry)
DE EGF receptor chimeric MAb chMint5 VL chain.

XX Mouse-human chimeric antibody; monoclonal antibody; chMint5;
KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
KW immunotoxin; immunocytokine; tumour; cancer.
XX
OS Mus musculus.

XX Key Location/Qualifiers
FH Region 24..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..97
FT /label= CDR3
XX W09627010-A1.
XX
XX 06-SEP-1996.
XX 01-MAR-1996; 96WO-EP00805.
XX 01-MAR-1995; 95IT-OFI0036.
XX
XX (ITU-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;
PI Ferrer Marsal C, Mele A;
XX
XX WPI; 1996-412776/41.
DR N-PSDB; T33446.
XX
XX Murine/human chimeric monoclonal antibody, chMint5 specific for
PT EGF-R - shows a lower immunogenicity when administered to humans
XX
XX Claim 7; Page 18; 28pp; English.

XX The amino acid sequence (W00241) of the light chain variable region
CC (VL) of the epidermal growth factor receptor (EGF-R)-specific mouse-
CC human chimeric antibody chMint5 was deduced from a cDNA clone
CC (T33446) obtd. by PCR amplification of murine Mint5 hybridoma DSM

CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
CC to human C-gamma1 and CK regions. Constructs were expressed in
CC CHO cell transfectants. chMint5 shows lower immunogenicity than
CC Mint5 when administered to humans. It can be used in diagnostic
CC assays or used to produce immunotoxins or immunocytokines useful
CC for tumour therapy.
XX
XX
SQ Sequence 108 AA;

Query Match 88.8%; Score 498; DB 17; Length 108;
Best Local Similarity 90.7%; Pred. No. 2.1e-31;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHESPRLLIKYRSQSISGIPS 60
DB 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHESPRLLIKYRSQSISGIPS 60
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTFGGKLEIK 107
DB 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHFTFGGKLEIK 107

RESULT 11
Y32405
ID Y32405 standard; Protein; 127 AA.
XX
AC Y32405;

XX 13-MAR-2000 (first entry)

XX Mouse anti-verotoxin II antibody VTml-1 light chain variable region.
XX
XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
KW monoclonal antibody; light chain; mouse; humanised antibody;
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW HUS; therapy.
XX
OS Mus musculus.

XX Key Location/Qualifiers
FH Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..127
FT /note= "mature protein"
FT Region 44..54
FT /note= "complementarity determining region 1"
FT Region 70..76
FT /note= "complementarity determining region 2"
FT Region 109..117
FT /note= "complementarity determining region 3"
FT Misc-difference 62
FT /note= "encoded by GAG"

XX W09959629-A1.

XX 25-NOV-1999.

XX 19-MAY-1999; 99WO-US11179.

XX 20-MAY-1998; 98US-0086570.

XX (TEIJ) TEIJIN LTD.
XX (PROT-) PROTEIN DESIGN LABS INC.

XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;

XX WPI; 2000-086580/07.

XX N-PSDB; Y35242.

XX Humanized antibody binding to verotoxin II used for treating Verotoxin
PT producing E. coli -

PS Claim 5; Fig 1b; 59pp; English.

CC This sequence represents the light chain variable region of murine
 CC monoclonal antibody Vm1-1 (MuVtm1-1), an antibody that specifically
 CC binds to the B subunit of verotoxin II (VT2). The invention relates
 CC to humanised antibodies against VT2 that are capable of neutralizing
 CC VT2 and/or VT2 variants. The humanised antibody is a humanized form
 CC of MuVtm1-1 comprising the complementarity determining regions of
 CC MuVtm1-1 and the heavy and light chain variable region frameworks
 CC from the human G4 antibody heavy and light chain frameworks,
 CC provided that at least 1 position selected from L49, H29, H30, H49
 CC and H98 is occupied by the amino acid at the equivalent position of
 CC the MuVtm1-1 antibody heavy or light chain variable region framework.
 CC Such humanized antibodies (see Y52406-07) have an affinity for VT2
 CC that is 3-, 5 or 10-times that of MuVtm1-1. They are used for
 CC treating a patient suffering from, or at risk of, the toxic effects
 CC from VT2 (claimed), especially for treating verotoxin producing
 CC Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome
 CC (HUS).

XX SQ Sequence 127 AA;

Query Match 87.3%; Score 490; DB 21; Length 127;
 Best Local Similarity 87.9%; Pred. No. 1e-30;
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSQASQSTSNHLHWYQOKSHSPRLLIKYSQSTSGIPS 60
 DB 21 dvlvtqspatlsvtpgdsvslscrasqtsinnlhwqkshksprlliksqsgisgips 80
 QY 61 RFGSGSGTDFALNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
 DB 81 rfsgsgsgtdftlsinsvtedfmgycqsgyswplttfgagtkleik 127

RESULT 12
 W89176
 ID W89176 standard; peptide; 109 AA.
 XX AC W89176;
 XX DT 25-MAR-1999 (first entry)
 XX DE Anti-p53 monoclonal antibody 248 variable light chain sequence.
 XX KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
 KW immune response; tumour associated antigen; metastatic cancer.
 OS Mus sp.
 OS Synthetic.
 XX PN W09856416-A1.
 XX PD 17-DEC-1998.
 XX PF 09-JUN-1998; 98WO-IL00266.
 XX PR 09-JUN-1997; 97IL-0121041.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
 PI Wolkowicz R;
 XX DR WPI; 1999-070296/06.
 XX PT Use of a monoclonal antibody to a tumour-associated antigen - to
 PT induce anti-tumour immunity or elicit an increased immune response
 PT to the antigen
 XX XX
 XX Example 3; Fig 3; 47pp; English.

CC The present invention describes the use of an immunogen (A) to induce
 CC anti-tumour immunity; to elicit an increased immune response to tumour
 CC associated antigen (TAA) and/or to induce an immune response to mutant
 CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
 CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
 CC (complementarity determining region) on the heavy or light chain of MAB
 CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
 CC variable (V) region of MAB, in a gene delivery vehicle. The present
 CC sequence represents the variable light chain sequence from anti-p53 MAB
 CC 248. Also described is a method for generating sequence-specific,
 CC anti-DNA antibodies (Ab) by immunising a mammal with a MAB directed to a
 CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
 CC used to treat a wide variety of primary and metastatic cancers,
 CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
 CC to determine critical sequences in animal or plant breeding); to
 CC identify bacteria and other parasites; to determine parentage; in
 CC forensic science; to isolate specific genes for DNA vaccination; in gene
 CC sequencing and cloning; also possibly for activation of selected
 CC therapeutic genes in plants, animals and humans. (A) induce an effective
 CC anti-tumour response without causing harm to the patient. The method
 CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.

XX SQ Sequence 109 AA;

Query Match 86.7%; Score 486.5; DB 20; Length 109;
 Best Local Similarity 89.6%; Pred. No. 1.6e-30;
 Matches 95; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDVSVLSQASQSTSNHLHWYQOKSHSPRLLIKYSQSTSGIPS 60
 DB 2 dvlvtqspatlsvtpgdsvslscrasqtsinnlhwqkshksprllikfasqsgisgips 61
 QY 61 RFGSGSGTDFALNSVETEDFGMYFCQSGSWP-HTTGGGTTKLE 105
 DB 62 rfsgsgsgtdftlsinsvtedfmgycqsgswpvharggggtkle 107

RESULT 13
 W76002
 ID W76002 standard; Protein; 107 AA.
 XX AC W76002;
 XX DT 02-NOV-1998 (first entry)
 XX DE Vitaxin antibody light chain variable region protein fragment.
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX PN W09833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX DR WPI; 1998-437472/37.
 XX DR N-PSDB; V49821.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal.

CC T cell mediated disorder. They can also be used to treat autoimmune
CC diseases, inflammatory diseases, and transplantation.

XX
SQ Sequence 214 AA; Query Match 82.9%; Score 465; DB 20; Length 214;
Best Local Similarity 84.1%; Pred. No. 1.3e-28;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIVLTQSPATLSVTPGDSVLSLCOASQISNHLHWYQOKSHESPRLLIKYRSQISGIPS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 divltqspatlsvtpgdrvsiscrasqsidsylhwyqqkshesprllikyashsisgips 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RFGSGSGTDFALINSVETEDFGMYFCQQSGSWPHTFEGGKLEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 rfsgsgsgsdfllsinsvepedvgiycqhghsfptwtfgggtkleik 107
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Search completed: March 28, 2001, 06:34:23
Job time: 503 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:01 ; Search time 269.55 Seconds
(without alignments)
7.128 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPGDSVS.....CQSGSWPHFTGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgnl_7/ptodata/1/1aa/5A-COMB.pep:*
2: /cgnl_7/ptodata/1/1aa/5B-COMB.pep:*
3: /cgnl_7/ptodata/1/1aa/6-COMB.pep:*
4: /cgnl_7/ptodata/1/1aa/PCPUS-COMB.pep:*
5: /cgnl_7/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	529	94.3	107	1	US-07-634-278-62
2	529	94.3	107	1	US-08-477-728-62
3	529	94.3	107	1	US-08-474-040-62
4	529	94.3	107	1	US-08-487-200-62
5	529	94.3	127	1	US-07-634-278-83
6	529	94.3	127	1	US-08-477-728-83
7	529	94.3	127	1	US-08-474-040-83
8	529	94.3	127	1	US-08-487-200-83
9	526	93.8	127	1	US-08-436-463-4
10	519	92.5	107	1	US-08-436-463-20
11	519	92.5	109	1	US-07-942-245-4
12	516	92.0	107	1	US-08-107-669D-1
13	516	92.0	107	1	US-08-472-788A-1
14	516	92.0	107	2	US-08-477-531B-1
15	516	92.0	107	2	US-08-082-842A-1
16	507	90.4	127	1	US-08-436-463-18
17	494	88.1	108	1	US-08-436-463-19
18	459	81.8	100	2	US-08-737-560A-11
19	453	80.7	103	1	US-08-436-463-21
20	432	77.0	107	1	US-07-634-278-63
21	432	77.0	107	1	US-07-634-278-87
22	432	77.0	107	1	US-08-477-728-63
23	432	77.0	107	1	US-08-477-728-87
24	432	77.0	107	1	US-08-474-040-63
25	432	77.0	107	1	US-08-474-040-87
26	432	77.0	107	1	US-08-487-200-63
27	432	77.0	107	1	US-08-487-200-87
28	426	75.9	107	2	US-08-476-176B-4

29 426 75.9 107 3 US-08-127-721A-4
30 426 75.9 107 3 US-08-485-246A-4
31 418 74.5 107 2 US-08-232-081B-40
32 418 74.5 240 2 US-07-956-399-2
33 415 74.0 106 2 US-08-800-198-4
34 415 74.0 106 3 US-09-296-595-4
35 415 74.0 127 2 US-08-476-176B-6
36 415 74.0 127 3 US-08-127-721A-6
37 415 74.0 127 3 US-08-485-246A-6
38 415 74.0 240 2 US-08-800-198-8
39 415 74.0 240 3 US-09-296-595-8
40 414 73.8 127 2 US-08-476-176B-10
41 414 73.8 127 3 US-08-127-721A-10
42 414 73.8 127 3 US-08-485-246A-10
43 411 73.3 127 2 US-08-476-176B-8
44 411 73.3 127 3 US-08-127-721A-8
45 411 73.3 127 3 US-08-485-246A-8

ALIGNMENTS

RESULT 1
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: 379 Lytton Avenue
; City: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 6e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDVSVLSQASQSIHNLHWYQOKSHSPRLTIKYRSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDVSVLSQASQSIHNLHWYQOKSHSPRLTIKYRSQISGIPS 60
QY 61 RFGSGSGTDFALNSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFGSGSGTDFLTVNGVETEDFGMYFCQSGSWPHTFGGKLEIK 107

RESULT 2
US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 94.3%; Score 529; DB 1; Length 107;

Best Local Similarity 93.5%; Pred. No. 6e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDVSVLSQASQSIHNLHWYQOKSHSPRLTIKYRSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDVSVLSQASQSIHNLHWYQOKSHSPRLTIKYRSQISGIPS 60
QY 61 RFGSGSGTDFALNSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFGSGSGTDFLTVNGVETEDFGMYFCQSGSWPHTFGGKLEIK 107

RESULT 3
US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLEY, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 6e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIISNHLHWYQKSHSPRLLIKYSQISGIPS 60
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Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIISNHLHWYQKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFALSINSETEDEFGMYFCQSGSWPHTFGGKLEIK 107
|||||
Db 61 RFSGSGGTDFALSINSETEDEFGMYFCQSGSWPHTFGGKLEIK 107

RESULT 4
US-08-487-200-62
: Sequence 62, Application US/08487200
: Patent No. 5693762
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,200
: FILING DATE: 7-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/634,278
: FILING DATE: 19-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002610
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 107 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 94.3%; Score 529; DB 1; Length 107;
Best Local Similarity 93.5%; Pred. No. 6e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIISNHLHWYQKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFALSINSETEDEFGMYFCQSGSWPHTFGGKLEIK 107
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Db 61 RFSGSGGTDFALSINSETEDEFGMYFCQSGSWPHTFGGKLEIK 107
RESULT 5
US-07-634-278-83
: Sequence 83, Application US/07634278
: Patent No. 5530101
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/634,278
: FILING DATE: 19-DEC-1990
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002600
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 83:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 127 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-07-634-278-83

Query Match 94.3%; Score 529; DB 1; Length 127;
Best Local Similarity 93.5%; Pred. No. 7.3e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCASQSIISNHLHWYQKSHSPRLLIKYSQISGIPS 60
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Db 21 DIVLTQSPATLSVTPGDSVSLSCASQSIISNHLHWYQKSHSPRLLIKYSQISGIPS 80
QY 61 RFSGSGGTDFALSINSETEDEFGMYFCQSGSWPHTFGGKLEIK 107
|||||
Db 81 RFSGSGGTDFALSINSETEDEFGMYFCQSGSWPHTFGGKLEIK 127

APPLICANT: COBLINCH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-200-83

Query Match 94.3%; Score 529; DB 1; Length 127;
Best Local Similarity 93.5%; Pred. No. 7.3e-44;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSSISNHLHWYQKSHSPRLLIKYSQISGIPS 60
DB 21 DIVLTQSPATLSVTPGDSVSLSCQASQSSISNHLHWYQKSHSPRLLIKYSQISGIPS 80
QY 61 RFSGSGGTDFALSINSVETEDFGMYFCQSGSNPHTFGGKLEIK 107
DB 81 RFSGSGGTDFALSINSVETEDFGMYFCQSGSNPHTFGGKLEIK 127
RESULT 9
US-08-436-463-4
Sequence 4, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-4
Query Match 93.8%; Score 526; DB 1; Length 127;
Best Local Similarity 93.5%; Pred. No. 1.4e-43;
Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSSISNHLHWYQKSHSPRLLIKYSQISGIPS 60
DB 21 DIVLTQSPATLSVTPGDSVSLSCQASQSSISNHLHWYQKSHSPRLLIKYSQISGIPS 80
QY 61 RFSGSGGTDFALSINSVETEDFGMYFCQSGSNPHTFGGKLEIK 107
DB 81 RFSGSGGTDFALSINSVETEDFGMYFCQSGSNPHTFGGKLEIK 127
RESULT 10
US-08-436-463-20
Sequence 20, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-20

Query Match          92.5%; Score 519; DB 1; Length 107;
Best Local Similarity 92.5%; Pred. No. 5.4e-43;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQISGNLNLHWYQKSHSPRLLIKYSQISGIPS 60
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFGSGSGTDFTLINSVETEDFGMYFCQSGNSWPYTFGGGKLEIK 107

RESULT 11
US-07-942-245-4
; Sequence 4, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Lion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-4

Query Match          92.5%; Score 519; DB 1; Length 109;
Best Local Similarity 92.5%; Pred. No. 5.5e-43;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQISGNLNLHWYQKSHSPRLLIKYSQISGIPS 60
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFGSGSGTDFTLINSVETEDFGMYFCQSGNSWPYTFGGGKLEIK 107

RESULT 12
US-08-107-669D-1
; Sequence 1, Application us/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-APR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-1

Query Match          92.0%; Score 516; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 1e-42;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLLIKYSQISGIPS. 60
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQISGNLNLHWYQKSHSPRLLIKYSQISGIPS 60
QY 61 RFGSGSGTDFALSINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
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Db 61 RFSGSGTDFTLINSVETEDFGMYCQSQNSWPYTFGGTKLDIK 107
|||||
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-1

Query Match 92.0%; Score 516; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 1e-42;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLIKYRSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLIKYRSQISGIPS 60
|||||
QY 61 RFSGSGTDFALSINSVETEDFGMYCQSQNSWPYTFGGTKLEIK 107
|||||
Db 61 RFSGSGTDFTLINSVETEDFGMYCQSQNSWPYTFGGTKLDIK 107
|||||
RESULT 14
US-08-477-531B-1
; Sequence 1, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-1

Query Match 92.0%; Score 516; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 1e-42;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLIKYRSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQKSHSPRLIKYRSQISGIPS 60
|||||
QY 61 RFSGSGTDFALSINSVETEDFGMYCQSQNSWPYTFGGTKLEIK 107
|||||
Db 61 RFSGSGTDFTLINSVETEDFGMYCQSQNSWPYTFGGTKLDIK 107
|||||
RESULT 15
US-08-082-842A-1
; Sequence 1, Application US/08082842A
; Patent No. 5869619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:49 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	86.5	94	2 S14580	Ig heavy chain V r
2	41	78.8	97	2 S26890	Ig heavy chain V r
3	40	76.9	113	2 S26468	Ig heavy chain V r
4	40	76.9	117	1 HVMS34	Ig heavy chain pre
5	40	76.9	121	2 D27888	Ig heavy chain V r
6	40	76.9	124	2 C27888	Ig heavy chain V r
7	39	75.0	548	2 S38864	Ig epsilon chain C
8	38	73.1	40	2 S33406	Ig heavy chain V r
9	38	73.1	83	2 C25913	Ig heavy chain V r
10	38	73.1	98	2 S26891	Ig heavy chain V r
11	38	73.1	108	2 PL0248	Ig heavy chain V r
12	38	73.1	108	2 PH1006	Ig heavy chain V r
13	38	73.1	114	1 AVDCGM	Ig heavy chain V r
14	38	73.1	117	1 HVMS84	Ig heavy chain pre
15	38	73.1	117	2 PL0249	Ig heavy chain V r
16	38	73.1	119	2 PL0252	Ig heavy chain V r
17	38	73.1	119	2 F27888	Ig heavy chain V r
18	38	73.1	122	2 E27888	Ig heavy chain V r
19	38	73.1	138	2 S09258	Ig heavy chain V r
20	37	71.2	92	2 S56009	Ig heavy chain var
21	37	71.2	92	2 S56008	Ig heavy chain var
22	37	71.2	97	1 HVMS91	Ig heavy chain var
23	37	71.2	97	2 PH0872	Ig heavy chain V r
24	37	71.2	98	2 S26889	Ig heavy chain V r
25	37	71.2	100	2 D48223	Ig heavy chain V r
26	37	71.2	102	2 S14581	Ig heavy chain V r
27	37	71.2	108	2 PH1648	Ig heavy chain V r
28	37	71.2	108	2 PH1011	Ig heavy chain V r
29	37	71.2	109	2 PH1649	Ig heavy chain V r

30	37	71.2	111	2 PH1659	Ig heavy chain V r
31	37	71.2	111	2 S40090	Ig heavy chain - m
32	37	71.2	111	2 PH1007	Ig heavy chain V r
33	37	71.2	112	2 S26327	Ig heavy chain V r
34	37	71.2	112	2 PH1647	Ig heavy chain V r
35	37	71.2	113	2 S25571	Ig heavy chain V r
36	37	71.2	117	1 H3H026	Ig heavy chain pre
37	37	71.2	117	2 A45953	Ig heavy chain pre
38	37	71.2	117	2 B34964	Ig heavy chain pre
39	37	71.2	117	2 S34012	Ig heavy chain V r
40	37	71.2	118	2 S31121	Ig heavy chain - h
41	37	71.2	119	2 C36005	Ig heavy chain V r
42	37	71.2	119	2 D36005	Ig heavy chain V r
43	37	71.2	119	2 S31107	Ig heavy chain - h
44	37	71.2	119	2 S31108	Ig heavy chain - h
45	37	71.2	120	2 S48798	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S14580
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14580
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyreactive antibodies differ from Ag-induced antibodies in v
A:Reference number: S14484
A:Accession: S14580
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94 <CHE>
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 45; DB 2; Length 94;
Best Local Similarity 90.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
DB 18 GTTFSSYDMS 27

RESULT 2
S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tromlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117.
A:Accession: S26890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 97;
Best Local Similarity 88.9%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| | | | | | | |
DB 26 GTTFSSYDM 34

RESULT 3

S26468

Ig heavy chain V region - mouse

A:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 113;

Best Local Similarity 80.0%; Pred. No. 0.72;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 10

| | | | | | | |

DB 22 GFAFSSYDM 31

RESULT 4

HVMS34

Ig heavy chain precursor V region (345) - mouse

A:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: J070502

R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J070501; MUID:89279149

A:Accession: J070502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 76.9%; Score 40; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.74;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 10

| | | | | | | |

DB 45 GFAFSSYDM 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

A:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 121;

Best Local Similarity 80.0%; Pred. No. 0.77;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 10

| | | | | | | |

DB 26 GFAFSSYDM 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 124;

Best Local Similarity 80.0%; Pred. No. 0.79;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 10

| | | | | | | |

DB 26 GFAFSSYDM 35

RESULT 7

S38864

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of

A:Reference number: S38864

A:Accession: S38864

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:D27397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C:Superfamily: immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length: 548;
 Best Local Similarity 80.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 26 GLTFSSYDMS 35

RESULT 8

S33406
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
 C:Accession: S33406
 R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
 Eur. J. Immunol. 23, 206-211, 1993
 A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes
 A:Reference number: S33391; MUID:93122092
 A:Accession: S33406
 A:Molecule type: mRNA
 A:Residues: 1-40 <KET>
 A:Cross-references: EMBL:X73009
 A:Experimental source: strain BALB/c
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 73.1%; Score 38; DB 2; Length 40;
 Best Local Similarity 80.0%; Pred. No. 0.58;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 26 GTFSSYDMS 35

RESULT 9

C25913
 Ig heavy chain V region (BFL14) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
 C:Accession: C25913
 R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
 A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
 A:Reference number: A94148; MUID:87175692
 A:Accession: C25913
 A:Molecule type: DNA
 A:Residues: 1-83 <LAW>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 73.1%; Score 38; DB 2; Length 83;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 11 GTFSSYDMS 20

RESULT 10

S26891
 Ig heavy chain V region (DP-58) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26891
 R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117
 A:Accession: S26891
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z12358; NID:932935; PTDN:CAA78226.1; PTD:932936
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 98;
 Best Local Similarity 70.0%; Pred. No. 1.5;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 26 GTFSSYDMS 35

RESULT 11

PL0248
 Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0248
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0248
 A:Molecule type: mRNA
 A:Residues: 1-108 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-24/Region: framework 1
 F:9-92/Domain: immunoglobulin homology <IMM>
 F:25-29/Region: complementarity-determining 1
 F:30-43/Region: framework 2
 F:44-60/Region: complementarity-determining 2
 F:61-92/Region: framework 3
 F:93-99/Region: complementarity-determining 3
 F:100-108/Region: framework 4

Query Match 73.1%; Score 38; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 20 GTFSSYDMS 29

RESULT 12

PH1006
 Ig heavy chain V region (clone 202.33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1006
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1006
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <PHL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | / | | | | | |
 DB 21 GTTFSSYDMS 30

RESULT 13
 AVDGM
 Ig heavy chain V region (Gom) - dog (tentative sequence)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 31-Mar-2000
 C:Accession: A02067
 R:Wasserman, R.L.; Capra, J.D.
 Biochemistry 16, 3160-3168, 1977
 A:Title: Primary structure of the variable regions of two canine immunoglobulin heavy chain
 A:Reference number: A90403; MUID:77242268
 A:Accession: A02067
 A:Molecule type: protein
 A:Residues: 1-114 <WAS>
 C:Comment: This chain was isolated from a myeloma protein.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:22-96/Disulfide bonds: #status predicted

Query Match 73.1%; Score 38; DB 1; Length 114;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
 | | | | | | |
 DB 26 GITFSGYDM 34

RESULT 14
 HWS84
 Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: J0505
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: J0501; MUID:89279149
 A:Accession: J0505
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: This sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 73.1%; Score 38; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 DB 45 GTTFSSYDMS 54

RESULT 15

PL0249
 Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0249
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0249
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 73.1%; Score 38; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | |
 DB 26 GTTFSSYDMS 35

Search completed: March 28, 2001, 06:41:49
 Job time: 872 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:41 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	76.9	117	1	HV55_MOUSE
2	38	73.1	114	1	HV01_CANFA
3	38	73.1	117	1	HV54_MOUSE
4	37	71.2	97	1	HV56_MOUSE
5	37	71.2	117	1	HV3C_HUMAN
6	36	69.2	117	1	HV53_MOUSE
7	35	67.3	117	1	HV52_MOUSE
8	35	67.3	117	1	HV59_MOUSE
9	35	67.3	569	1	AMY_STRVL
10	34	65.4	114	1	HV00_MOUSE
11	34	65.4	153	1	RISC_METH
12	34	65.4	153	1	RISC_METH
13	34	65.4	527	1	GUAD_SCHPO
14	34	65.4	641	1	FIB2_PETMA
15	34	65.4	703	1	CDGT_BACS2
16	34	65.4	704	1	CDGT_BACOH
17	33	63.5	115	1	HV3D_HUMAN
18	33	63.5	650	1	RAEL_RAT
19	33	63.5	710	1	CDGT_THETU
20	33	63.5	1024	1	RIP3_MOUSE
21	33	63.5	2211	1	FA5_BOVIN
22	32	61.5	314	1	RHRA_RHME
23	32	61.5	441	1	DNB2_ADEG1
24	32	61.5	444	1	CIAB_STRPN
25	32	61.5	576	1	RICI_RICCO
26	31	59.6	116	1	HV1A_RABIT
27	31	59.6	117	1	HV2B_RABIT
28	31	59.6	120	1	HV3E_HUMAN
29	31	59.6	121	1	HV3J_HUMAN
30	31	59.6	326	1	YQBQ_BACSU
31	31	59.6	391	1	Y534_METJA
32	31	59.6	401	1	ODO2_RICPR
33	31	59.6	409	1	ODO2_FUGRU

ALIGNMENTS

RESULT 1
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE: 89279149
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0502; HVMS34.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 76.9%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2;

QY 1 GTTFSYDMS 10
Db 45 GRAFSSYDMS 54

RESULT 2
HV01_CANFA
ID HV01_CANFA STANDARD; PRT; 114 AA.
AC P01784;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION GOM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

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RN SEQUENCE.
RX MEDLINE; 77242268.
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
  immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A02067; AVDGM.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;

Query Match 73.18; Score 38; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.69;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
DB 26 GTTFSSYDM 34

RESULT 3
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
  the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO504; HVMS91.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTTFSSYAMS 35

RESULT 5
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81101090.
RA Matthyssens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
  heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3H026.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

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AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
  the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO504; HVMS91.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTTFSSYAMS 35

RESULT 5
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81101090.
RA Matthyssens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
  heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3H026.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

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Query Match 71.2%; Score 37; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 Db 45 GTTFSSYAMS 54

RESULT 6
 HV53_MOUSE STANDARD; PRT; 117 AA.
 ID HV53_MOUSE
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Last Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION RF PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-BALB/CJ;
 RX MEDLINE: 89279149.
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0503; HVMSRF.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 69.2%; Score 36; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 Db 45 GTTFSSYMS 54

RESULT 7
 HV52_MOUSE STANDARD; PRT; 117 AA.
 ID HV52_MOUSE
 AC P06327;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 85099340.
 RA Yancopoulos G.D., Alt F.W.;
 RT "Developmentally controlled and tissue-specific expression of
 unrearranged VH gene segments.";
 RL Cell 40:271-281(1985).
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DR EMBL: M13787; AAA38499.1; -.
 DR PIR: A02029; HVMSA1.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 67.3%; Score 35; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 2.8;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 Db 45 GVTFTSYDIN 54

RESULT 8
 HV59_MOUSE STANDARD; PRT; 117 AA.
 ID HV59_MOUSE
 AC P18530;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-BALB/CJ;
 RX MEDLINE: 89279149.
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0507; HVMS39.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 67.3%; Score 35; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| |||:| | |
Db 45 GTTFSSYDMS 54

RESULT 9
AMY_STRVL
ID AMY_STRVL STANDARD; PRT; 569 AA.
AC P22998;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
GLUCANOHYDROLASE).
GN AML.
OS Streptomyces violaceus (Streptomyces venezuelae).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=ATCC 15068;
RX MEDLINE: 89232724.
RA Virolle M.-J., Long C.M., Chang S., Bibb M.J.;
RT "Cloning, characterisation and regulation of an alpha-amylase gene
from Streptomyces venezuelae";
RL Gene 74:321-334(1988).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -!- INDUCTION: BY MALTOSSE, AND REPRESSION BY GLUCOSE.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M25263; AAB36561.1; -
DR PIR: J50101; J50101.
DR HSSP: P00690; 10SE.
DR INTERPRO: IPR000461; -
DR INTERPRO: IPR002044; -
DR PFAM: PF00686; CBD_4; 1.
DR PFAM: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
FT SIGNAL 1 28
FT CHAIN 29 569
FT ACT_SITE 205 205
FT ACT_SITE 209 209
FT ACT_SITE 296 296
SQ SEQUENCE 569 AA; 60637 MW; 14CA5B1D56720043 CRC64;

Query Match 67.3%; Score 35; DB 1; Length 569;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
| |||:| | |
Db 132 GTTFSSYD 139

RESULT 10
HV00_MOUSE
ID HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE 1G HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE: 79195438.
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
specificities. VII. The complete amino acid sequence of the heavy
chain variable region of anti-p-azophenylarsenate antibodies from A/J
mice bearing a cross-reactive idio type.";
RL J. Immunol. 123:279-284(1979).
CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
THE IG G1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
REGION SEQUENCE.
CC PIR: A02022; GIMSAA.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 65.4%; Score 34; DB 1; Length 114;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| ||||:| | |
Db 26 GTTFSSYEL 34

RESULT 11
RISC_METTH
ID RISC_METTH STANDARD; PRT; 153 AA.
AC 026237;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RIBOFLAVIN SYNTHASE (EC 2.5.1.9).
GN RIBO OR MTH134.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE: 98037514.
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -!- CATALYTIC ACTIVITY: 2,6,7-DIMETHYL-8-(1-D-RIBITYL) LUMAZINE -
RIBOFLAVIN + 4-(1-D-RIBITYLAMINO)-5-AMINO-2,6-DIHYDROXYPYRIMIDINE.
CC -!- COFACTOR: FLAVOPROTEIN AND MAGNESIUM (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY EDTA (BY SIMILARITY).
CC -!- PATHWAY: FINAL STEP OF RIBOFLAVIN SYNTHESIS.
CC -!- SUBUNIT: HOMODIGOMER (BY SIMILARITY).
CC -----
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CC -----

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CC -----
 DR EMBL; AE000802; AAB84640.1; -
 DR INTERPRO; IPR002180; -
 DR PRAM; PF00885; DMRL_synthase; 1.
 KW Riboflavin biosynthesis; Transferase; Flavoprotein; Magnesium.
 SQ SEQUENCE 153 AA; 16908 MW; 79DD08CCBABB785 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 153;
 Best Local Similarity 75.0%; Pred. No. 5.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTFSSYDM 9
 |||: |||
 Db 9 TTFARYDM 16

RESULT 12

RISC_METTM STANDARD; PRT; 153 AA.
 AC Q59587;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE RIBOFLAVIN SYNTHASE (EC 2.5.1.9).
 GN RIBC.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 CC Methanobacterium.
 CC [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-42 AND 129-151.
 RA Eberhardt S., Korn S., Lortsch F., Bacher A.;
 RT "Biosynthesis of riboflavin: an unusual riboflavin synthase of
 RT Methanobacterium thermoautotrophicum.";
 RL J. Bacteriol. 179:2938-2943(1997).
 CC -1- FUNCTION: THE RELATIVELY LOW ACTIVITY OF THIS ENZYME SUGGESTED
 CC THAT 6,7-DIMETHYL-8-RIBITYLLUMAZINE MIGHT NOT BE ITS NATURAL
 CC SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: 2,6,7-DIMETHYL-8-(1-D-RIBITYL)UMAZINE -
 CC RIBOFLAVIN + 4-(1-D-RIBITYLAMINO)-5-AMINO-2,6-DIHYDROXYPYRIMIDINE.
 CC -1- COFACTOR: FLAVOPROTEIN AND MAGNESIUM.
 CC -1- ENZYME REGULATION: INHIBITED BY EDTA.
 CC -1- PATHWAY: FINAL STEP OF RIBOFLAVIN SYNTHESIS.
 CC -1- SUBUNIT: HOMODIGLIMER.
 CC -----

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CC EMBL; X94292; CAA63959.1; -
 DR INTERPRO; IPR002180; -
 DR PRAM; PF00885; DMRL_synthase; 1.
 KW Riboflavin biosynthesis; Transferase; Flavoprotein; Magnesium.
 SQ SEQUENCE 153 AA; 16969 MW; CAAE34FDA348F534 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 153;
 Best Local Similarity 75.0%; Pred. No. 5.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTFSSYDM 9
 |||: |||
 Db 9 TTFARYDM 16

RESULT 13

GUAD_SCHPO

ID GUAD_SCHPO STANDARD; PRT; 527 AA.
 AC O14057;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE GUANINE DEAMINASE (EC 3.5.4.3) (GUANASE) (GUANINE AMINASE)
 DE (GUANINE AMINOHYDROLASE) (GAH).
 GN SPCC1672.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 CC Schizosaccharomycetaceae; Schizosaccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE HYDROLYTIC DEAMINATION OF GUANINE,
 CC PRODUCING XANTHINE AND AMMONIA (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GUANINE + H(2)O = XANTHINE + NH(3).
 CC -1- COFACTOR: CONTAINS 1 MOLE OF ZINC PER SUBUNIT (BY SIMILARITY).
 CC -1- PATHWAY: PURINE NUCLEOTIDE CATABOLISM.
 CC -1- SIMILARITY: BELONGS TO THE ATZ/TRZ FAMILY.
 CC -----
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DR EMBL; AL031324; CAA20441.1; -
 DR INTERPRO; IPR002604; -
 DR PRAM; PF01685; ATZ_TRZ; 1.
 KW Hydrolase; Zinc.
 SQ SEQUENCE 527 AA; 58047 MW; 23D9A3F1117601C1 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 527;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTFSSY 7
 |||: |||
 Db 132 GTTFASY 138

RESULT 14

FIB2_PETMA STANDARD; PRT; 641 AA.
 ID FIB2_PETMA
 AC P33573;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIBRINOGEN ALPHA-2 CHAIN PRECURSOR.
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercartia;
 CC Petromyzontiformes; Petromyzontidae; Petromyzon.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE; 92196058.

RA Pan Y., Doolittle R.F.;
 RT "cDNA sequence of a second fibrinogen alpha chain in lamprey: an
 RT archetypal version alignable with full-length beta and gamma
 RT chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2066-2070(1992).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC
 CC -1- SIMILARITY: ITS N-TERMINAL HALF IS HOMOLOGOUS TO THE ALPHA CHAINS,
 CC WHILE ITS C-TERMINAL HALF IS HOMOLOGOUS TO THE C-TERMINI OF THE
 CC BETA AND THE GAMMA CHAINS.
 CC
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M84565; AAA73183.1; -;
 CC EMBL; M84482; AAA49264.1; -;
 CC PIR; S27940; S27940.
 CC HSP; P02671; IZSD.
 CC
 CC INTERPRO; IPR002181; -;
 CC PFAM; PF00147; fibrinogen_C; 1.
 CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 CC Blood coagulation; Plasma; Signal; Repeat.
 CC SIGNAL 1 23 POTENTIAL.
 CC PEPTIDE 24 31 FIBRINOPEPTIDE A (BY SIMILARITY).
 CC CHAIN 32 641 FIBRINOGEN ALPHA-2 CHAIN.
 CC SITE 31 32 CLEAVAGE (BY THROMBIN; RELEASE
 CC FIBRINOPEPTIDE A).
 CC
 CC DOMAIN 293 316 SER-RICH.
 CC DISULFID 45 45 INTERCHAIN (WITH THE ALPHA CHAIN)
 CC (BY SIMILARITY).
 CC DISULFID 54 54 INTERCHAIN (WITH THE BETA CHAIN)
 CC (BY SIMILARITY).
 CC DISULFID 63 63 INTERCHAIN (WITH THE GAMMA CHAIN)
 CC (BY SIMILARITY).
 CC DISULFID 67 67 INTERCHAIN (WITH THE BETA CHAIN)
 CC (BY SIMILARITY).
 CC DISULFID 179 179 INTERCHAIN (WITH THE GAMMA CHAIN)
 CC (BY SIMILARITY).
 CC DISULFID 183 183 INTERCHAIN (WITH THE BETA CHAIN)
 CC (BY SIMILARITY).
 CC DISULFID 404 435 (BY SIMILARITY).
 CC DISULFID 571 584 BY SIMILARITY.
 CC CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 641 AA; 70756 MW; CA991A8DD698BFB5 CRC64;
 CC
 CC Query Match 65.4%; Score 34; DB 1; Length 641;
 CC Best Local Similarity 75.0%; Pred. No. 29;
 CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 GTTFSSYD 8
 CC I I I I I I
 CC Db 553 GMTFTSYD 560
 CC
 CC RESULT 15
 CC CDGT_BACS2
 CC ID CDGT_BACS2 STANDARD; PRT; 703 AA.
 CC AC P31746;
 CC DT 01-JUL-1993 (Rel. 26, Created)
 CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
 CC DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
 CC DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
 CC GN CGT.
 CC OS Bacillus sp. (strain 1-1).

OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RA SEQUENCE FROM N.A., AND SEQUENCE OF 30-52.
 RA Schmid G., Englbrecht A., Schmid D.;
 RT "Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase
 RT gene from the alkalophilic Bacillus 1-1.";
 RL (in) Huber O., Szejtli J. (eds.);
 RL Proceedings of the fourth international symposium on cyclodextrins,
 RL pp.71-76, Kluwer Academic Publishers, Dordrecht and Boston (1988).
 CC -1- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION
 CC OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.
 CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC PIR; S26399; ALBSX1.
 DR HSP; P31797; ICYG.
 DR INTERPRO; IPR000461; -;
 DR INTERPRO; IPR002044; -;
 DR INTERPRO; IPR002909; -;
 DR PFAM; PF00586; CBD_4; 1.
 DR PFAM; PF01833; TIG; 1.
 DR PFAM; PF00128; alpha-amylase; 1.
 KW Transferase; Glycosyltransferase; Calcium; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 703 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
 FT DOMAIN 30 160 A1.
 FT DOMAIN 161 224 B.
 FT DOMAIN 225 428 A2.
 FT DOMAIN 429 516 C.
 FT DOMAIN 517 600 D.
 FT DOMAIN 601 703 E.
 FT DISULFID 68 75 BY SIMILARITY.
 FT ACT_SITE 251 251 BY SIMILARITY.
 FT ACT_SITE 279 279 BY SIMILARITY.
 FT ACT_SITE 350 350 BY SIMILARITY.
 SQ SEQUENCE 703 AA; 78663 MW; 4D973FB21D0D9B0A CRC64;

Query Match 65.4%; Score 34; DB 1; Length 703;
 Best Local Similarity 70.0%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 I I I I I I I
 Db 202 GTDFSSYDMS 211

Search completed: March 28, 2001, 07:29:43
 Job time: 1650 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:27 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_15:*
- 1: sp.archaea:*
 - 2: sp.bacteria:*
 - 3: sp.fungi:*
 - 4: sp.human:*
 - 5: sp.invertebrate:*
 - 6: sp.mammal:*
 - 7: sp.mhc:*
 - 8: sp.organelle:*
 - 9: sp.phage:*
 - 10: sp.plant:*
 - 11: sp.rodent:*
 - 12: sp.virus:*
 - 13: sp.vertebrate:*
 - 14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	73.1	370	Q52474	Q52474 pseudomonas
2	37	71.2	437	Q9RIA4	Q9RIA4 mus musculus
3	36	69.2	118	Q9UL91	Q9UL91 homo sapien
4	35	67.3	95	Q9ULB6	Q9ULB6 homo sapien
5	35	67.3	125	Q9RZR0	Q9RZR0 deinococcus
6	35	67.3	147	Q9Y509	Q9Y509 homo sapien
7	35	67.3	892	P91644	P91644 drosophila
8	35	67.3	894	Q9VKG1	Q9VKG1 drosophila
9	34	65.4	92	Q9MXB2	Q9MXB2 barbus inte
10	34	65.4	113	Q9UL90	Q9UL90 homo sapien
11	34	65.4	191	Q9ZEB4	Q9ZEB4 rickettsia
12	34	65.4	217	Q9IHH6	Q9IHH6 frog adenov
13	34	65.4	314	Q97279	Q97279 plasmodium
14	34	65.4	481	Q9X405	Q9X405 streptococc
15	34	65.4	692	Q30565	Q30565 bacillus br
16	34	65.4	704	Q82984	Q82984 bacillus br
17	34	65.4	725	Q59239	Q59239 bacillus sp
18	34	65.4	855	Q15797	Q15797 p strain dd
19	34	65.4	1892	Q9QY40	Q9QY40 mus musculus

20	34	65.4	2325	10	Q41743	Q41743 zeu mayas (m
21	33	63.5	116	4	Q9UL93	Q9UL93 homo sapien
22	33	63.5	116	4	Q9UL89	Q9UL89 homo sapien
23	33	63.5	157	8	Q9MJR3	Q9MJR3 taenia pisi
24	33	63.5	159	5	Q9N7T2	Q9N7T2 leishmania
25	33	63.5	251	11	Q63800	Q63800 rattus norv
26	33	63.5	292	3	Q05533	Q05533 saccharomyc
27	33	63.5	297	2	Q70010	Q70010 salmonella
28	33	63.5	531	2	Q9RJ14	Q9RJ14 streptomyc
29	33	63.5	708	2	Q9RUA4	Q9RUA4 deinococcus
30	33	63.5	1837	5	Q9VC29	Q9VC29 drosophila
31	32	61.5	118	1	Q9Y9X2	Q9Y9X2 aeropyrum p
32	32	61.5	124	4	Q9UL92	Q9UL92 homo sapien
33	32	61.5	130	2	Q25823	Q25823 helicobacte
34	32	61.5	130	2	Q9ZK01	Q9ZK01 helicobacte
35	32	61.5	147	4	Q9NT38	Q9NT38 homo sapien
36	32	61.5	258	2	Q83768	Q83768 treponema p
37	32	61.5	373	10	Q9LZFO	Q9LZFO arabidopsis
38	32	61.5	377	5	Q9VDL7	Q9VDL7 drosophila
39	32	61.5	464	2	Q66863	Q66863 aquifex ae
40	32	61.5	491	2	P94289	P94289 bacillus ci
41	32	61.5	541	10	Q41174	Q41174 ricinus com
42	32	61.5	558	2	Q9R9W8	Q9R9W8 pseudomonas
43	32	61.5	773	2	Q9PP35	Q9PP35 campylobact
44	32	61.5	820	12	Q89364	Q89364 paramecium
45	32	61.5	1318	5	Q9NE11	Q9NE11 leishmania

ALIGNMENTS

RESULT 1
Q52474
ID Q52474 PRELIMINARY; PRT; 370 AA.
AC Q52474;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE (SPRAIN DC3000).
GN HRPZ.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
OC Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=96025089; PubMed=7579616;
RA Preston G., Huang H.C., He S.Y., Collmer A.;
RT "The HrpZ proteins of Pseudomonas syringae pvs. syringae, glycinea,
RT and tomato are encoded by an operon containing Yersinia ysc homologs
RT and elicit the hypersensitive response in tomato but not soybean.";
RL Mol. Plant Microbe Interact. 8:717-732(1995).
DR EMBL: L41861; AAB00127.1;
SQ SEQUENCE 370 AA; 36584 MW; D22E43784ACDIE51 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 370;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 159 GTTFSSDDM 167
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RESULT 2
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

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DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -
DR HSPF; P01842; 7FAB.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 71.2%; Score 37; DB 11; Length 437;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 25 GTTFSSYAMS 34
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RESULT 3
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Young D.C.;
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 69.2%; Score 36; DB 4; Length 118;
Best Local Similarity 70.0%; Pred. No. 7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTTFSSYSMN 35
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RESULT 4
Q9ULB6 PRELIMINARY; PRT; 95 AA.
ID Q9ULB6
AC Q9ULB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -
DR HSPF; P01772; 2FB4.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 67.3%; Score 35; DB 4; Length 95;
Best Local Similarity 80.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 25 GTTFSSYWS 34
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RESULT 5
Q9RZR0 PRELIMINARY; PRT; 125 AA.
ID Q9RZR0
AC Q9RZR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 13.7 KDA PROTEIN.
GN DRB0060.
OS Deinococcus radiodurans.
OG Plasmid MPI.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome Sequence of the Radioresistant Bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AF001826; AAF12636.1; -
DR TIGR; DRB0060; -
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 125 AA; 13670 MW; 009E5806FAA172A0 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
DB 23 GTTFGRKYD 30
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RESULT 6
Q9Y509 ID Q9Y509 PRELIMINARY: PRT: 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
DR HSP: P01772; 2F84.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 67.3%; Score 35; DB 4; Length 147;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTTFSTYGMS 35
!|||||!

RESULT 7
P91644 ID P91644 PRELIMINARY: PRT: 892 AA.
AC P91644;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE KEK2 PRECURSOR (FRAGMENT).
GN KEK2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN RP SEQUENCE FROM N.A.
RX STRAIN=OREGON;
RA Musacchio M., Perrimon N.;
RA "The Drosophila kekkon genes: novel members of both the leucine-rich
RT repeat and immunoglobulin superfamilies expressed in the CNS.";
RL Dev. Biol. 178:63-76(1996).
DR EMBL: U42768; AAC47405.1; -.
DR FLYBASE: FBgn0015400; kek2.
DR INTERPRO: IPR000483; -.
DR INTERPRO: IPR001611; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
DR PFAM: PF00560; LRR; 5.
DR PFAM: PF01463; LRRT; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 17 POTENTIAL.
FT CHAIN 18 892 KEK2.
SQ SEQUENCE 892 AA; 97294 MW; 61FB07968E9FF880 CRC64;

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Query Match 67.3%; Score 35; DB 5; Length 892;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
DB 349 GTTFSTNYTL 357
|||||!

RESULT 8
Q9VKG1 ID Q9VKG1 PRELIMINARY: PRT: 894 AA.
AC Q9VKG1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE KEK2 PROTEIN.
GN KEK2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake R.G., Champ M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003633; AAF53111.1; -.
DR FLYBASE: FBgn0015400; kek2.
DR INTERPRO: IPR000483; -.
DR INTERPRO: IPR001611; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.

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DR PFAM: PF00560; LRR: 5.
 DR PFAM: PF01463; LRRCT: 1.
 SQ SEQUENCE 894 AA; 97466 MW; 58C04C0931B655B8 CRC64;

Query Match 67.3%; Score 35; DB 5; Length 894;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDM 9
 |||||:
 Db 351 GTTFSSNYTL 359

RESULT 9
 Q9MVB2 PRELIMINARY; PRT; 92 AA.
 AC Q9MVB2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE MHC CLASS I ANTIGEN (FRAGMENT).
 GN BAIN-UA*L08.
 OS Barbus intermedius (Lake tana barbels).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Barbus.
 OX NCBI_TaxID=40831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kruiwijk C.P., Stet R.J.M.;
 RT "Characterization of MHC genes in lake Tana barbus species.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ007892; CAB57336.1; -
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 10632 MW; ED7D11C82CBD35F7 CRC64;

Query Match 65.4%; Score 34; DB 7; Length 92;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
 | : : : :
 Db 29 GADFNFDMS 38

RESULT 10
 Q9UL90 PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RL EMBL: AF035024; AAD56260.1; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; Ig; 1.
 FT NON_TER 1 1

FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.4%; Score 34; DB 4; Length 113;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDM 9
 | : : : :
 Db 26 GTTFSSYGM 34

RESULT 11
 Q9ZEB4 PRELIMINARY; PRT; 191 AA.
 AC Q9ZEB4;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE SCO2 PROTEIN PRECURSOR (SCO2).
 GN RP031.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsieae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HADRID E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
 RL Nature 396:133-140(1998).
 DR EMBL: AJ235270; CAAL4502.1; -
 SQ SEQUENCE 191 AA; 22254 MW; 74B8EAD74CED2698 CRC64;

Query Match 65.4%; Score 34; DB 2; Length 191;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYD 8
 | : : : :
 Db 77 GTTYSLYD 84

RESULT 12
 Q9IIH6 PRELIMINARY; PRT; 217 AA.
 AC Q9IIH6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PVI PROTEIN.
 GN PVI.
 OS frog adenovirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Siadenovirus.
 OX NCBI_TaxID=114102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davison A.J., Wright K.M., Harrach B.;
 RT "Phylogenetic position of an amphibian adenovirus.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF224336; AAF86931.1; -
 SQ SEQUENCE 217 AA; 23529 MW; 9683496440E90087 CRC64;

Query Match 65.4%; Score 34; DB 12; Length 217;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTFSSYDM 9
|||||:
Db 12 TTFSGYDI 19

RESULT 13

O97279 ID O97279 PRELIMINARY; PRT; 314 AA.
AC O97279;
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE PFC0885C PROTEIN.
GN PFC0885C.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Oliver K., Bowman S., Harris D., Lawson D., Quail M., Barrell B.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL034559; CAB39025.1; -;
SQ SEQUENCE 314 AA; 36143 MW; C2ELED6F14ED40F0 CRC64;

Query Match 65.4%; Score 34; DB 5; Length 314;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTFSSYDMS 10
|||||:
Db 70 TTFSSYDMS 78

RESULT 14

Q9X4U5 ID Q9X4U5 PRELIMINARY; PRT; 481 AA.
AC Q9X4U5;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE CPS2A.
GN CPS2A.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10;
RX MEDLINE=99184998; PubMed=10085014;
RA Smith H.E., Damman M., Van der Velde J., Wagenaar F., Wisselink H.J.,
RA Stockhofe-zurwieden N., Smits M.A.;
RT "Identification and characterization of the cps locus of Streptococcus
RT suis serotype 2: the capsule protects against phagocytosis and is an
RT important virulence factor."
RL Infect. Immun. 67:1750-1756(1999).
DR EMBL; AF118389; AAD24447.1; -;
SQ SEQUENCE 481 AA; 53291 MW; DFFE1BF750C56CA8 CRC64;

Query Match 65.4%; Score 34; DB 2; Length 481;
Best Local Similarity 66.7%; Pred. No. 95;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTFSSYDMS 10
|||||:
Db 106 TTFSEYEMS 114

RESULT 15

O30565 ID O30565 PRELIMINARY; PRT; 692 AA.
AC O30565;
DT 01-JAN-1998 (TREMREL. 05, Created)
DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
DT 01-JUN-2000 (TREMREL. 14, Last annotation update)
DE CYCLODEXTRIN GLYCOSYLTRANSFERASE (EC 2.4.1.19) (CYCLOMALTODEXTRIN
DE GLUCANOTRANSFERASE) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (BACILLUS
DE MACERANS AMYLASE) (CYCLODEXTRIN GLUCANOTRANSFERASE).
OS Bacillus brevis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Brevibacillus.
OX NCBI_TaxID=1393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD162;
RA Kim M.H., Sohn C.B., Oh T.K.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: DEGRADATES STARCH TO CYCLODEXTRINS BY FORMATION
CC OF A 1,4-ALPHA-D- GLUCOSIDIC BOND.
DR EMBL; AF011388; AAB65420.1; -;
DR HSP; P31797; 1CYG.
DR INTERPRO; IPR000461; -;
DR INTERPRO; IPR002044; -;
DR INTERPRO; IPR002909; -;
DR PFAM; PF00128; alpha-amylase; 1.
DR PFAM; PF00686; CBD_4; 1.
DR PFAM; PF01833; TIG; 1.
DR PRODOM; PD001568; -; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 692 AA; 77404 MW; 8CF5AD8CB9EFF57E CRC64;

Query Match 65.4%; Score 34; DB 2; Length 692;
Best Local Similarity 70.0%; Pred. No. 14e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
|||||:
Db 193 GTDFSSYEDS 202

Search completed: March 28, 2001, 07:27:30
Job time: 1643 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:31 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: us-09-016-061-48

Perfect score: 52

Sequence: 1 GTTFSSYDMS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT:*
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- 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT:*
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- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	19 W76014	LM609 grafted anti
2	45	86.5	10	19 W76007	LM609 grafted anti
3	45	86.5	117	19 W76001	Vitaxin antibody h
4	42	80.8	117	20 W86137	Protein sequence o
5	42	80.8	123	18 W15536	Anti-TGF beta-1 sc
6	42	80.8	128	19 W54000	Anti-CD4 antibody
7	42	80.8	134	13 R24713	Sequence encoded b
8	42	80.8	466	13 R24812	Sequence encoded b
9	41	78.8	139	18 W21652	Humanised reshaped
10	40	76.9	10	19 W76015	LM609 grafted anti
11	40	76.9	117	19 W76003	LM609 antibody hea
12	40	76.9	117	20 Y06381	Murine monoclonal

13	40	76.9	130	20 Y06379	Murine monoclonal
14	40	76.9	239	14 R34511	Fv(FU25). Homo sa
15	40	76.9	247	16 W1917	Murine MAB SK48-E2
16	39	75.0	10	19 W76016	LM609 grafted anti
17	39	75.0	117	20 W86141	Protein sequence o
18	39	75.0	119	16 W1919	Humanised MAB SK48
19	39	75.0	123	19 W53998	Anti-CD4 antibody
20	38	73.1	10	21 Y73322	Anti-zeta-chain an
21	38	73.1	98	19 W59614	Anti-RSV F protein
22	38	73.1	116	16 R66307	Human immunoglobul
23	38	73.1	116	18 W13529	Anti-melanoma anti
24	38	73.1	118	19 W57591	Chimeric antibody
25	38	73.1	118	19 W57576	Chimeric H chain S
26	38	73.1	118	20 W89636	Human antibody hea
27	38	73.1	118	20 W89627	Mouse humanised an
28	38	73.1	118	21 Y77502	Peptide seq ID No:
29	38	73.1	118	21 Y77512	Peptide seq ID No:
30	38	73.1	119	16 R79876	Anti-EGFR antibody
31	38	73.1	119	16 R79887	Anti-EGFR antibody
32	38	73.1	119	16 R79888	Anti-EGFR antibody
33	38	73.1	121	20 W86122	Protein sequence o
34	38	73.1	122	15 R54301	Anti-HIV gp120 imm
35	38	73.1	122	17 W01259	VH region of HIV n
36	38	73.1	122	20 W78432	Antibody heavy cha
37	38	73.1	122	21 Y95111	Anti-gp120 antibod
38	38	73.1	122	21 Y98220	Anti-gp120 antibod
39	38	73.1	123	18 W08582	Human antibody C4.
40	38	73.1	123	21 Y78325	Anti-zeta-chain an
41	38	73.1	128	16 R69085	Anti-HIV Fab rev16
42	38	73.1	128	16 R69086	Anti-HIV Fab rev20
43	38	73.1	128	18 W08734	Human anti-HIV Fab
44	38	73.1	128	18 W08735	Human anti-HIV Fab
45	38	73.1	137	19 W57603	Chimeric antibody

ALIGNMENTS

RESULT 1

W76014
ID W76014 standard; Protein: 10 AA.

XX W76014;

DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR1 protein fragment #2.

XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer: V-H region; CDR;
KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49851.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 60; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 52; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 1 gttfssydms 10
RESULT 2
W76007
ID W76007 standard; Protein; 10 AA.
XX
XX W76007;
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDRL1 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX N-PSDB; V49844.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 10 AA;
SQ
Query Match 86.5%; Score 45; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 1 gttfssydms 10
RESULT 3
W76001
ID W76001 standard; Protein; 117 AA.
XX
XX W76001;
XX
XX 02-NOV-1998 (first entry)
XX Vitaxin antibody heavy chain variable region protein fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX N-PSDB; V49820.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 1; Fig 1a; 129pp; English.
XX
XX This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC So are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 86.5%; Score 45; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10

Db 26 gftfssydm 35

RESULT 4

ID W86137 standard; Protein; 117 AA.

AC W86137;

DT 03-MAR-1999 (first entry)

DE Protein sequence of de-immunised humanised A33 Vh.

XX Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;

KW Immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.

XX Homo sapiens.

OS

XX WO9852976-A1.

PN

XX 26-NOV-1998.

PD

XX 21-MAY-1998; 98WO-GB01473.

PF

XX 14-APR-1998; 98GB-0007751.

PR 21-MAY-1997; 97GB-0010480.

PR 31-JUL-1997; 97GB-0016197.

PR 28-NOV-1997; 97GB-0025270.

PR 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

PA Carr FJ;

PI WPI; 1998-045301/04.

XX

XX Reducing immunogenicity of proteins - by modifying the amino acid

PT sequence of the protein to eliminate potential epitopes for T-cells

PT of a given species

XX

PS Example 5; Fig 25; 77pp; English.

XX

XX The invention relates to a method for the production of non-immunogenic

CC proteins. The method comprises determining at least part of the amino

CC acid sequence of the protein; (b) identifying in the amino acid sequence

CC one or more potential epitopes for T-cells (T-cell epitopes) of the given

CC species; and (c) modifying the amino acid sequence to eliminate at least

CC one of the T-cell epitopes identified in step (b) thereby to eliminate or

CC reduce the immunogenicity of the protein when exposed to the immune

CC system of the given species. A method of analysing a pre-existing protein

CC to predict the basis for immunogenic responses is also provided. The

CC methods can be used particularly for reducing the immunogenicity of

CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The

CC products can be used for diagnosis and therapy. The present sequence

CC represents the protein sequence of de-immunised humanised A33 Vh.

XX

SQ Sequence 117 AA;

Query Match 80.8%; Score 42; DB 20; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.58;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10

Db 26 gftfssydm 35

RESULT 5

ID W15536 standard; Protein; 123 AA.

XX

AC W15536;

XX

DT 27-NOV-1997 (first entry)

XX

DE Anti-TGF beta-1 scFv antibody 27C1 VH domain.

XX

KW Transforming growth factor beta-1; TGF-beta-1; human;

KW antibody engineering; scFv; phage display; lung fibrosis;

KW arterial injury; proliferative retinopathy; retinal detachment;

KW adult respiratory distress syndrome; liver cirrhosis;

KW post myocardial infarction; post-angioplasty restenosis;

KW scleroderma; vascular disease; cataract; glaucoma; scarring;

KW glomerulonephritis; osteoporosis; immune disease; inflammation;

KW rheumatoid arthritis; macrophage deficiency disease;

KW macrophage pathogen infection; therapy.

XX Homo sapiens.

OS

XX GB2305921-A.

PN

XX 23-APR-1997.

PD

XX 07-OCT-1996; 96GB-0020920.

PF

XX 19-JAN-1996; 96GB-0001081.

PR

XX 06-OCT-1995; 95GB-0020486.

PR

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PA

XX Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;

PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;

PI Wilton AJ;

XX

XX WPI; 1997-215360/20.

DR N-PSDB; T60382.

DR

XX Agent contg. antigen-binding domain of human antibody to

PT transforming growth factor beta 1 or 2 - and nucleic acid encoding

PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,

PT immune and inflammatory disease

XX

PS Claim 16; Fig 1c(i); 184pp; English.

XX

XX This polypeptide sequence comprises the VH domain of human scFv

CC antibody 31G9, which is specific for transforming growth factor

CC (TGF) beta-1. It is encoded by a gene (T60382) obtained from a

CC CDR3 spiking experiment. The antigen-binding domains of human

CC antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be

CC used to counter the adverse effects of TGF beta, such as (i)

CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung

CC fibrosis, arterial injury, proliferative retinopathy, retinal

CC detachment, adult respiratory distress syndrome, liver cirrhosis,

CC post myocardial infarction, post-angioplasty restenosis,

CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural

CC scarring and glomerulonephritis, also (not claimed) osteoporosis,

CC or (ii) immune and inflammatory diseases (e.g. rheumatoid

CC arthritis, macrophage deficiency diseases or macrophage pathogen

CC infection). Nucleic acids encoding human antibody VH and VL can be

CC used for prodn. of recombinant antigen-binding domains. These are

CC highly specific, have low dissociation constants (pref. less than 5

CC nM) and low IC50s for neutralisation.

SQ Sequence 123 AA;

Query Match 80.8%; Score 42; DB 18; Length 123;
Best Local Similarity 88.9%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| | | | | | | |
Db 26 gltfssydm 34

RESULT 6

ID W54000 standard; Protein; 128 AA.

XX AC W54000;

XX DT 29-JUL-1998 (first entry)

DE Anti-CD4 antibody VH3 monkey clone 3-40.

XX KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;

XX KW Old World monkey; constant domain; eczema; immuno-modulated disease;
XX KW rheumatoid arthritis.

OS Primate sp.

FX Key Location/Qualifiers

FT Misc-difference 1..128

FT /note= "Xaa= unspecified amino acid"

PN US5750105-A.

PD 12-MAY-1998.

XX PF 07-JUN-1995; 95US-0476349.

XX PR 10-JUL-1992; 92US-0912292.

XX PR 25-JUL-1991; 91US-0735064.

XX PR 23-MAR-1992; 92US-0856281.

XX PR 05-DEC-1995; 95US-0379072.

XX PR 07-JUN-1995; 95US-0476349.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Hanna N, Newman RA, Raab RW;

XX DR WPI; 1998-296690/26.

XX PT Improved method for antibody treatment - uses an antibody comprising
an Old World monkey variable region and a human constant domain

XX PS Example 1; Fig 9c; 84pp; English.

XX CC This sequence represents the VH3 domain of an anti-CD4 antibody
(Ab). This sequence can be used in the method of the invention for
treating a subject, where the treatment comprises administration of an
Ab. The method comprises the administration of an antibody which has an
Old World monkey (e.g. baboon or macaque) variable region which binds to
an antigen (Ag) (or Ag binding portion), and a human constant domain. The
method is useful for the treatment of eczema and immuno-modulated
diseases and especially rheumatoid arthritis. The recombinant antibodies
used are sufficiently different from native monkey antibodies to allow
human antigens to raise these antibodies, but similar enough to human
antibody so there is no immune response to the antibodies in humans.
XX CC Compared to antibodies used in therapy in prior art, these antibodies do
not induce human anti-antibodies on repeated administration. They also
have longer half-lives and do not have a lack of effector function with
human cells.

XX Sequence 128 AA;

Query Match 80.8%; Score 42; DB 19; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 gltfssydmn 35

RESULT 7

R24713

ID R24713 standard; Protein; 134 AA.

XX AC R24713;

XX DT 28-DEC-1992 (first entry)

XX DE Sequence encoded by the genomic chimeric heavy chain variable region
(VFH) gene.

XX KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;

XX KW antithrombotic agent; myocardial infarction therapy.

XX OS Mus musculus.

XX FX Key Location/Qualifiers

FT Peptide 1..19

FT /label= leader

FT Region 23..49

FT /label= Framework Region (FR) 1

FT Region 50..54

FT /label= Complementarity determining region(CDR)1

FT Region 55..68

FT /label= FR-2

FT Region 69..84

FT /label= CDR-2

FT Region 85..114

FT /label= FR-3

FT Region 115..123

FT /label= CDR-3

FT Region 124..134

FT /label= FR-4

XX EP491351-A.

XX PN 24-JUN-1992.

XX PF 17-DEC-1991; 91EP-0121591.

XX PR 18-DEC-1990; 90JP-0413829.

XX PR 11-NOV-1991; 91JP-0294464.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Iwasa S, Taka H, Watanabe T, Tada H;

XX WPI; 1992-209528/26.

XX DR N-PSDP; Q25666.

XX CC Chimeric monoclonal antibodies - contain anti-human fibrin

XX PT antibody light and heavy chain variable and constant for treating

XX PT thrombotic conditions e.g. myocardial infarction

XX PS Example; Figure 4; 87pp; English.

XX CC PCR primers 5'mVH and 3'mVH were used to produce a VH gene-contg.

XX CC fragment of about 330bp. The fragment was isolated and subcloned in

XX CC pUC119. The fragment was found to be a functional VH structural

XX CC gene, referred to as VFH, comprising a VH gene belonging to the

XX CC subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot

XX CC analysis using the whole RNA of FIB1-11 cells confirmed that VFH

XX CC was the gene expressed in FIB1-11 cells. The sequence is given in

CC *Q25666.

XX Sequence 134 AA;

SQ Query Match 80.8%; Score 42; DB 13; Length 134;

Best Local Similarity 80.0%; Pred. No. 0.66;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10

| | | | |

Db 45 gtfssnydms 54

RESULT 8

R24812 ID R24812 standard; Protein; 466 AA.

XX AC R24812;

XX DT 28-DEC-1992 (first entry)

XX DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373.

XX KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;

XX KW antithrombotic agent; myocardial infarction therapy.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 13..19

FT /label= Leader

FT Region 20..134

FT /label= VH

FT Region 135..232

FT /label= CH1

FT Region 233..247

FT /label= hinge

FT Region 248..357

FT /label= CH2

FT Region 358..464

FT /label= CH3

FT Misc-difference 465

FT /note= "translated stop codon"

XX EP491351-A.

XX PD 24-JUN-1992.

XX PF 17-DEC-1991; 91EP-0121591.

XX PR 18-DEC-1990; 90JP-0413829.

XX PR 11-NOV-1991; 91JP-0294464.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Iwasa S, Taka H, Watanabe T, Tada H;

XX WPI; 1992-209528/26.

XX DR N-PSDB; Q25692.

XX Chimeric monoclonal antibodies - contain anti-human fibrin

PT antibody light and heavy chain variable and constant for treating

PT thrombotic conditions e.g. myocardial infarction

XX Example; Figure 11; 87pp; English.

XX Plasmid pTB1373 contains the whole length of a mouse-human

CC chimeric anti-human fibrin heavy chain cDNA open reading

CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin

CC chimeric Ab-producing transformant FIB1-H01/X63 as a template

CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as

CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH

CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding

CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain

CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader

CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CIH

CC respectively as a primer for first strand cDNA synthesis and the

CC primer combination of 5'CIH and 3'C2H, of 5'LIH and 3'CIH and of

CC 5'SH and 3'LIH respectively as primers for PCR. The amplified gene

CC products were isolated and used to produce plasmids. After

CC confirmation of the cDNA sequence of each plasmid, the cDNA

CC encoding LH, VH, CH1 and CH2CH3 were joined together to give

CC plasmid pTB1373 contg. the whole length chimeric H chain

CC (LH, VH, CH1, CH2CH3), also abbreviated as Igh-FIB,

XX SQ Sequence 466 AA;

Query Match 80.8%; Score 42; DB 13; Length 466;

Best Local Similarity 80.0%; Pred. No. 2.5;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10

| | | | |

Db 45 gtfssnydms 54

RESULT 9

W21652 ID W21652 standard; Protein; 139 AA.

XX AC W21652;

XX DT 03-JAN-1998 (first entry)

XX DE Humanised reshaped MAb 15 heavy chain variable region.

XX KW Humanised antibody; monoclonal antibody; MAb 15; tumour;

XX KW Lung cancer; therapy.

XX OS Chimeric Mus musculus.

XX OS Chimeric Homo sapiens.

XX OS Chimeric synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Protein 20..139

FT /label= Mat_protein

FT Region 20..49

FT /label= Framework-1

FT Region 50..54

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 55..68

FT /label= Framework-2

FT Region 69..85

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 86..117

FT /label= Framework-3

FT Region 118..128

FT /label= CDR3

FT /note= "complementarity determining region 3"

FT Region 129..138

FT /label= Framework-4

XX EP781847-A1.

XX PD 02-JUL-1997.

XX PF 25-OCT-1996; 96EP-0117154.

XX PR 06-NOV-1995; 95EP-0117407.

PA (MERE) MERCK PATENT GMBH.
XX
PI Bendig M, Jones T, Saidana J;
XX
XX WPI: 1997-334904/31.
DR N-PSDB; T72237.
DR
XX
PT Humanised form of murine monoclonal antibody MAB 15 - useful for
PT treating lung cancer
PT
XX
PS Claim 2; Fig 12; 71pp; English.
XX
CC This polypeptide comprises the heavy chain variable region VH
CC of humanised reshaped monoclonal antibody (MAB) 15 comprising
CC complementarity determining regions of murine MAB 15 (DSM ACC2117),
CC and reshaped human 30p1 framework regions. It is expressed by a
CC cDNA clone (see W72237) prepared using PCR mutagenesis methods. A
CC claimed process for preparation of humanised reshaped MAB 15
CC involves: cloning and sequencing murine MAB 15 VL and VH regions
CC (see W21653 and W21654); constructing, expressing and analysing
CC chimeric MAB 15 antibody (see W21655-56); modelling the structure
CC of murine MAB 15 variable regions; designing reshaped human MAB 15
CC variable regions; preparing an oligonucleotide sequence which codes
CC for the constant regions of the light and heavy chain of a human
CC immunoglobulin; and constructing, expressing and analysing the
CC complete reshaped human MAB 15. The humanised MAB can be used for
CC treating tumours, especially lung cancer, and for the manufacture
CC of a drug related to tumours, especially lung cancer.
XX
SQ Sequence 139 AA;
Query Match 78.8%; Score 41; DB 18; Length 139;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db 45 gftfsdydms 54
RESULT 10
W76015 ID W76015 standard; Protein; 10 AA.
AC W76015;
XX
XX 02-NOV-1998 (first entry)
DT LM609 grafted antibody V-H region CDR1 protein fragment #3.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX W09833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI: 1998-437472/37.
DR N-PSDB; V49822.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 43; Fig 2a; 129pp; English.

DR N-PSDB; V49852.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 60; Page 41; 129pp; English.
PS
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;
Query Match 76.9%; Score 40; DB 19; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTFSSYDMS 10
Db 1 gftwssydsms 10
RESULT 11
W76003 ID W76003 standard; Protein; 117 AA.
XX
XX W76003;
AC
XX
XX 02-NOV-1998 (first entry)
DT LM609 antibody heavy chain variable region protein fragment.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
XX W09833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI: 1998-437472/37.
DR N-PSDB; V49822.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX

SQ Sequence 117 AA;

Query Match 76.9%; Score 40; DB 19; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
 I | | | | | | |
 Db 26 gfafssyds 35

RESULT 12
 Y06381
 ID Y06381: standard; Protein; 117 AA.
 XX
 AC Y06381;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Murine monoclonal antibody LM609 VH region.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; Integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 52-53; 55pp; English.
 XX
 CC This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 117 AA;

Query Match 76.9%; Score 40; DB 20; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
 I | | | | | | |
 Db 26 gfafssyds 35

RESULT 13
 Y06379
 ID Y06379: standard; Protein; 130 AA.
 XX
 AC Y06379;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Murine monoclonal antibody LM609 V kappa.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.
 XX
 FH Key
 FT Peptide 1.2
 FT Region /note= "vector-encoded residues"
 FT Region /note= "CDR1"
 FT Region /note= "CDR2"
 FT Region /note= "CDR3"
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 49-50; 55pp; English.
 XX
 CC This sequence represents the light chain V kappa region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 130 AA;

Query Match 76.9%; Score 40; DB 20; Length 130;
 Best Local Similarity 80.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 Db 23 gfafssyds 32

RESULT 14

R34511 ID R34511 standard; Protein; 239 AA.

XX AC

XX R34511;

XX AC

XX DT 20-AUG-1993 (first entry)

XX DE Fv(TU25).

XX KW pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;

XX KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition;

XX KW immunomodulator; immunosuppressant; graft rejection; allergy;

XX KW autoimmune disease; leukemia; cyclosporin.

XX OS Homo sapiens.

XX PN EP539748-A.

XX PD 05-MAY-1993.

XX PF 30-SEP-1992; 92EP-0116746.

XX PR 03-OCT-1991; 91JP-0256335.

XX PA (AJIN) AJINOMOTO KK.

XX PI Hamuro J, Shimamura T, Taki S;

XX DR WPI; 1993-145163/18.

XX DR N-PSDB; Q40463.

XX PT Polypeptide(s) which bind H chain of human IL-2 receptors - for

XX PT treating inflammatory, allergic and auto-immune disorders,

XX PT leukaemias etc.

XX PS Claim 4; Page 19; 27pp; English.

XX CC The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express

XX CC polypeptides consisting only of the V regions were purified and

XX CC sequenced. The polypeptides are capable of binding to the beta

XX CC chain of IL-2 receptor and of inhibiting the binding of IL-2 to the

XX CC receptor. They are useful as immunomodulators and

XX CC immunosuppressants, e.g. to prevent graft rejection or to treat

XX CC inflammatory allergic and autoimmune diseases, or leukemia. Unlike

XX CC cyclosporin etc. they are both effective and safe.

XX SQ Sequence 239 AA;

Query Match 76.9%; Score 40; DB 14; Length 239;

Best Local Similarity 80.0%; Pred. No. 2.9;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

| | | | | | | |

Db 148 gfafssyds 157

RESULT 15

W11917

ID W11917 standard; Protein; 247 AA.

XX W11917;
 AC 24-JUN-1997 (first entry)
 DT Murine MAb SK48-E26 heavy chain.
 DE Interleukin-1 beta; IL-1 beta; recombinant antibody;
 XX KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Sig_peptide
 FT Region 20..49
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 (Claim 10, page 48)"
 FT Region 55..68
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 (Claim 10, page 48)"
 FT Region 86..117
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 118..127
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 (Claim 10, page 48)"
 FT Region 128..138
 FT /label= FR4
 FT /note= "framework region 4"
 FT Region 139..247
 FT /label= Constant_region
 XX WO9501997-A1.
 PN 19-JAN-1995.
 PD 07-JUL-1994; 94WO-US07659.
 XX 09-JUL-1993; 93US-0090534.
 PR 04-MAR-1994; 94US-0206190.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA Gross MS, Hurie MR, Jackson JR, Jonak ZL, Theisen TW;
 XX Young PR;
 PI WPI; 1995-066868/09.
 XX N-PSDB; T51436.
 DR Recombinant and humanised chimeric antibodies against human
 XX interleukin-1-beta - for preventing and treating
 PT interleukin-mediated inflammatory disorders
 XX Claim 5; Page 36-37; 62pp; English.
 XX Amino acid sequences of the heavy chain (W11917) and light chain
 CC (W11918) of anti-human interleukin-1 beta (IL-1 beta) murine
 CC monoclonal antibody (MAb) SK48-E26 were deduced from nucleic acids
 CC (T51436-37) derived from hybridoma SK48-E26. The heavy and light
 CC chains, esp. the complementarity determining region sequences,
 CC can be utilised in novel recombinant chimeric and humanised
 CC antibodies (see also W11919-20) useful for the treatment and

CC Prevention of IL-1 mediated inflammatory disorders.

XX
SQ Sequence 247 AA;

Query Match 76.9%; Score 40; DB 16; Length 247;
Best Local Similarity 80.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | |
Db 45 gfafssydms 54

Search completed: March 28, 2001, 06:34:32
Job time: 512 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:09 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: us-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep:*
 - 2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep:*
 - 3: /cgnl_7/ptodata/1/iaa/6_COMB.pep:*
 - 4: /cgnl_7/ptodata/1/iaa/PTUS_COMB.pep:*
 - 5: /cgnl_7/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	80.8	128	1	US-08-478-039-73
2	42	80.8	128	1	US-08-478-039-73
3	42	80.8	128	1	US-08-476-349A-73
4	42	80.8	128	1	US-08-476-349A-102
5	40	76.9	239	2	US-07-956-399-4
6	40	76.9	247	4	PCT-US94-07659-2
7	39	75.0	119	4	PCT-US94-07659-6
8	39	75.0	123	1	US-08-478-039-71
9	39	75.0	123	1	US-08-478-039-104
10	39	75.0	123	1	US-08-476-349A-71
11	39	75.0	123	1	US-08-476-349A-104
12	38	73.1	98	2	US-08-665-202-31
13	38	73.1	116	3	US-08-545-809A-101
14	38	73.1	116	3	US-08-983-607-36
15	38	73.1	122	1	US-08-276-852-80
16	38	73.1	122	1	US-08-899-575-80
17	38	73.1	122	1	US-08-899-575-80
18	38	73.1	122	4	PCT-US93-08743-80
19	38	73.1	123	2	US-08-665-202-30
20	38	73.1	239	2	US-08-553-497A-18
21	37	71.2	35	2	US-08-765-179B-1
22	37	71.2	98	2	US-08-428-197-48
23	37	71.2	98	4	PCT-US93-10555-48
24	37	71.2	102	2	US-08-273-146-65
25	37	71.2	110	1	US-08-211-202-117
26	37	71.2	113	3	US-08-974-899-6
27	37	71.2	116	2	US-08-428-197-2
28	37	71.2	116	4	PCT-US93-10555-2

Sequence 109, Appl
Sequence 46, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 43, Appl
Sequence 38, Appl
Sequence 51, Appl
Sequence 99, Appl
Sequence 1, Appl

117 3 US-08-545-809A-109
117 3 US-08-983-607-46
118 2 US-08-652-816A-12
118 4 PCT-US93-08435-10
121 1 US-08-339-582-2
122 2 US-07-934-373C-21
122 3 PCT-US93-07832-21
122 4 PCT-US93-08435-12
122 4 PCT-US93-08435-14
122 4 PCT-US93-08435-43
123 2 US-08-428-197-38
123 4 PCT-US93-10555-38
124 3 US-08-983-607-51
125 1 US-08-478-039-99
125 1 US-08-476-349A-99
125 2 US-08-428-197-1

ALIGNMENTS

RESULT 1
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
DB 26 GTTFSSYDMN 35

RESULT 2
US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40

US-08-478-039-102

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
DB 26 GTTFSSYDMN 35

RESULT 3
US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.6;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GTTFSSYDMN 35

RESULT 4

US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:

; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | |
Db 26 GTTFSSYDMN 35

RESULT 5

US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:

; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-4

Query Match 76.9%; Score 40; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | |
Db 148 GFATSSYDMS 157

RESULT 6

PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:

; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5024
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 76.9%; Score 40; DB 4; Length 247;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
DB 45 GFATSSYDMS 54

RESULT 7
PCT-US94-07659-6
Sequence 6, Application PC/TUS9407659
GENERAL INFORMATION:
APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurlle, Mark
APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
TITLE OF INVENTION: Disorders in Man
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corp.
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5024
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 75.0%; Score 39; DB 4; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
DB 26 GTTFSSYDMS 35

RESULT 8
US-08-478-039-71
Sequence 71, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-478-039-71

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| |||:| |:
Db 26 GTTFSTYDMT 35

RESULT 9
US-08-478-039-104
Sequence 104, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #34
US-08-478-039-104

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| |||:| |:
Db 26 GTTFSTYDMT 35

RESULT 10
US-08-476-349A-71
Sequence 71, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:

CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-476-349A-71

Query Match 75.0%; Score 39; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 26 GFTFTYDWT 35

RESULT 11
US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA

; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476.349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34

US-08-476-349A-104

Query Match, 75.0%; Score 39; DB 1; Length 123;

Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 26 GFTFTYDWT 35

RESULT 12
US-08-665-202-31
; Sequence 31, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crèw LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-665-202-31

Query Match 73.1%; Score 38; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 26 GFTFTSYEMN 35

RESULT 13
US-08-545-809A-101
; Sequence 101, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko

```

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-101

Query Match 73.1%; Score 38; DB 3; Length 116;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 45 GTTFNSYDM 53

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
;

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-101

Query Match 73.1%; Score 38; DB 3; Length 116;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 45 GTTFNSYDM 53

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
;

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scfv antibodies obtained from
; LIBRARY: fuses fusion phage construct
; CLONE: V474
; FEATURE:
; NAME/KEY: heavy chain
; US-08-983-607-36

Query Match 73.1%; Score 38; DB 3; Length 116;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYDMS 35

RESULT 15
US-08-276-852-80
; Sequence 80, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
;
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;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCL1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 80:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-276-852-80

Query Match 73.1%; Score 38; DB 1; Length 122;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | : |
Db 23 GTTFSSYEMN 32

Search completed: March 28, 2001, 06:39:09
Job time: 763 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:49 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	82.8	94	2 S14580	Ig heavy chain V r
2	44	75.9	97	2 S26890	Ig heavy chain V r
3	43	74.1	113	2 S26468	Ig heavy chain V r
4	43	74.1	117	1 HWM534	Ig heavy chain pre
5	43	74.1	121	2 D27888	Ig heavy chain V r
6	43	74.1	124	2 C27888	Ig heavy chain V r
7	41	70.7	40	2 S33406	Ig heavy chain V r
8	41	70.7	83	2 C25913	Ig heavy chain V r
9	41	70.7	98	2 S26891	Ig heavy chain V r
10	41	70.7	108	2 PL0248	Ig heavy chain V r
11	41	70.7	108	2 PH1006	Ig heavy chain V r
12	41	70.7	117	1 HWM584	Ig heavy chain pre
13	41	70.7	117	2 PL0249	Ig heavy chain V r
14	41	70.7	117	2 PL0252	Ig heavy chain V r
15	41	70.7	118	2 S38491	Ig heavy chain - h
16	41	70.7	119	2 F27888	Ig heavy chain V r
17	41	70.7	122	2 E27888	Ig heavy chain V r
18	41	70.7	138	2 S09258	Ig heavy chain V r
19	41	70.7	325	2 T25122	hypothetical prote
20	40	69.0	92	2 S56009	Ig heavy chain var
21	40	69.0	92	2 S56008	Ig heavy chain var
22	40	69.0	97	1 HWM591	Ig heavy chain V r
23	40	69.0	97	2 PH0872	Ig heavy chain V r
24	40	69.0	98	2 S26889	Ig heavy chain V r
25	40	69.0	100	2 D48223	Ig heavy chain V r
26	40	69.0	102	2 S14581	Ig heavy chain V r
27	40	69.0	108	2 PH1648	Ig heavy chain V r
28	40	69.0	108	2 PH1011	Ig heavy chain V r
29	40	69.0	109	2 PH1649	Ig heavy chain V r

30	40	69.0	111	2 PH1659	Ig heavy chain V r
31	40	69.0	111	2 S40090	Ig heavy chain - m
32	40	69.0	111	2 PH1007	Ig heavy chain V r
33	40	69.0	112	2 S26327	Ig heavy chain V r
34	40	69.0	112	2 PH1647	Ig heavy chain V r
35	40	69.0	113	2 S25571	Ig heavy chain V r
36	40	69.0	117	1 H3H026	Ig heavy chain pre
37	40	69.0	117	2 A45953	Ig heavy chain pre
38	40	69.0	117	2 B34964	Ig heavy chain pre
39	40	69.0	117	2 S34012	Ig heavy chain V r
40	40	69.0	118	2 S31121	Ig heavy chain - h
41	40	69.0	119	2 C36005	Ig heavy chain V r
42	40	69.0	119	2 D36005	Ig heavy chain V r
43	40	69.0	119	2 S31107	Ig heavy chain - h
44	40	69.0	119	2 S31108	Ig heavy chain - h
45	40	69.0	120	2 S48798	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14580
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-Induced antibodies in v
A:Reference number: S14484
A:Accession: S14580
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94 <CHE>
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 48; DB 2; Length 94;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFTWSSYDMS 10
|||:|||||
DB 18 GFTFSSYDMS 27

RESULT 2

S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117
A:Accession: S26890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 97;
Best Local Similarity 88.9%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 9
 |||:|||||
 Db 26 GFTSSYDM 34

RESULT 3

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 74.1%; Score 43; DB 2; Length 113;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 10

|||:|||||

Db 22 GFAPSSYDM 31

RESULT 4

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: J070502

R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J070501; MUID:89279149

A:Accession: J070502

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: This sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 74.1%; Score 43; DB 1; Length 117;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 10

|||:|||||

Db 45 GFAPSSYDM 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 74.1%; Score 43; DB 2; Length 121;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 10

|||:|||||

Db 26 GFAPSSYDM 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 74.1%; Score 43; DB 2; Length 124;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 10

|||:|||||

Db 26 GFAPSSYDM 35

RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998

C:Accession: S33406

R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes

A:Reference number: S33391; MUID:93122092

A:Accession: S33406

A:Molecule type: mRNA

A:Residues: 1-40 <KET>

A:Cross-references: EMBL:X73009

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 70.7%; Score 41; DB 2; Length 40;
 Best Local Similarity 80.0%; Pred. No. 0.83;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 |||:||||
 Db 26 GFTFSSYTMS 35

RESULT 8

Ig heavy chain V region (BF114) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
 C:Accession: C25913
 R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
 A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
 A:Reference number: A94148; MUID:87175692
 A:Accession: C25913
 A:Molecule type: DNA
 A:Residues: 1-83 <LAW>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.7%; Score 41; DB 2; Length 83;
 Best Local Similarity 80.0%; Pred. No. 1.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 |||:||||
 Db 11 GFTFSSYCMS 20

RESULT 9

Ig heavy chain V region (DP-58) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26891
 R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26895; MUID:93021117
 A:Accession: S26891
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 C:Cross-references: EMBL:Z12358; PIDN:CAA78228.1; PID:932936
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 98;
 Best Local Similarity 70.0%; Pred. No. 2.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 |||:||||
 Db 26 GFTFSSYEMN 35

RESULT 10

Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0248
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0248
 A:Molecule type: mRNA
 A:Residues: 1-108 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-24/Region: framework 1
 F:9-92/Domain: immunoglobulin homology <IMM>
 F:25-29/Region: complementarity-determining 1
 F:30-43/Region: framework 2
 F:44-60/Region: complementarity-determining 2
 F:61-92/Region: framework 3
 F:93-99/Region: complementarity-determining 3
 F:100-108/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 2.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 |||:||||
 Db 20 GFTFSSYTMS 29

RESULT 11

Ig heavy chain V region (clone 202.33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1006
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
 J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1006

A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 2.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 |||:||||
 Db 21 GFTFSSYCMS 30

RESULT 12

Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0505

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0505

A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: This sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 70.7%; Score 41; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||||
 Db 45 GFTFSSTMS 54

RESULT 13

PL0249
 Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0249
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0249
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||||
 Db 26 GFTFSSTMS 35

RESULT 14

PL0252
 Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0252
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0252
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||||
 Db 26 GFTFSSTMS 35

RESULT 15

S38491
 Ig heavy chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S38491
 R:Warks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
 submitted to the EMBL Data Library, June 1993
 A:Description: Human antibody fragments specific for human blood group antigens from
 A:Reference number: S38488
 A:Accession: S38491
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-118 <WAR>
 A:Cross-references: EMBL:223032; NID:9414029; PIDN:CAA80567.1; PID:9414030
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 118;
 Best Local Similarity 88.9%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 9
 |||:||||||
 Db 26 GFTLSSYDM 34

Search completed: March 28, 2001, 06:41:49
 Job time: 872 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:43 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-50

Perfect score: 58

Sequence: 1 GFTWSSYDMS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	117	1	HV55_MOUSE
2	41	70.7	117	1	HV54_MOUSE
3	40	69.0	97	1	HV56_MOUSE
4	40	69.0	117	1	HV3C_HUMAN
5	39	67.2	117	1	HV53_MOUSE
6	38	65.5	117	1	HV59_MOUSE
7	38	65.5	304	1	NKR7_HUMAN
8	38	65.5	450	1	NMT_CAEEL
9	37	63.8	116	1	HV1A_RABIT
10	37	63.8	117	1	HV2B_RABIT
11	37	63.8	311	1	PLC_STAAR
12	36	62.1	115	1	HV3D_HUMAN
13	36	62.1	367	1	DIAC_RAT
14	36	62.1	385	1	DIAC_HUMAN
15	36	62.1	416	1	NMT1_HUMAN
16	36	62.1	423	1	IDH_BACSU
17	36	62.1	496	1	NMT1_MOUSE
18	36	62.1	503	1	AMPY_RAT
19	36	62.1	508	1	AMPY_MOUSE
20	36	62.1	511	1	AMYS_MOUSE
21	36	62.1	517	1	YB3C_SCHPO
22	36	62.1	565	1	SYG_METTH
23	36	62.1	707	1	TRFL_MOUSE
24	36	62.1	781	1	GCS1_CAEEL
25	35	60.3	117	1	HV52_MOUSE
26	35	60.3	396	1	CBG_RAT
27	35	60.3	434	1	SLS4_BRAOL
28	35	60.3	435	1	SLS2_BRAOA
29	35	60.3	558	1	AMAL_PLACH
30	34	58.6	105	1	ARSR_BACSU
31	34	58.6	114	1	HV00_MOUSE
32	34	58.6	114	1	HV01_CANFA
33	34	58.6	118	1	ABBB_TRIAB

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34      34      58.6      120      1      HV3E_HUMAN      P01766      homo sapien
35      34      58.6      121      1      HV3J_HUMAN      P01771      homo sapien
36      34      58.6      127      1      P044_RAT       P38718      rattus norv
37      34      58.6      193      1      YLBO_BACSU     O34549      bacillus su
38      34      58.6      213      1      COBO_PSEDE     P29930      pseudomonas
39      34      58.6      264      1      STEA_SCHPO     P36622      schizosacch
40      34      58.6      304      1      YQOB_CAEEL     Q09300      caenorhabdl
41      34      58.6      455      1      NKR4_HUMAN     P43630      homo sapien
42      34      58.6      491      1      NMT_CRYNE      P34809      cryptococcu
43      34      58.6      498      1      NMT2_HUMAN     O60551      homo sapien
44      34      58.6      529      1      NMT2_MOUSE     O70311      mus musculu
45      34      58.6      632      1      YA28_SCHPO     Q09699      schizosacch

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ALIGNMENTS

```

*RESULT 1
HV55_MOUSE      STANDARD;      PRT;      117 AA.
ID      HV55_MOUSE
AC      P18526;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALE/CJ;
RX      MEDLINE; 89279149.
RA      Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT      "Early onset of somatic mutation in immunoglobulin VII genes during
RT      the primary immune response.";
RL      J. Exp. Med. 169:2007-2019(1989).
CC      -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR      PIR; JT0502; HVMS34.
DR      INTERPRO; IPR003006;
DR      PFAM; PF00047; ig; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL      1      19
FT      CHAIN      20      117      IG HEAVY CHAIN V REGION 345.
FT      DOMAIN      20      49      FRAMEWORK 1.
FT      DOMAIN      50      54      COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN      55      68      FRAMEWORK 2.
FT      DOMAIN      69      85      COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN      86      117      FRAMEWORK 3.
FT      DISULFID      41      115      BY SIMILARITY.
FT      NON_TER      117      117
SQ      SEQUENCE      117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match      74.1%; Score 43; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.71;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY      1 GFTWSSYDMS 10
      || :|||
Db      45 GFATSSYDMS 54

RESULT 2
HV54_MOUSE      STANDARD;      PRT;      117 AA.
ID      HV54_MOUSE
AC      P18525;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RA MEDLINE: 89279149.
 RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0505; HVMS84.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFD 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 Db 45 GFTFSSYAMS 54
 III:III II

RESULT 3

ID HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 914.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RA MEDLINE: 89279149.
 RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0504; HVMS91.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 97;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 Db 26 GFTFSSYAMS 35
 III:III II

RESULT 4

HV3C_HUMAN

ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 81101090.
 RA Matthyssens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 heavy chain variable region."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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 DR EMBL: J00236; AAA53516.1; -.
 DR EMBL: M35415; AAA58735.1; -.
 DR PIR: A02047; H3H026.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 Db 45 GFTFSSYAMS 54
 III:III II

RESULT 5

ID HV53_MOUSE STANDARD; PRT; 117 AA.
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION RF PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN SEQUENCE FROM N.A.
 RP STRAIN=BALB/CJ;
 RC MEDLINE: 89279149.
 RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0503; HVMSRF.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
 FT DOMAIN 20 49 FRAMEWORK 1.

FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	55	68	FRAMEWORK 2.
FT	DOMAIN	59	85	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	86	117	FRAMEWORK 3.
FT	DISULFID	41	115	BY SIMILARITY.
FT	NON_TER	117	117	
SQ	SEQUENCE	117 AA;	12866 MW;	2CE3295F390F725B CRC64;

Query Match	67.2%	Score 39;	DB 1;	Length 117;
Best Local Similarity	80.0%;	Pred. No. 3.4;		
Matches 8;	Conservative	-1;	Mismatches	1;
			Indels	0;
			Gaps	0;

```
Qy      1 GFTWSSYDMS 10
        |||:||||
Db      45 GFTSSYYMS 54
```

RESULT	6
HV59_MOUSE	
ID	HV59_MOUSE STANDARD; PRT; 117 AA.
AC	P18530;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DE	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
RN	[1]
RP	SEQUENCE FROM N.A.

Query Match	65.5%	Score 38;	DB 1;	Length 117;
Best Local Similarity	70.0%;	Pred. No. 5;		
Matches 7;	Conservative	2;	Mismatches	1;
			Indels	0;
			Gaps	0;

Qy 1 GFTWSSYDMS 10
 |||:|:|
 Db 45 GFTFSNYGMS 54

RESULT	7	
NRK7_HUMAN		
ID	NRK7_HUMAN	STANDARD;
AC	Q14952: O00644;	PRT; 304 AA.
DT	01-NOV-1997 (Rel. 35; Created)	
DT	01-NOV-1997 (Rel. 35; Last sequence update)	
DT	15-JUL-1999 (Rel. 39; Last annotation update)	
DE	MHC CLASS I NK CELL RECEPTOR PRECURSOR (NATURAL KILLER ASSOCIATED	
DE	DE TRANSCRIPT 7) (NKAT7).	
OS	Homo sapiens (Human).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96270004.
RA Doehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOID;
RA Blassoni R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C
CC ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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Query Match	65.5%	Score 38:	DB 1:	Length 304:
Best Local Similarity	85.7%	Pred. No. 13:		
Matches	6:	Conservative	1:	Mismatches
				0: Indels
				0: Caps
				0: 0:

Qy 3 TWSSYDM 9
:|||||
Db 151 SWSSYDM 157

```

RESULT      8
NMT_CAEEL
ID      NMT_CAEEL      STANDARD;      PRT;      450 AA.
AC      P46548;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update) ,
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      PROBABLE GLYCYLEPTIDE N-TETRADECANOYLTRANSFERASE
DE      (PEPTIDE N-MYRISTOYLTRANSFERASE) (MYRISTOYL-COA:PROTEIN N-
DE      MYRISTOYLTRANSFERASE) (NMT).
GN      T1E9.2.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
RN      [1]
RP      SEQUENCE FROM N.A.

```

RC STRAIN-BRISTOL N2;
 RA Du Z.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ADDS MYRISTOYL GROUP TO N-TERMINAL GLYCINE RESIDUE
 CC OF CERTAIN CELLULAR AND VIRAL PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: TETRADECANOYL-COA + GLYCYL-PEPTIDE = COA +
 CC N-TETRADECANOYLGLYCYL-PEPTIDE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U11280; AAA19436.1; .
 DR WORMPEP; T17E9.2; CE01406.
 DR INTERPRO; IPR000903; .
 DR PFAM; PF01233; NMT_1.
 DR PROSITE; PS00975; NMT_1; 1.
 DR PROSITE; PS00976; NMT_2; 1.
 KW Hypothetical protein; Transferase; Acyltransferase.
 SQ SEQUENCE 450 AA; 50889 MW; 5A639808F7DDA38E CRC64;

 Query Match 65.5%; Score 38; DB 1; Length 450;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 || || | | |
 DB 108 GFRWNVNLS 117

 RESULT 9
 HV1A_RABIT
 ID HV1A_RABIT STANDARD; PRT; 116 AA.
 AC P01826;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-AL REGION BS-5.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE OF 1-69.
 RX MEDLINE; 73220191.
 RA Jaton J.-C.; Braun D.G.;
 RT "Amino acid sequence of the N-terminal sixty-nine residues of heavy
 RT chain derived from a homogeneous rabbit antibody."
 RL Biochem. J. 130:539-546(1972).
 RN [2]
 RP SEQUENCE OF 64-116.
 RX MEDLINE; 75183340.
 RA Jaton J.-C.;
 RT "Completion of the analysis of the primary structure of the variable
 RT domain of a homogeneous rabbit antibody to type III pneumococcal
 RT polysaccharide."
 RL Biochem. J. 143:723-732(1974).
 CC -!- MISCELLANEOUS: THIS GAMMA CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE
 CC -!- PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE
 CC RABBIT.
 DR PIR; A02102; GARB15.
 DR INTERPRO; IPR003006; .
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12349 MW; 95C6FAC93C788C42 CRC64;

 Query Match 65.5%; Score 38; DB 1; Length 450;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 || || | | |
 DB 108 GFRWNVNLS 117

 RESULT 9
 HV1A_RABIT
 ID HV1A_RABIT STANDARD; PRT; 116 AA.
 AC P01826;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-AL REGION BS-5.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE OF 1-69.
 RX MEDLINE; 73220191.
 RA Jaton J.-C.; Braun D.G.;
 RT "Amino acid sequence of the N-terminal sixty-nine residues of heavy
 RT chain derived from a homogeneous rabbit antibody."
 RL Biochem. J. 130:539-546(1972).
 RN [2]
 RP SEQUENCE OF 64-116.
 RX MEDLINE; 75183340.
 RA Jaton J.-C.;
 RT "Completion of the analysis of the primary structure of the variable
 RT domain of a homogeneous rabbit antibody to type III pneumococcal
 RT polysaccharide."
 RL Biochem. J. 143:723-732(1974).
 CC -!- MISCELLANEOUS: THIS GAMMA CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE
 CC -!- PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE
 CC RABBIT.
 DR PIR; A02102; GARB15.
 DR INTERPRO; IPR003006; .
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12349 MW; 95C6FAC93C788C42 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 116;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTWSSYDM 9
 || | | | | |
 DB 25 GFSLSYDM 33

RESULT 10
 HV2B_RABIT
 ID HV2B_RABIT STANDARD; PRT; 117 AA.
 AC P01828;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-A2 REGION K-25.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 76039436.
 RA Jaton J.-C.;
 RT "Comparison of the amino acid sequences of the variable domains of
 RT two homogeneous rabbit antibodies to type III pneumococcal
 RT polysaccharide."
 RL Biochem. J. 147:235-247(1975).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
 CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
 DR PIR; A02104; GARB2K.
 DR INTERPRO; IPR003006; .
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT DISULFID 21 91
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12580 MW; 28DD87FDB7AEE9B8 CRC64;

 Query Match 63.8%; Score 37; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 || | | | | |
 DB 25 GFSLSGYDMS 34

RESULT 11
 PLC_STAAU
 ID PLC_STAAU STANDARD; PRT; 311 AA.
 AC P45723;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE 1-PHOSPHATIDYLINOSITOL PHOSPHOTERASE PRECURSOR (EC 3.1.4.10)
 DE (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).
 GN PLC.
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Staphylococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NEWMAN;
 RX MEDLINE; 94041628.
 RA Daugherty S.; Low M.G.;
 RT "Cloning, expression, and mutagenesis of
 RT phosphatidylinositol-specific phospholipase C from Staphylococcus
 RT aureus: a potential staphylococcal virulence factor."
 RL Infect. Immun. 61:5078-5089(1993).

CC -!- FUNCTION: CLEAVES GLYCOSYLPHOSPHATIDYLINOSITOL (GPI) AND
 CC PHOSPHATIDYLINOSITOL (PI) ANCHORS BUT NOT PI PHOSPHATES. POTENTIAL
 CC VIRULENCE FACTOR.
 CC -!- CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL = D-MYO-INOSITOL
 CC 1,2-CYCLIC PHOSPHATE + DIACYLGLYCEROL.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: TO OTHER BACTERIAL PI-PLC.
 CC -!- SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
 CC ESSENTIAL FOR CATALYTIC ACTIVITY.

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CC EMBL; L19298; AAA16442.1; -.
 CC HSP; P14262; 6PTD.
 CC INTERPRO: IPR000909; -.
 CC PFAM; PF00388; PI-PLC-X; 1.
 CC PROSITE; PS00007; PIP2C_X DOMAIN; 1.
 CC Hydrolase; Lipid degradation; Signal; Virulence.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 311 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE.
 CC FT DOMAIN 27 311
 CC FT ACT_SITE 40 40 GENERAL BASE (BY SIMILARITY).
 CC FT ACT_SITE 90 90 GENERAL ACID (BY SIMILARITY).
 CC FT ACT_SITE 90 90
 CC SEQUENCE 311 AA; 3235 MW; CC5A1F830776741F CRC64;

Query Match 63.8%; Score 37; DB 1; Length 311;
 Best Local Similarity 62.5%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSVD 8

Db 293 GYTWPGYD 300

RESULT 12

ID HV3D_HUMAN STANDARD; PRT; 115 AA.
 AC P01765;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG HEAVY CHAIN V-III REGION TIL.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC [1]
 RN MEDLINE; 78005528.
 RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
 RT "Immunoglobulin structure and genetics. Identity between variable
 RT regions of a mu and a gamma2 chain.";
 RL J. Biol. Chem. 252:7192-7199(1977).
 CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
 CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
 CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
 CC IDENTICAL.
 DR PIR; A02048; H3HUTL.
 DR INTERPRO: IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 115 115
 FT SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 115;
 Best Local Similarity 70.0%; Pred. No. 11;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 Db 26 GTFSTYVMS 35

RESULT 13

ID DIAC_RAT STANDARD; PRT; 367 AA.
 AC Q01460;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE DI-N-ACETYLCHITOBIASE PRECURSOR (EC 3.2.1.-).
 GN CTBS OR CTB.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 24-32.
 RC TISSUE=LIVER;
 RX MEDLINE; 92406917.
 RA Fisher K.J., Aronson N.N. Jr.;
 RT "Cloning and expression of the cDNA sequence encoding the lysosomal
 RT glycosidase di-N-acetylchitobiasase.";
 RL J. Biol. Chem. 267:19607-19616(1992).
 CC -!- FUNCTION: INVOLVED IN THE DEGRADATION OF ASPARAGINE-LINKED
 CC GLYCOPROTEINS. HYDROLYSE OF N-ACETYL-BETA-D-GLUCOSAMINE
 CC (1-4)-N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END
 CC OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -!- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.

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CC EMBL; M95768; AAA40924.1; -.
 CC PIR; S27882; S27882.
 CC PIR; C44102; C44102.
 CC INTERPRO: IPR001223; -.
 CC INTERPRO: IPR001579; -.
 CC PFAM; PF00704; Glyco_hydro_18; 1.
 CC PROSITE; PS01095; CHITINASE_18; 1.
 CC Hydrolase; Glycosidase; Signal; Lysosome; Glycoprotein.
 CC FT SIGNAL 1 23
 CC FT CHAIN 24 367 DI-N-ACETYLCHITOBIASE.
 CC FT ACT_SITE 128 128 PROTON DONOR (BY SIMILARITY).
 CC FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 367 AA; 41531 MW; 29AB8BE4FC157C16 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 367;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TWSSYDMS 10

Db 54 TWKSYDWS 61

RESULT 14

ID DIAC_HUMAN STANDARD; PRT; 385 AA.
 ID DIAC_HUMAN

AC 001459;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE DI-N-ACETYLCHITOBIOSE PRECURSOR (EC 3.2.1.-).
 GN CTBS OR CTB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE; 92406917.
 RA Fisher K.J., Aronson N.N. Jr.;
 RT "Cloning and expression of the cDNA sequence encoding the lysosomal
 glycosidase di-N-acetylchitobiase";
 RL J. Biol. Chem. 267:19607-19616(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liu B., Aronson N.N. Jr.;
 RT "Structure of the human gene for lysosomal di-N-acetylchitobiase";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE DEGRADATION OF ASPARAGINE-LINKED
 CC GLYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCOSAMINE
 CC (1-4)-N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END
 CC OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -!- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
 CC
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 CC
 CC EMBL; M95767; AAC35684.1;
 DR EMBL; AF085706; AAC35852.1; JOINED.
 DR EMBL; AF085700; AAC35852.1; JOINED.
 DR EMBL; AF085701; AAC35852.1; JOINED.
 DR EMBL; AF085702; AAC35852.1; JOINED.
 DR EMBL; AF085703; AAC35852.1; JOINED.
 DR EMBL; AF085704; AAC35852.1; JOINED.
 DR EMBL; AF085705; AAC35852.1; JOINED.
 DR PIR; A44102; A44102.
 DR PIR; S27959; S27959.
 DR MIN; 600873; -.
 DR INTERPRO; IPR001579; -.
 DR PROSITE; PS01095; CHITINASE_18; 1.
 KW Hydrolase; Glycosidase; Signal; Lysosome; Glycoprotein.
 FT SIGNAL 1 38
 FT CHAIN 39 385
 FT ACT_SITE 143 143 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 385 AA; 43759 MW; 0A9D14C8B26B52EE CRC64;

 Query Match 62.1%; Score 36; DB 1; Length 385;
 Best Local Similarity 75.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 3 TWSSYDMS 10
 Db 69 TWKSYDWS 76

 RESULT 15
 ID NMT1_HUMAN STANDARD; PRT; 416 AA.

AC P30419;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE 1 (EC 2.3.1.97) (PEPTIDE N-
 DE MYRISTOYLTRANSFERASE 1) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE
 DE 1) (NMT 1).
 GN NMT1 OR NMT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLY-412.
 RX MEDLINE; 92237320.
 RA Duronio R.J., Reed S.I., Gordon J.I.;
 RT "Mutations of human myristoyl-CoA:protein N-myristoyltransferase
 RT cause temperature-sensitive myristic acid autotrophy in Saccharomyces
 RT cerevisiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
 CC -!- FUNCTION: ADDS MYRISTOYL GROUP TO N-TERMINAL GLYCINE RESIDUE
 CC OF CERTAIN CELLULAR AND VIRAL PROTEINS.
 CC -!- CATALYTIC ACTIVITY: TETRADECANOYL-COA + GLYCYL-PEPTIDE - COA +
 CC N-TETRADECANOYLGLYCYL-PEPTIDE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA.
 CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.
 CC
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 CC
 CC EMBL; M86707; -; NOT_ANNOTATED_CDS.
 DR PIR; JC1343; JC1343.
 DR MIN; 160993; -.
 DR INTERPRO; IPR000903; -.
 DR PFAM; PF01233; NMT_1.
 DR PROSITE; PS00975; NMT_1; 1.
 DR PROSITE; PS00976; NMT_2; 1.
 KW Transferase; Acyltransferase.
 FT MUTAGEN 412 412 G->D,K: REDUCED ACTIVITY.
 FT SEQUENCE 416 AA; 48140 MW; CF08D233B6DD9383 CRC64;

 Query Match 62.1%; Score 36; DB 1; Length 416;
 Best Local Similarity 55.6%; Pred. No. 38;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 GFTWSSYDM 9
 Db 75 GFTWDALDL 83

Search completed: March 28, 2001, 07:29:45
 Job time: 1652 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:30 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-50

Perfect score: 58

Sequence: 1 GFTWSSYDMS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

1: sp-archaea:*

2: sp-bacteria:*

3: sp-fungi:*

4: sp-human:*

5: sp-invertebrate:*

6: sp-mammal:*

7: sp-mhc:*

8: sp-organelle:*

9: sp-phage:*

10: sp-plant:*

11: sp-rodent:*

12: sp-virus:*

13: sp-vertebrate:*

14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	70.7	325	5	O02322
2	40	69.0	437	11	O9RLA4
3	39	67.2	118	4	O9UL91
4	39	67.2	511	2	O9PM91
5	38	65.5	95	4	O9ULB6
6	38	65.5	147	4	O9V509
7	38	65.5	228	5	O02109
8	38	65.5	325	5	O23244
9	38	65.5	327	10	O9S260
10	38	65.5	335	10	O64692
11	38	65.5	356	10	O04710
12	38	65.5	2408	5	O22184
13	37	63.8	113	4	O9UL90
14	37	63.8	256	10	O9S7F0
15	37	63.8	286	3	O60065
16	37	63.8	309	5	O9N7W6
17	37	63.8	476	5	O9V935
18	37	63.8	510	10	O9ST51
19	37	63.8	537	3	O42801

20	37	63.8	702	10	O9LNL6
21	37	63.8	889	5	O9NEE9
22	37	63.8	993	5	P91157
23	37	63.8	1156	5	O61137
24	36	62.1	116	4	O9UL93
25	36	62.1	159	10	O9SDR8
26	36	62.1	174	12	O9QRM4
27	36	62.1	232	11	O61297
28	36	62.1	422	2	O9K848
29	36	62.1	425	2	O06893
30	36	62.1	483	1	O9VEL8
31	36	62.1	497	6	O9N177
32	36	62.1	506	5	O9V7P1
33	36	62.1	509	5	O9W3F6
34	36	62.1	577	5	P91823
35	36	62.1	673	4	O43895
36	36	62.1	690	10	O9L1B7
37	36	62.1	876	2	O53576
38	36	62.1	1324	2	O44103
39	36	62.1	1372	5	P91526
40	35	60.3	101	1	O06103
41	35	60.3	263	13	O91622
42	35	60.3	275	10	O9ZUA6
43	35	60.3	282	5	O02335
44	35	60.3	299	4	O9NYW4
45	35	60.3	327	5	O25688

ALIGNMENTS

RESULT 1
O02322 PRELIMINARY; PRT; 325 AA.
AC O02322;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE T22G5.1 PROTEIN.
GN T22G5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Favello A., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 281127; CAB03386.1;
SQ SEQUENCE 325 AA; 36754 MW; EE9D338E16F8AC9F CRC64;

Query Match 70.7%; Score 41; DB 5; Length 325;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

Db 218 GFTWSSYDMS 227
||||| : : : : |

RESULT 2

Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -
DR HSSP; P01842; 7FAB.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 69.0%; Score 40; DB 11; Length 437;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
||||| : : : : |
Db 25 GFTSSYAMS 34

RESULT 3

Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 67.2%; Score 39; DB 4; Length 118;
Best Local Similarity 70.0%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
||||| : : : : |
Db 26 GFTSSYSMN 35

RESULT 4

Q9PM91 PRELIMINARY; PRT; 511 AA.
AC Q9PM91;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PUTATIVE PEPTIDE ABC-TRANSPORT SYSTEM PERIPLASMIC PEPTIDE-BINDING
DE PROTEIN.
DE DE
GN CJ1584C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA Jagels K., Karlyshev A., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139079; CAB73572.1; -
DR INTERPRO; IPR000914; -
DR INTERPRO; IPR002052; -
DR PFAM; PF00496; SBP_bac_5; 2.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 511 AA; 58856 MW; 7139374B316CBBEB CRC64;

Query Match 67.2%; Score 39; DB 2; Length 511;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
||||| : : : : |
Db 501 GFTWNVIEWS 510

RESULT 5

Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -
DR HSSP; P01772; 2FBA.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
FT NON_TER 1 95
SQ SEQUENCE 95 AA; 95

SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 65.5%; Score 38; DB 4; Length 95;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
| | | : | | | | |

DB 25 GFTFSSYMS 34

RESULT 6

QY509 PRELIMINARY; PRT; 147 AA.

AC QY509;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE VH3 PROTEIN (FRAGMENT).

GN VH3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96071149; PubMed=7475288;

RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,

Lichtenstein A.K., Berenson J.R.;

RT "A CD10-positive subset of malignant cells is identified in multiple

myeloma using PCR with patient-specific immunoglobulin gene primers.";

RL Leukemia 9:1948-1953(1995).

DR EMBL; S80860; AAD14339.1; -

DR HSP; P01772; 2FB4.

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; ig; 1.

FT NON_TER 1 1

SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match

Best Local Similarity 70.0%; Score 38; DB 4; Length 147;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
| | | : | | | | |

DB 26 GFTFSSYMS 35

RESULT 7

QY509 PRELIMINARY; PRT; 228 AA.

AC QY509;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE CODED FOR BY C. ELEGANS CDNA IK97B2.3.

GN W08F4.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94150718; PubMed=79063198;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Madsen C., Graves T.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF000266; AAC71167.1; -

SQ SEQUENCE 228 AA; 25615 MW; 2EC0801189EB1985 CRC64;

Query Match

Best Local Similarity 65.5%; Score 38; DB 5; Length 228;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
| | | : | | | | |

DB 24 GLRWKSYDIS 33

RESULT 8

Q23244 PRELIMINARY; PRT; 325 AA.

AC Q23244;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)

DE HYPOTHETICAL 36.5 KDA PROTEIN ZC155.4 IN CHROMOSOME III.

GN ZC155.4.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Miller N.;

RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U00064; AAB52706.1; -

DR WORMPEP; ZC155.4; CE01434.

KW Hypothetical protein.

SQ SEQUENCE 325 AA; 36467 MW; A7285FFA1A97ACFA CRC64;

Query Match

Best Local Similarity 65.5%; Score 38; DB 5; Length 325;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
| | | : | | | | |

DB 218 GFTWRNWSLS 227

RESULT 9

Q9SZ60 PRELIMINARY; PRT; 327 AA.

ID Q9SZ60

AC Q9SZ60;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 35.8 KDA PROTEIN.
 GN F16J13.20 OR AT4G11950.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049638; CAB40936.1; -;
 DR EMBL; AL161533; CAB78238.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 327 AA; 35845 MW; B2BB47DF4A83E635 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 327;
 Best Local Similarity 85.7%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSY 7
 |||||
 Db 107 GFNWSY 113

RESULT 10
 O64692
 ID O64692 PRELIMINARY; PRT; 335 AA.
 AC O64692;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PUTATIVE GA4 PROTEIN.
 GN T31E10.11 OR GA20X3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
 RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
 RA Somerville C.R., Venter J.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99218343; PubMed=10200325;
 RA Thomas S.G., Phillips A.L., Hedden P.;
 RT "Molecular cloning and functional expression of gibberellin 2-
 RT oxidases, multifunctional enzymes involved in gibberellin
 RT deactivation."
 RT Proc. Natl. Acad. Sci. U.S.A. 96:4698-4703(1999).
 DR EMBL; AC004077; AAC26696.1; -;
 DR EMBL; AJ132437; CAB41009.1; -;

DR INTERPRO; IPR002419; -;
 DR PFAM; PF00671; Fe_Asc_Oxidorel; 1.
 SQ SEQUENCE 335 AA; 38216 MW; 181F6EAA1EE1C331 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 335;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FTWSSYDMS 10
 |||||
 Db 302 FTWSQYKLS 310

RESULT 11

O04710
 ID O04710 PRELIMINARY; PRT; 356 AA.
 AC O04710;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ANIONIC PEROXIDASE.
 GN YPR9 OR API.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97433264; PubMed=9288904;
 RA Teichmann T., Guan C., Kristoffersen P., Muster G., Tietz O.,
 RA Palme K.;
 RT "Cloning and biochemical characterization of an anionic peroxidase
 RT from Zea mays."
 RL Eur. J. Biochem. 247:826-832(1997).
 DR EMBL; Y13905; CAA74203.1; -;
 DR HSSP; P00433; 2ATJ.
 DR MENDEL; 14986; Zeama; Ypr9; 14986.
 DR INTERPRO; IPR002016; -;
 DR PFAM; PF00141; peroxidase; 1.
 DR PRINTS; PR00458; PEROXIDASE.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; 1.
 KW Peroxidase.
 SQ SEQUENCE 356 AA; 37774 MW; A392241467C863F0 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 356;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 |::|
 Db 36 GLSWSFYDVS 45

RESULT 12

Q22184
 ID Q22184 PRELIMINARY; PRT; 2408 AA.
 AC Q22184;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE T05A1.4 PROTEIN.
 GN T05A1.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lloyd C.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton A., Dear S., Du Z., Durbin R., Favellio A., Fulton L.,
 RA Gardner A., Green S., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: 268219; CAA92477.1; -;
 DR INTERPRO: IPR001584; -;
 DR INTERPRO: IPR001969; -;
 DR INTERPRO: IPR002106; -;
 DR PFAM: PF00665; rve; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN1.
 DR PROSITE: PS00339; AA_TRNA_LIGASE_II.2; UNKNOWN1.
 SQ SEQUENCE 2408 AA; 269763 MW; 6C9542F1FA80AC09 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 2408;
 Best Local Similarity 62.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8
 Db 1420 GTWDSFD 1427
 I:|:|:|:|

RESULT 13
 Q9UL90
 ID Q9UL90 PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035024; AAD56260.1; -;
 DR INTERPRO: IPR003006; -;
 DR PFAM: PF00047; ig; 1.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 63.8%; Score 37; DB 4; Length 113;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYD 9
 Db 26 GFTFSSYGM 34
 I:|:|:|:|

RESULT 14

Q9S7P0
 ID Q9S7P0 PRELIMINARY; PRT; 256 AA.
 AC Q9S7P0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 EST D15357(C0514) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
 DE Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone-P0711E10.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone-P0705D01.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP000570; BAA85196.1; -;
 DR EMBL: AP000492; BAA84621.1; -;
 SQ SEQUENCE 256 AA; 29068 MW; 6D504E88F5BBB605 CRC64;

Query Match 63.8%; Score 37; DB 10; Length 256;
 Best Local Similarity 85.7%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTWSSYD 8
 Db 116 FKSSYD 122
 I:|:|:|:|

RESULT 15
 O60065
 ID O60065 PRELIMINARY; PRT; 286 AA.
 AC O60065;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE PUTATIVE PEROXISOMAL MEMBRANE PROTEIN C13G1.03C.
 GN SPBC13G1.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 OC Schizosaccharomycetaceae; Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Badcock K.,
 RA Churcher C.M.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: PEROXISOMAL MEMBRANE-ASSOCIATED. OUTER FACE
 (BY SIMILARITY).
 CC EMBL: AL022600; CAA18656.1; -;
 KW Hypothetical protein; Peroxisome; Membrane; Coiled coil.
 FT DOMAIN 107 177
 FT COILED COIL (POTENTIAL).
 SQ SEQUENCE 286 AA; 32813 MW; 26A73B1A935E6D77 CRC64;

Query Match 63.8%; Score 37; DB 3; Length 286;
 Best Local Similarity 55.6%; Pred. No. 52;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYD 9
 Db 81 GFANSAISL 89
 I:|:|:|:|

Search completed: March 28, 2001, 07:27:33
Job time: 1646 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:32 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*
1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19 W76015	LM609 grafted anti
2	48	82.8	10	19 W76007	LM609 grafted anti
3	48	82.8	117	19 W76001	Vitaxin antibody h
4	45	77.6	117	20 W86137	Protein sequence o
5	45	77.6	128	19 W54000	Anti-CD4 antibody
6	45	77.6	134	13 R24713	Sequence encoded b
7	45	77.6	466	13 R24812	Sequence encoded b
8	44	75.9	139	18 W21652	Humanised reshaped
9	43	74.1	117	19 W76003	Humanised antibody
10	43	74.1	117	20 Y06381	LM609 antibody hea
11	43	74.1	130	20 Y06379	Murine monoclonal
12	43	74.1	239	14 R34511	Fv(TU25). Homo sa

13	43	74.1	247	16 W1917	Murine MAB SK48-E2
14	42	72.4	10	19 W76016	LM609 grafted anti
15	42	72.4	117	20 W86141	Protein sequence o
16	42	72.4	119	16 W1919	Humanised MAB SK48
17	42	72.4	123	19 W53998	Anti-CD4 antibody
18	41	70.7	98	19 W59614	Anti-RSV F protein
19	41	70.7	116	16 R6307	Human immunoglobul
20	41	70.7	116	18 W13529	Anti-melanoma anti
21	41	70.7	118	19 W57591	Chimeric antibody
22	41	70.7	118	19 W57576	Chimeric H chain S
23	41	70.7	118	20 W89636	Human antibody hea
24	41	70.7	118	20 W89627	Mouse humanised an
25	41	70.7	118	21 Y77502	Peptide seq ID No:
26	41	70.7	118	21 Y77512	Peptide seq ID No:
27	41	70.7	119	16 R79876	Anti-EGFR antibody
28	41	70.7	119	16 R79887	Anti-EGFR antibody
29	41	70.7	119	16 R79888	Anti-EGFR antibody
30	41	70.7	121	20 W86122	Protein sequence o
31	41	70.7	122	15 R54301	Anti-HIV gp120 imm
32	41	70.7	122	17 W01259	VH region of HIV n
33	41	70.7	122	20 W78432	Antibody heavy cha
34	41	70.7	122	21 Y95111	Anti-gp120 antibod
35	41	70.7	122	21 Y98220	Anti-gp120 antibod
36	41	70.7	123	18 W08582	Human antibody C4.
37	41	70.7	128	16 R69085	Anti-HIV Fab rev16
38	41	70.7	128	16 R69086	Anti-HIV Fab rev20
39	41	70.7	128	18 W08734	Human anti-HIV Fab
40	41	70.7	128	18 W08735	Human anti-HIV Fab
41	41	70.7	137	19 W57603	Chimeric antibody
42	41	70.7	137	19 W57592	Chimeric antibody
43	41	70.7	137	20 W89635	Human antibody hea
44	41	70.7	137	20 W89625	Mouse humanised an
45	41	70.7	137	21 Y77513	Mouse antibody H c

ALIGNMENTS

RESULT 1

W76015
ID W76015 standard; Protein; 10 AA.
XX
AC W76015;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR1 protein fragment #3.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI: 1998-437472/37.
XX
DR N-PSDB; V49852.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 60; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db |||||
1 gftwssyds 10

RESULT 2
W76007
ID W76007 standard; Protein; 10 AA.
XX
AC W76007;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609-grafted antibody V-H region CDRI protein fragment #1.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49844.
XX
CC Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Disclosure; Page 40; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.017;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db |||||
1 gftwssyds 10

RESULT 3
W76001
ID W76001 standard; Protein; 117 AA.
XX
AC W76001;
XX
DT 02-NOV-1998 (first entry)
XX
DE Vitaxin antibody heavy chain variable region protein fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49820.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 1; Fig 1a; 129pp; English.
XX
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 82.8%; Score 48; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.26;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 DB 26 gftfssydm 35

RESULT 4

ID W86137 standard; Protein; 117 AA.

AC W86137;

XX 03-MAR-1999 (first entry)

DE Protein sequence of de-immunised humanised A33 Vh.

XX Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW Immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.

XX Homo sapiens.

OS WO9852976-A1.

PN 26-NOV-1998.

PD 21-MAY-1998; 98WO-GB01473.

PF 14-APR-1998; 98GB-0007751.

PR 21-MAY-1997; 97GB-0010480.

PR 31-JUL-1997; 97GB-0016197.

PR 28-NOV-1997; 97GB-0025270.

PR 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FJ;

XX WPI; 1998-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species

PS Example 5; Fig 25; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.

XX Sequence 117 AA;

Query Match 77.6%; Score 45; DB 20; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.83;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

DB 26 gftfssydm 35

RESULT 5

ID W54000 standard; Protein; 128 AA.

XX W54000;

XX 29-JUL-1998 (first entry)

XX Anti-CD4 antibody VH3 monkey clone 3-40.

XX Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
 KW Old world monkey; constant domain; eczema; immuno-modulated disease;
 KW rheumatoid arthritis.

OS Primate sp.

XX Location/Qualifiers

FT Misc-difference 1..128

FT /note= "xaa= unspecified amino acid"

PN US5750105-A.

XX 12-MAY-1998.

XX 07-JUN-1995; 95US-0476349.

XX 10-JUL-1992; 92US-0912292.

PR 25-JUL-1991; 91US-0735064.

PR 23-MAR-1992; 92US-0856281.

PR 05-DEC-1995; 95US-0379072.

PR 07-JUN-1995; 95US-0476349.

XX (IDEC-) IDEC PHARM CORP.

XX Hanna N, Newman RA, Raab RW;

XX WPI; 1998-296690/26.

XX Improved method for antibody treatment - uses an antibody comprising
 PT an Old World monkey variable region and a human constant domain

PS Example 1; Fig 9c; 84pp; English.

XX This sequence represents the VH3 domain of an anti-CD4 antibody for
 CC (AB). This sequence can be used in the method of the invention for
 CC treating a subject, where the treatment comprises administration of an
 CC Ab. The method comprises the administration of an antibody which has an
 CC Old World monkey (e.g. baboon or macaque) variable region which binds to
 CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
 CC method is useful for the treatment of eczema and immuno-modulated
 CC diseases and especially rheumatoid arthritis. The recombinant antibodies
 CC used are sufficiently different from native monkey antibodies to allow
 CC human antigens to raise these antibodies, but similar enough to human
 CC antibody so there is no immune response to the antibodies in humans.
 CC Compared to antibodies used in therapy in prior art, these antibodies do
 CC not induce human anti-antibodies on repeated administration. They also
 CC have longer half-lives and do not have a lack of effector function with
 CC human cells.

XX Sequence 128 AA;

Query Match 77.6%; Score 45; DB 19; Length 128;

Best Local Similarity 80.0%; Pred. No. 0.92;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||||
 Db 26 gftfssydmn 35

RESULT 6

R24713
 ID R24713 standard; Protein; 134 AA.

XX
 AC R24713;

XX 28-DEC-1992 (first entry)

XX Sequence encoded by the genomic chimeric heavy chain variable region (VFH) gene.

XX Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
 KW antithrombotic agent; myocardial infarction therapy.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= leader

FT Region 23..49

FT /label= Framework Region (FR) 1

FT Region 50..54

FT /label= Complementarity determining region(CDR)1

FT Region 55..68

FT /label= FR-2

FT Region 69..84

FT /label= CDR-2

FT Region 85..114

FT /label= FR-3

FT Region 115..123

FT /label= CDR-3

FT Region 124..134

FT /label= FR-4

XX EP491351-A.

XX 24-JUN-1992.

XX 17-DEC-1991; 91EP-0121591.

XX 18-DEC-1990; 90JP-0413829.

XX 11-NOV-1991; 91JP-0294464.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa S, Taka H, Watanabe T, Tada H;

XX WPI; 1992-209528/26.

XX N-PSDP; Q25666.

XX Chimeric monoclonal antibodies - contain anti-human fibrin

XX antibody light and heavy chain variable and constant for treating

XX thrombotic conditions e.g. myocardial infarction

XX Example; Figure 4; 87pp; English.

XX PCR primers 5'mVH and 3'mVH were used to produce a VH gene-contg.

XX fragment of about 330bp. The fragment was isolated and subcloned in

XX pUC119. The fragment was found to be a functional VH structural

XX gene, referred to as VFH, comprising a VH gene belonging to the

XX subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot

XX analysis using the whole RNA of FIB1-11 cells confirmed that VFH

XX was the gene expressed in FIB1-11 cells. The sequence is given in

XX Q25666.

XX Sequence 134 AA;

Query Match 77.6%; Score 45; DB 13; Length 134;
 Best Local Similarity 80.0%; Pred. No. 0.96;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

Db 45 gftfssydmn 54

RESULT 7

R24812

ID R24812 standard; Protein; 466 AA.

XX

XX R24812;

XX 28-DEC-1992 (first entry)

XX Sequence encoded by the chimeric H chain cDNA contained in pTb1373.

XX Chimeric monoclonal antibody; anti-fibrin antibody; primer;
 KW antithrombotic agent; myocardial infarction therapy.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 13..19

FT /label= Leader

FT Region 20..134

FT /label= VH

FT Region 135..232

FT /label= CH1

FT Region 233..247

FT /label= hinge

FT Region 248..357

FT /label= CH2

FT Region 358..464

FT /label= CH3

FT Misc-difference 465

FT /note= "translated stop codon"

XX EP491351-A.

XX 24-JUN-1992.

XX 17-DEC-1991; 91EP-0121591.

XX 18-DEC-1990; 90JP-0413829.

XX 11-NOV-1991; 91JP-0294464.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa S, Taka H, Watanabe T, Tada H;

XX WPI; 1992-209528/26.

XX N-PSDB; Q25692.

XX Chimeric monoclonal antibodies - contain anti-human fibrin

XX antibody light and heavy chain variable and constant for treating

XX thrombotic conditions e.g. myocardial infarction

XX Example; Figure 11; 87pp; English.

XX Plasmid pTb1373 contains the whole length of a mouse-human

XX chimeric anti-human fibrin heavy chain cDNA open reading

XX frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin

XX chimeric Ab-producing transformant FIB1-H01/X63 as a template

XX to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as

XX a primer for first strand cDNA synthesis and the 5'C2H and 3'EH

XX primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding

XX cDNA was amplified. Similarly a human gamma-1 chain CH1 domain

XX encoding cDNA and an anti-fibrin antibody VH cDNA and a leader

XX peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CH

XX respectively as a primer for first strand cDNA synthesis and the

CC primer combination of 5'CH and 3'C2H, of 5' LH and 3'CH and of
 CC 5' SH and 3' LH respectively as primers for PCR. The amplified gene
 CC products were isolated and used to produce plasmids. After
 CC confirmation of the cDNA sequence of each plasmid, the cDNA
 CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
 CC plasmid pTB1373 contg. the whole length chimeric H chain
 CC (LH, VH, CH1, CH2CH3), also abbreviated as Igh-FIB,
 XX
 SQ Sequence 466 AA;

Query Match 77.68; Score 45; DB 13; Length 466;
 Best Local Similarity 80.0%; Pred. No. 3.8;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFTWSSYDMS 10
 DB 45 gftfsdydms 54
 |||:|:||||

RESULT 8
 ID W21652 standard; Protein; 139 AA.
 AC W21652;
 XX
 XX 03-JAN-1998 (first entry)
 DT
 XX
 DE Humanised reshaped MAB 15 heavy chain variable region.
 XX
 KW Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy.
 XX
 OS Chimeric Mus musculus.
 OS Chimeric Homo sapiens.
 OS Chimeric synthetic.
 XX

Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..139
 FT /label= Mat_protein
 FT Region 20..49
 FT /label= Framework-1
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 55..68
 FT /label= Framework-2
 FT Region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 86..117
 FT /label= Framework-3
 FT Region 118..128
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 129..138
 FT /label= Framework-4
 XX
 XX EP781847-A1.
 XX
 PD 02-JUL-1997.
 XX
 XX 25-OCT-1996; 96EP-0117154.
 XX
 XX 06-NOV-1995; 95EP-0117407.
 XX
 XX (MERE) MERCK PATENT GMBH.
 XX
 XX Bendig M, Jones T, Saldana J;
 XX
 XX WPI; 1997-334904/31.

DR N-PSDB; T72237.
 XX
 PT Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer
 XX
 PS Claim 2; Fig 12; 71pp; English.
 XX
 CC This polypeptide comprises the heavy chain variable region VH
 CC of humanised reshaped monoclonal antibody (MAB) 15 comprising
 CC complementarity determining regions of murine MAB 15 (DSM ACC2117),
 CC and reshaped human 30P1 framework regions. It is expressed by a
 CC cDNA clone (see T72237) prepared using PCR mutagenesis methods. A
 CC claimed process for preparation of humanised reshaped MAB 15
 CC involves: cloning and sequencing murine MAB 15 VL and VH regions
 CC (see W21653 and W21654); constructing, expressing and analysing
 CC chimeric MAB 15 antibody (see W21655-56); modelling the structure
 CC of murine MAB 15 variable regions; designing reshaped human MAB 15
 CC variable regions; preparing an oligonucleotide sequence which codes
 CC for the constant regions of the light and heavy chain of a human
 CC immunoglobulin; and constructing, expressing and analysing the
 CC complete reshaped human MAB 15. The humanised MAB can be used for
 CC treating tumours, especially lung cancer, and for the manufacture
 CC of a drug related to tumours, especially lung cancer.
 XX
 SQ Sequence 139 AA;

Query Match 75.9%; Score 44; DB 18; Length 139;
 Best Local Similarity 80.0%; Pred. No. 1.5;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFTWSSYDMS 10
 DB 45 gftfsdydms 54
 |||:|:||||

RESULT 9
 ID W76003 standard; Protein; 117 AA.
 XX
 AC W76003;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 XX WPI; 1998-437472/37.
 DR N-PSDB; V49822.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 74.1%; Score 43; DB 19; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:|||||
 Db 26 gfaissydms 35

RESULT 10
 Y06381
 ID Y06381 standard; Protein; 117 AA..

XX AC Y06381;
 XX DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

XX W09929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences

CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 74.1%; Score 43; DB 20; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:|||||
 Db 26 gfaissydms 35

RESULT 11
 Y06379
 ID Y06379 standard; Protein; 130 AA..

XX AC Y06379;

XX DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 28..32 /note= "CDR1"

FT Region 47..63 /note= "CDR2"

FT Region 96..103 /note= "CDR3"

XX W09929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V kappa region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 130 AA;

Query Match 74.1%; Score 43; DB 20; Length 130;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
II :|||||
Db 23 gfafssydm 32

RESULT 12

ID R34511 standard; Protein; 239 AA.

XX AC R34511;

DT 20-AUG-1993 (first entry)

XX DE Fv(TU25).

XX KW pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
KW immunomodulator; immunosuppressant; graft rejection; allergy;
KW autoimmune disease; leukemia; cyclosporin.

XX OS Homo sapiens.

XX PN EP539748-A.

XX PD 05-MAY-1993.

XX PF 30-SEP-1992; 92EP-0116746.

XX PR 03-OCT-1991; 91JP-0256335.

XX PA (AJIN) AJINOMOTO KK.

XX PI Hamuro J, Shimamura T, Taki S;

XX DR WPI; 1993-145163/18.

XX DR N-PSDB; Q40463.

XX PT Polypeptide(s) which bind H chain of human IL-2 receptors - for
PT treating inflammatory, allergic and auto-immune disorders,
PT leukaemias etc.

XX PS Claim 4; Page 19; 27pp; English.

XX CC The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
CC polypeptides consisting only of the V regions were purified and
CC sequenced. The polypeptides are capable of binding to the beta
CC chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
CC receptor. They are useful as immunomodulators and
CC immunosuppressants, e.g. to prevent graft rejection or to treat
CC inflammatory allergic and autoimmune diseases, or leukemia. Unlike
CC cyclosporin etc. they are both effective and safe.

XX SQ Sequence 239 AA;

Query Match 74.1%; Score 43; DB 14; Length 239;
Best Local Similarity 80.0%; Pred. No. 3.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
II :|||||
Db 148 gfafssydm 157

RESULT 13

W11917

XX ID W11917 standard; Protein; 247 AA.

XX AC W11917;

XX DT 24-JUN-1997 (first entry)

XX DE Murine MAB SK48-E26 heavy chain.

XX KW Interleukin-1 beta; IL-1 beta; recombinant antibody;
KW humanised antibody; chimeric antibody; antibody engineering;
KW monoclonal antibody; MAB; SK48-E26; inflammation; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..19

XX FT Region /label= Sig_peptide
20..49

XX FT FT /label= FR1

XX FT FT /note= "framework region 1"

XX FT FT /label= CDR1

XX FT FT /note= "complementarity determining region 1
(Claim 10, page 48)"

XX FT FT 55..68

XX FT FT /label= FR2

XX FT FT /note= "framework region 2"

XX FT FT 69..85

XX FT FT /label= CDR2

XX FT FT /note= "complementarity determining region 2
(Claim 10, page 48)"

XX FT FT 86..117

XX FT FT /label= FR3

XX FT FT /note= "framework region 3"

XX FT FT 118..127

XX FT FT /label= CDR3

XX FT FT /note= "complementarity determining region 3
(Claim 10, page 48)"

XX FT FT 128..138

XX FT FT /label= FR4

XX FT FT /note= "framework region 4"

XX FT FT 139..247

XX FT FT /label= Constant_region

XX PN WO9501997-A1.

XX PD 19-JAN-1995.

XX PF 07-JUL-1994; 94WO-US07659.

XX PR 09-JUL-1993; 93US-0090534.

XX PR 04-MAR-1994; 94US-0206190.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Gross MS, Hurler MR, Jackson JR, Jonak ZL, Theisen TW;

XX PI Young PR;

XX DR WPI; 1995-066868/09.

XX DR N-PSDB; T51436.

XX PT Recombinant and humanised chimeric antibodies against human
PT interleukin-1-beta - for preventing and treating
PT interleukin-mediated inflammatory disorders

XX PS Claim 5; Page 36-37; 62pp; English.

XX CC Amino acid sequences of the heavy chain (W11917) and light chain
CC (W11918) of anti-human interleukin-1 beta (IL-1 beta) murine
CC monoclonal antibody (MAB) SK48-E26 were deduced from nucleic acids
CC (T51436-37) derived from hybridoma SK48-E26. The heavy and light
CC chains, esp. the complementarity determining region sequences,

CC can be utilised in novel recombinant chimeric and humanised
 CC antibodies (see also W1919-20) useful for the treatment and
 CC prevention of IL-1 mediated inflammatory disorders.

XX
 SQ Sequence 247 AA;

Query Match 74.1%; Score 43; DB 16; Length 247;
 Best Local Similarity 80.0%; Pred. No. 4.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:|||||
 Db 45 gftfssydds 54

RESULT 14

W76016
 ID W76016 standard; Protein; 10 AA.

XX
 AC W76016;

XX
 DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR1 protein fragment #4.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX PS WPI; 1998-437472/37.

DR N-PSDB; V49853.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 60; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 72.4%; Score 42; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.18;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:|||||
 Db 1 gftfssydds 10

RESULT 15

W86141
 ID W86141 standard; Protein; 117 AA.

XX
 AC W86141;

XX 03-MAR-1999 (first entry)

XX DE Protein sequence of de-immunised murine A33 Vh.

XX KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunogl bulin; therapeutic; streptokinase; murine; de-immunised.

OS Mus sp.

XX WO9852976-A1.

XX PD 26-NOV-1998.

XX PF 21-MAY-1998; 98WO-GB01473.

XX PR 14-APR-1998; 98GB-0007751.

XX PR 21-MAY-1997; 97GB-0010480.

XX PR 31-JUL-1997; 97GB-0016197.

XX PR 28-NOV-1997; 97GB-0025270.

XX PR 02-DEC-1997; 97US-0067235.

XX PA (BIOV-) BIOVATION LTD.

XX PI Carr FJ;

XX DR WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species

XX PS Example 6; Fig 27; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.

XX SQ Sequence 117 AA;

Query Match 72.4%; Score 42; DB 20; Length 117;
 Best Local Similarity 70.0%; Pred. No. 2.7;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:|||||
 Db 26 gftfssydds 35

Search completed: March 28, 2001, 06:34:32
Job time: 512 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:09 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-50

Perfect score: 58

Sequence: 1 GFTWSSVDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgnl_7/prodata/1/1aa/5A_COMB.pep.*

2: /cgnl_7/prodata/1/1aa/5B_COMB.pep.*

3: /cgnl_7/prodata/1/1aa/6_COMB.pep.*

4: /cgnl_7/prodata/1/1aa/PCTUS_COMB.pep.*

5: /cgnl_7/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	77.6	128	1	US-08-478-039-73
2	45	77.6	128	1	US-08-478-039-102
3	45	77.6	128	1	US-08-476-349A-73
4	45	77.6	128	1	US-08-476-349A-102
5	43	74.1	239	2	US-07-956-399-4
6	43	74.1	247	4	PCT-US94-07659-2
7	42	72.4	119	4	PCT-US94-07659-6
8	42	72.4	123	1	US-08-478-039-71
9	42	72.4	123	1	US-08-478-039-104
10	42	72.4	123	1	US-08-476-349A-71
11	42	72.4	123	1	US-08-476-349A-104
12	41	70.7	98	2	US-08-665-202-31
13	41	70.7	116	3	US-08-545-809A-101
14	41	70.7	116	3	US-08-983-607-36
15	41	70.7	122	1	US-08-276-852-80
16	41	70.7	122	1	US-08-899-575-80
17	41	70.7	122	1	US-08-899-575-80
18	41	70.7	122	4	PCT-US95-08743-80
19	41	70.7	123	2	US-08-665-202-30
20	41	70.7	239	2	US-08-553-497A-18
21	40	69.0	35	2	US-08-765-179B-1
22	40	69.0	98	2	US-08-428-197-48
23	40	69.0	98	4	PCT-US93-10555-48
24	40	69.0	102	2	US-08-273-146-65
25	40	69.0	110	1	US-08-211-202-117
26	40	69.0	113	3	US-08-974-899-6
27	40	69.0	116	2	US-08-428-197-2
28	40	69.0	116	4	PCT-US93-10555-2

29 40 69.0 117 3 US-08-545-809A-109 Sequence 109, Appl
30 40 69.0 117 3 US-08-983-607-46 Sequence 46, Appl
31 40 69.0 118 2 US-08-652-816A-12 Sequence 12, Appl
32 40 69.0 118 4 PCT-US93-08435-10 Sequence 10, Appl
33 40 69.0 121 1 US-08-339-582-2 Sequence 2, Appl
34 40 69.0 122 2 US-07-934-373C-21 Sequence 21, Appl
35 40 69.0 122 3 US-08-437-642B-21 Sequence 21, Appl
36 40 69.0 122 4 PCT-US93-07832-21 Sequence 21, Appl
37 40 69.0 122 4 PCT-US93-08435-12 Sequence 12, Appl
38 40 69.0 122 4 PCT-US93-08435-14 Sequence 14, Appl
39 40 69.0 122 4 PCT-US93-08435-43 Sequence 43, Appl
40 40 69.0 123 2 US-08-428-197-38 Sequence 38, Appl
41 40 69.0 123 4 PCT-US93-10555-38 Sequence 38, Appl
42 40 69.0 124 3 US-08-983-607-51 Sequence 51, Appl
43 40 69.0 125 1 US-08-478-039-99 Sequence 99, Appl
44 40 69.0 125 1 US-08-476-349A-99 Sequence 99, Appl
45 40 69.0 125 2 US-08-428-197-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:

ORGANISM: Monkey
POSITION IN GENOME:

CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMN 35

RESULT 2

US-08-478-039-102
Sequence 102, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064

FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:

ORGANISM: Monkey
POSITION IN GENOME:

CHROMOSOME/SEGMENT: #40

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 1.4;

US-08-478-039-102

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMN 35

RESULT 3

US-08-476-349A-73
Sequence 73, Application US/08476349A
Patent No. 5750105

GENERAL INFORMATION:
APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria

STATE: VA
COUNTRY: USA
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064

FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:

ORGANISM: Monkey
POSITION IN GENOME:

CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|||:|||||
Db 26 GFTFSSYDMN 35

RESULT 4
US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match 77.6%; Score 45; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|||:|||||
Db 26 GFTFSSYDMN 35

RESULT 5
US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; NUMBER OF SEQUENCES: 4
; TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5876717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-4

Query Match 74.1%; Score 43; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
||:|||||
Db 148 GFAPSSYDMS 157

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TU59407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 74.1%; Score 43; DB 4; Length 247;
Best Local Similarity .80.0%; Pred. No. 5.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GFTWSSYDMS 10
DB 45 GFAPSSYDMS 54

RESULT 7
PCT-US94-07659-6
Sequence 6, Application PC/TUS9407659
GENERAL INFORMATION:
APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
TITLE OF INVENTION: Disorders in Man
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corp.
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 72.4%; Score 42; DB 4; Length 119;
Best Local Similarity 80.0%; Pred. No. 3.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 26 GFIFSSYDMS 35

RESULT 8
US-08-478-039-71
Sequence 71, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 123 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Monkey
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-478-039-71

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 26 GFTFSTYDMT 35

RESULT 9
US-08-478-039-104
; Sequence 104, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Monkey
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT: #34
US-08-478-039-104

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
DB 26 GFTFSTYDMT 35

RESULT 10
US-08-476-349A-71
; Sequence 71, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:

CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-476-349A-71

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|:|:|:
Db 26 GFTFSTYDMT 35

RESULT 11
US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME: #34
; CHROMOSOME/SEGMENT: #34
US-08-476-349A-104

Query Match 72.4%; Score 42; DB 1; Length 123;

Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|:|:|:
Db 26 GFTFSTYDMT 35

RESULT 12
US-08-665-202-31
; Sequence 31, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schlier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-31

Query Match 70.7%; Score 41; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 4.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|:|:|:
Db 26 GFTFSSYEMN 35

RESULT 13
US-08-545-809A-101
; Sequence 101, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko

;
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200134
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-101

Query Match 70.7%; Score 41; DB 3; Length 116;
Best Local Similarity 77.8%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 9
|||:|:|:|
Db 45 GFTFSNYDM 53

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/08983607
; Patent No. 614070
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998

;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V474
; FEATURE:
; NAME/KEY: heavy chain
; US-08-983-607-36

Query Match 70.7%; Score 41; DB 3; Length 116;
Best Local Similarity 80.0%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|:|:|
Db 26 GFTFSYDMS 35

RESULT 15
US-08-276-852-80
; Sequence 80, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10566 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop Tpc8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SC1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-80

Query Match 70.7%; Score 41; DB 1; Length 122;
Best Local Similarity 70.0%; Pred. No. 5.6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:||||:
Db 23 GFTSSYEMN 32

Search completed: March 28, 2001, 06:39:09
Job time: 763 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:49 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	88.7	94	2 S14580	Ig heavy chain V r
2	43	81.1	97	2 S26890	Ig heavy chain V r
3	42	79.2	113	2 S26468	Ig heavy chain V r
4	42	79.2	117	1 HVMS34	Ig heavy chain pre
5	42	79.2	121	2 D27888	Ig heavy chain V r
6	42	79.2	124	2 C27888	Ig heavy chain V r
7	40	75.5	40	2 S33406	Ig heavy chain V r
8	40	75.5	83	2 C25913	Ig heavy chain V r
9	40	75.5	98	2 S26891	Ig heavy chain V r
10	40	75.5	108	2 PL0248	Ig heavy chain V r
11	40	75.5	108	2 PH1006	Ig heavy chain V r
12	40	75.5	117	1 HVMS84	Ig heavy chain pre
13	40	75.5	117	2 PL0249	Ig heavy chain V r
14	40	75.5	117	2 PL0252	Ig heavy chain V r
15	40	75.5	119	2 F27888	Ig heavy chain V r
16	40	75.5	122	2 E27888	Ig heavy chain V r
17	40	75.5	138	2 S09258	Ig heavy chain V r
18	40	75.5	138	2 I47205	Ig heavy chain V r
19	39	73.6	92	2 S56009	Ig heavy chain var
20	39	73.6	92	2 S56008	Ig heavy chain var
21	39	73.6	97	1 HVMS91	Ig heavy chain V r
22	39	73.6	97	2 PH0872	Ig heavy chain V r
23	39	73.6	98	2 S26889	Ig heavy chain V r
24	39	73.6	100	2 D48223	Ig heavy chain V r
25	39	73.6	102	2 S14581	Ig heavy chain V r
26	39	73.6	108	2 PH1648	Ig heavy chain V r
27	39	73.6	108	2 PH1011	Ig heavy chain V r
28	39	73.6	109	2 PH1649	Ig heavy chain V r
29	39	73.6	111	2 PH1659	Ig heavy chain V r

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30      39      73.6      111      2      S40090      Ig heavy chain - m
31      39      73.6      111      2      PH1007      Ig heavy chain V r
32      39      73.6      112      2      S26327      Ig heavy chain V r
33      39      73.6      112      2      PH1647      Ig heavy chain V r
34      39      73.6      113      2      S25571      Ig heavy chain V r
35      39      73.6      117      1      H3H026      Ig heavy chain pre
36      39      73.6      117      2      A45953      Ig heavy chain pre
37      39      73.6      117      2      B34964      Ig heavy chain pre
38      39      73.6      117      2      S34012      Ig heavy chain V r
39      39      73.6      118      2      S31121      Ig heavy chain - h
40      39      73.6      119      2      C36005      Ig heavy chain V r
41      39      73.6      119      2      D36005      Ig heavy chain V r
42      39      73.6      119      2      S31107      Ig heavy chain - h
43      39      73.6      119      2      S31108      Ig heavy chain - h
44      39      73.6      120      2      S48798      Ig heavy chain V r
45      39      73.6      120      2      S55538      Ig heavy chain V r

```

ALIGNMENTS

RESULT 1

S14580

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S14580

R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.

submitted to the EMBL Data Library, March 1991

A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in V

A:Reference number: S14484

A:Accession: S14580

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-94 <CHE>

A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.7%; Score 47; DB 2; Length 94;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

Db 18 GFTFLSYDMS 27

RESULT 2

S26890

Ig heavy chain V region (BP-48) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26890

R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o

A:Reference number: S26885; MUID:93021117

A:Accession: S26890

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-97 <TOM>

A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.1%; Score 43; DB 2; Length 97;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTFLSYDM 9
 |||||
 Db 26 GTFSSYDM 34

RESULT 3

S26458

Ig heavy chain V region - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26458
 R:Kavalet, J.
 Submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26458
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <KAV>
 A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

QY 1 GTFLSYDMS 10
 |||||
 Db 22 GFATSSYDMS 31

RESULT 4

HWS34

Ig heavy chain precursor V region (345) - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: J00502
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: J00501; MUID:89279149
 A:Accession: J00502
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: This sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

QY 1 GTFLSYDMS 10
 |||||
 Db 45 GFATSSYDMS 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
 C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
 EMBO J. 5, 1577-1587, 1986
 A:Title: Structural and functional implications of a restricted antibody response to
 A:Reference number: A91043; MUID:86300658
 A:Accession: D27888
 A:Molecule type: DNA
 A:Residues: 1-121 <CAT>
 A:Experimental source: strain Balb/c
 A:Note: This sequence was determined from the germline gene
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 121;
 Best Local Similarity 80.0%; Pred. No. 0.24;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTFLSYDMS 10
 |||||
 Db 26 GFATSSYDMS 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
 C:Accession: C27888
 R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
 EMBO J. 5, 1577-1587, 1986
 A:Title: Structural and functional implications of a restricted antibody response to
 A:Reference number: A91043; MUID:86300658
 A:Accession: C27888
 A:Molecule type: DNA
 A:Residues: 1-124 <CAT>
 A:Experimental source: strain Balb/c
 A:Note: This sequence was determined from the germline gene
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 124;
 Best Local Similarity 80.0%; Pred. No. 0.25;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTFLSYDMS 10
 |||||
 Db 26 GFATSSYDMS 35

RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
 C:Accession: S33406
 R:Kettleborough, C.A.; Saidanha, J.; Ansell, K.H.; Bendig, M.M.
 Eur. J. Immunol. 23, 206-211, 1993
 A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes
 A:Reference number: S33391; MUID:93122092
 A:Accession: S33406
 A:Molecule type: mRNA
 A:Residues: 1-40 <KET>
 A:Cross-references: EMBL:X73009
 A:Experimental source: strain BALB/c
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 75.5%; Score 40; DB 2; Length 40;
 Best Local Similarity 80.0%; Pred. No. 0.18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 DB 26 GFTFSYDMS 35

RESULT 8
 C25913
 Ig heavy chain V region (BFL14) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
 C:Accession: C25913
 R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
 A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
 A:Reference number: A94148; MUID:87175692
 A:Accession: C25913
 A:Molecule type: DNA
 A:Residues: 1-83 <LAW>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 75.5%; Score 40; DB 2; Length 83;
 Best Local Similarity 80.0%; Pred. No. 0.4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 DB 11 GFTFSYDMS 20

RESULT 9
 S26891
 Ig heavy chain V region (DP-58) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26891
 R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117
 A:Accession: S26891
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: EMBL:Z12358; NID:932935; PIDN:CAA78228.1; PID:932936
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 98;
 Best Local Similarity 70.0%; Pred. No. 0.48;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 DB 26 GFTFSYDMS 35

RESULT 10
 PL0248
 Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0248
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0248
 A:Molecule type: mRNA
 A:Residues: 1-108 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-24/Region: framework 1
 F:9-92/Domain: immunoglobulin homology <IMM>
 F:25-29/Region: complementarity-determining 1
 F:30-43/Region: framework 2
 F:44-60/Region: complementarity-determining 2
 F:61-92/Region: framework 3
 F:93-99/Region: complementarity-determining 3
 F:100-108/Region: framework 4

Query Match 75.5%; Score 40; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 0.54;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 DB 20 GFTFSYDMS 29

RESULT 11
 PH1006
 Ig heavy chain V region (clone 202.33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1006
 R:Tillman, D.M.; Jow, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1006
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <HIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 0.54;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 DB 21 GFTFSYDMS 30

RESULT 12
 HWS84
 Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0505
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primer
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0505
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: This sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 75.5%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 45 GFTFSSYTMS 54

RESULT 13

PL0249
Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0249

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990

A>Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618

A:Accession: PL0249

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match 75.5%; Score 40; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 GFTFSSYTMS 35

RESULT 14

PL0252

Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0252

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990

A>Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618

A:Accession: PL0252

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match 75.5%; Score 40; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 GFTFSSYTMS 35

RESULT 15

F27888

Ig heavy chain V region (H158-89H4) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: F27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A>Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658

A:Accession: F27888

A:Molecule type: DNA

A:Residues: 1-119 <CAT>

A:Experimental source: strain Balb/c

A>Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 GFTFSSYTMS 35

Search completed: March 28, 2001, 06:41:49
Job time: 872 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:45 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	42	79.2	117	1 HV55_MOUSE	P18526 mus musculus
2	40	75.5	117	1 HV54_MOUSE	P18525 mus musculus
3	39	73.6	97	1 HV3C_MOUSE	P18527 mus musculus
4	39	73.6	117	1 HV3C_HUMAN	P01764 homo sapien
5	38	71.7	117	1 HV52_MOUSE	P06327 mus musculus
6	38	71.7	117	1 HV53_MOUSE	P18524 mus musculus
7	37	69.8	117	1 HV59_MOUSE	P18530 mus musculus
8	36	67.9	3106	1 LMA2_MOUSE	Q60675 mus musculus
9	35	66.0	115	1 HV3D_HUMAN	P01765 homo sapien
10	35	66.0	117	1 HV17_MOUSE	P01786 mus musculus
11	34	64.2	117	1 HV58_MOUSE	P18529 mus musculus
12	34	64.2	326	1 YE08_SCHPO	O13805 schizosacch
13	34	64.2	451	1 ARP2_PLAFA	P13824 plasmodium
14	33	62.3	114	1 HV00_MOUSE	P01741 mus musculus
15	33	62.3	114	1 HV01_CANFA	P01784 canis famil
16	33	62.3	116	1 HV1A_RABIT	P01826 oryctolagus
17	33	62.3	117	1 HV2E_RABIT	P01828 oryctolagus
18	33	62.3	120	1 HV3E_HUMAN	P01766 homo sapien
19	33	62.3	121	1 HV3J_HUMAN	P01771 homo sapien
20	33	62.3	396	1 EFTU_STIAU	P42479 stigmatella
21	33	62.3	706	1 VGLH_EBV	P03231 epstein-bar
22	32	60.4	114	1 HV3E_HUMAN	P01763 homo sapien
23	32	60.4	117	1 HV14_MOUSE	P01758 mus musculus
24	32	60.4	122	1 HV3G_HUMAN	P01768 homo sapien
25	32	60.4	136	1 HV16_MOUSE	P01783 mus musculus
26	32	60.4	247	1 ATP6_ACACA	Q37385 acanthamoeb
27	32	60.4	281	1 Y373_MYCGE	P47613 mycoplasma
28	32	60.4	281	1 Y373_MYCPN	P75227 mycoplasma
29	32	60.4	465	1 YGLX_RHIME	O87394 rhizobium m
30	32	60.4	550	1 INV1_HANAN	P40912 hanseniella a
31	32	60.4	747	1 FHUA_EGOLI	P06971 escherichia
32	31	58.5	111	1 HV35_MOUSE	P01804 mus musculus
33	31	58.5	113	1 HV27_MOUSE	P01796 mus musculus

ALIGNMENTS

RESULT 1

ID	HV55_MOUSE	STANDARD:	PRT:	117 AA.
AC	P18526;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG HEAVY CHAIN V REGION 345 PRECURSOR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/CJ;			
RX	MEDLINE: 89279149;			
RA	Ley N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;			
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";			
RL	J. Exp. Med. 169:2007-2019(1989).			
CC	-1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH17183 SUBFAMILY.			
DR	PIR: JT0502; HVMS34;			
DR	INTERPRO: IPR003006; -;			
DR	PFAM: PF00047; Ig; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 19			
FT	CHAIN 20 117			
FT	DOMAIN 20 49			
FT	DOMAIN 50 54			
FT	DOMAIN 55 68			
FT	DOMAIN 69 85			
FT	DOMAIN 86 117			
FT	DISULFID 41 115			
FT	NON_TER 117 117			
SO	SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;			

Query Match 79.2%; Score 42; DB 1; Length 117;

Best Local Similarity 80.0%; Pred No. 0.17; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 0;

Qy 1 GFTFLSYDMS 10

Db 45 GFATSSYDMS 54

RESULT 2

ID	HV54_MOUSE	STANDARD:	PRT:	117 AA.
AC	P18525;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG HEAVY CHAIN V REGION 5-84 PRECURSOR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/CJ;
RX  MEDLINE; 89279149.
RA  Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during
RT  the primary immune response.";
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR  PIR; JT0505; HVMS84.
DR  INTERPRO; IPR003006; -.
DR  PFAM; PF00047; Ig; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 19
FT  CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT  DOMAIN 20 49 FRAMEWORK 1.
FT  DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT  DOMAIN 55 68 FRAMEWORK 2.
FT  DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT  DOMAIN 86 117 FRAMEWORK 3.
FT  DISULFID 41 115 BY SIMILARITY.
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db 45 GFTFSYTMS 54

RESULT 3
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db 26 GFTFSYAMS 35

RESULT 4
HV3C_HUMAN

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ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81101090.
RA Matthyssens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL heavy chain variable region.;
CC Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC -----
DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F3A3CB0F1 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
Db 45 GFTFSYAMS 54

RESULT 5
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85099340.
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).
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DR EMBL: M13787; AAA38499.1; -.
DR PIR: A02029; HVMSAL.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 AL/M4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 50 54 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 71.7%; Score 38; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 1;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 45 GYTFSSYDMS 54

RESULT 6
HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION RF PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO503; HVMSRF.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 71.7%; Score 38; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 45 GYTFSSYDMS 54

RESULT 7
HV59_MOUSE

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ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO507; HVMS39.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 45 GYTFSSYDMS 54

RESULT 8
LMA2_MOUSE STANDARD; PRT; 3106 AA.
ID LMA2_MOUSE STANDARD; PRT; 3106 AA.
AC Q60675; Q05003; Q64061;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY
CHAIN).
DE CHAIN.
DE LMA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN STRAIN-FVB/N; TISSUE-EMBRYO, AND HEART;
RX MEDLINE; 95316259.
RA Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,
RA Yanada Y.;
RT "Cloning and expression of laminin alpha 2 chain (M-chain) in the
mouse.";
RL Matrix Biol. 14:447-455(1995).
[2]
RN STRAIN-C57BL/6; TISSUE-THYMUS;
RX MEDLINE; 93346725.
RA Chang A.C., Wadsworth S., Colligan J.E.;
RT "Expression of merosin in the thymus and its interaction with
thymocytes.";
RL J. Immunol. 151:1789-1801(1993).

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FT DISULFID 1467 1490 BY SIMILARITY.
FT DISULFID 1493 1502 BY SIMILARITY.
FT DISULFID 1505 1520 BY SIMILARITY.
FT DISULFID 1523 1535 BY SIMILARITY.
FT DISULFID 1525 1542 BY SIMILARITY.
FT DISULFID 1544 1553 BY SIMILARITY.
FT DISULFID 1556 1567 BY SIMILARITY.
FT DISULFID 1570 1570 INTERCHAIN (PROBABLE).
FT DISULFID 1574 1574 INTERCHAIN (PROBABLE).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 742 742 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 919 919 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1031 1031 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1057 1057 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1593 1593 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1610 1610 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1696 1696 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1806 1806 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1897 1897 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1912 1912 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1916 1916 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 67.9%; Score 36; DB 1; Length 3106;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
Db 2817 GPFPSYDL 2825

RESULT 9
HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 78005528.
RA Wang A.-C., Wang I.-Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
DR PIR; A02048; H3HUTL.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 115;
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 10
Db 26 GFTFTSYVM 35

RESULT 10
HV17_MOUSE STANDARD; PRT; 117 AA.
ID HV17_MOUSE
AC P01786;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 47A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 80049769.
RA Robinson E.A., Appella E.;
RT "Amino acid sequence of a mouse myeloma immunoglobulin heavy chain
(MOPC 47 A) with a 100-residue deletion.";
RL J. Biol. Chem. 254:11418-11430(1979).
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,
CC LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA
CC MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A
CC LIGHT-HEAVY CHAIN DISULFIDE BOND.
DR PIR; A02069; ALMS47.
DR HSSP; P01789; 2MCP.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12975 MW; 0C74B8BBI54BDF4 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 10
Db 26 GFTFTSYVM 35

RESULT 11
HV58_MOUSE STANDARD; PRT; 117 AA.
ID HV58_MOUSE
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALEB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin V genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70506; HVMS57.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.

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FT DOMAIN      86 117 FRAMEWORK 3.
FT DISULFID    41 115 BY SIMILARITY.
FT NON_TER     117
SQ SEQUENCE    117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match      64.2%; Score 34; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 45 GFTFNKIAMS 54

RESULT 12
YE08_SCHPO STANDARD; PRT; 326 AA.
AC 013805;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE PUTATIVE MITOCHONDRIAL CARRIER C17H9.08.
GN SPAC17H9.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -!- INNER MEMBRANE (POTENTIAL).
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M13021; AAA29485.1; -
CC PIR; A23535; A23535.
CC INTERPRO: IPR000504; -
CC PFAM; PF00076; rrm; 2.
CC Malaria.
KW
FT NON_TER 1
SQ SEQUENCE 451 AA; 52204 MW; B686354D85F8C293 CRC64;

Query Match      64.2%; Score 34; DB 1; Length 451;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
Db 407 GGFVSVSYD 414

RESULT 14
HV00_MOUSE STANDARD; PRT; 114 AA.
ID HV00_MOUSE
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE; 79195438.
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idioype."
RL J. Immunol. 123:279-284(1979).
CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC PIR; A02022; GIMSA.
CC INTERPRO: IPR003006; -
CC PFAM; PF00047; ig; 1.
CC Immunoglobulin V region; Antiarsonate antibody.
KW
FT NON_TER 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

```

Query Match 62.3%; Score 33; DB 1; Length 114;
 Best Local Similarity 55.6%; Pred. No. 9.2;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTFELSYDM 9
 |::|::|::|
 Db 26 GYTFSYEL 34

RESULT 15
 HV01_CANFA
 ID HV01_CANFA STANDARD; PRT; 114 AA.
 AC P01784;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION GOM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 77242268.
 RA Wasserman R.L., Capra J.D.;
 RT "Primary structure of the variable regions of two canine
 RT immunoglobulin heavy chains";
 RL Biochemistry 16:3160-3168(1977).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A02067; AVDGM.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig: 1.
 KW Immunoglobulin V region.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;

Query Match 62.3%; Score 33; DB 1; Length 114;
 Best Local Similarity 66.7%; Pred. No. 9.2;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTFELSYDM 9
 |::|::|::|
 Db 26 GTFESGYDM 34

Search completed: March 28, 2001, 07:29:46
 Job time: 1653 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:33 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organellae:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	73.6	437	11 Q9RIA4	Q9RIA4 mus musculu
2	38	71.7	118	4 Q9UL31	Q9UL31 homo sapien
3	37	69.8	95	4 Q9ULB6	Q9ULB6 homo sapien
4	37	69.8	147	4 Q9Y509	Q9Y509 homo sapien
5	36	67.9	113	4 Q9UL90	Q9UL90 homo sapien
6	36	67.9	312	12 Q67551	Q67551 garlic late
7	36	67.9	1924	12 Q67554	Q67554 garlic late
8	36	67.9	1967	12 Q65652	Q65652 blueberry s
9	36	67.9	2183	12 Q64962	Q64962 apple stem
10	35	66.0	116	4 Q9UL93	Q9UL93 homo sapien
11	35	66.0	314	10 Q9ZQR7	Q9ZQR7 arabidopsis
12	35	66.0	363	10 Q9ZU66	Q9ZU66 arabidopsis
13	35	66.0	577	5 P91823	P91823 caenorhabdi
14	34	64.2	289	10 Q9ZU04	Q9ZU04 arabidopsis
15	34	64.2	347	8 Q34096	Q34096 crithidia f
16	34	64.2	349	12 Q65125	Q65125 african swi
17	34	64.2	364	10 Q9LIR8	Q9LIR8 arabidopsis
18	34	64.2	398	5 Q9WLP8	Q9WLP8 drosophila
19	34	64.2	475	5 Q9XWR7	Q9XWR7 caenorhabdi

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20 34 64.2 690 10 Q9LIB7
21 34 64.2 702 10 Q9LNL6
22 34 64.2 868 10 Q38710
23 34 64.2 1418 5 O01837
24 34 64.2 1456 5 O19127
25 33 62.3 85 2 Q53774
26 33 62.3 128 3 O94499
27 33 62.3 223 12 Q9VP85
28 33 62.3 300 5 Q9V3G3
29 33 62.3 315 5 Q20116
30 33 62.3 355 8 Q34937
31 33 62.3 430 10 Q9W159
32 33 62.3 455 2 O87953
33 33 62.3 470 8 Q32371
34 33 62.3 472 8 Q32364
35 33 62.3 491 2 P94289
36 33 62.3 723 11 Q35193
37 33 62.3 763 3 Q12653
38 33 62.3 852 11 Q35192
39 33 62.3 879 2 Q9PIG2
40 33 62.3 928 2 O86164
41 33 62.3 949 2 Q9K299
42 33 62.3 968 10 O04623
43 33 62.3 1045 5 Q9W124
44 33 62.3 1378 11 Q07314
45 33 62.3 1395 11 Q07313

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ALIGNMENTS

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RESULT 1
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -
DR HSSP; P01842; 7FAB.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 437
FT TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

```

Query Match 73.6%; Score 39; DB 11; Length 437;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 25 GFTFLSYDMS 34

RESULT 2

Q9UL91 PRELIMINARY; PRT; 118 AA.

ID Q9UL91

AC Q9UL91;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035023; RAD56259.1; -;
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 FT NON_TER 1
 FT 118
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 71.7%; Score 38; DB 4; Length 118;

Best Local Similarity 70.0%; Pred. No. 4.6;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db ||||| ||

Db 26 GFTFSSYMN 35

RESULT 3

Q9ULB6 PRELIMINARY; PRT; 95 AA.

AC Q9ULB6;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
 GN VH.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Tange Y., Kayano H.;
 RT "Human VH gene sequence";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB035268; BAA87067.1; -;
 DR HSP; P01772; 2FB4.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 FT NON_TER 1
 FT 95
 FT NON_TER 95
 SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 69.8%; Score 37; DB 4; Length 95;

Best Local Similarity 80.0%; Pred. No. 5.7;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db ||||| ||

Db 25 GFTFSSYWN 34

RESULT 4

Q9Y509 PRELIMINARY; PRT; 147 AA.

QY Q9Y509

AC Q9Y509

DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE VH3 PROTEIN (FRAGMENT).
 GN VH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96071149; PubMed=7475288;
 RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
 RA Lichtenstein A.K., Berenson J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple
 RT myeloma using PCR with patient-specific immunoglobulin gene primers";
 RL Leukemia 9:1948-1953(1995).
 DR EMBL; S80860; RAD14339.1; -;
 DR HSP; P01772; 2FB4.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 FT NON_TER 1
 FT 1
 FT NON_TER 1
 SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 69.8%; Score 37; DB 4; Length 147;

Best Local Similarity 70.0%; Pred. No. 9.1;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db ||||| ||

Db 26 GFTFSTYGM 35

RESULT 5

Q9UL90 PRELIMINARY; PRT; 113 AA.

AC Q9UL90;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035024; AAD56260.1; -;
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 FT NON_TER 1
 FT 113
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 67.9%; Score 36; DB 4; Length 113;

Best Local Similarity 77.8%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9

Db ||||| ||

Db 26 GFTFSSYGM 34

RESULT 6

Q67551

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ID Q67551 PRELIMINARY; PRT; 312 AA.
AC Q67551;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE RNA REPLICASE (FRAGMENT).
OS garlic latent virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlaviruses.
OX NCBI_TaxID=12458;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsuneyoshi T., Sumi S.;
RT "Differentiation among garlic viruses in mixed infections based on RT-PCR procedures and direct tissue blotting immunoassays.";
RL Phytopathology 86:253-259(1996).
DR EMBL; D11161; BAA01931.1; -
FT NON_TER
SQ SEQUENCE 312 AA; 36230 MW; C79E6563DA488175 CRC64;

Query Match 67.9%; Score 36; DB 12; Length 312;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTFLSYDMS 10
Db 168 FTFLRYDLN 176

RESULT 7
ID Q67654 PRELIMINARY; PRT; 1924 AA.
AC Q67654;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE REPLICASE.
OS garlic latent virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlaviruses.
OX NCBI_TaxID=12458;
RN [1]
RP SEQUENCE FROM N.A.
RA Jin Nam C., Sang Ik S., Jong Seob L., Yang Do C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z68502; CA92815.1; -
DR MEROPS; C23.001; -
DR INTERPRO; IPR000606; -
DR INTERPRO; IPR000923; -
DR INTERPRO; IPR001202; -
DR PFAM; PF01443; Viral_helicase1; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
SQ SEQUENCE 1924 AA; 218937 MW; 8C814AEC96526654 CRC64;

Query Match 67.9%; Score 36; DB 12; Length 1924;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTFLSYDMS 10
Db 1780 FTFLRYDLN 1788

RESULT 8
ID Q65652 PRELIMINARY; PRT; 1967 AA.
AC Q65652;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE BLUEBERRY SCORCH CARLAVIRUS MRNA.

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OS blueberry scorch virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlaviruses.
OX NCBI_TaxID=31722;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NJ-2;
RX MEDLINE=94201746; PubMed=8151289;
RA Cavileer T.D., Halpern B.T., Lawrence D.M., Podleckis E.V.,
RA Martin R.R., Hillman B.I.;
RT "Nucleotide sequence of the carlaviruses associated with blueberry scorch and similar diseases.";
RL J. Gen. Virol. 75:711-720(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NJ-2;
RX MEDLINE=95176530; PubMed=7871721;
RA Lawrence D.M., Rozanov M.N., Hillman B.I.;
RT "Autocatalytic processing of the 223-kDa protein of blueberry scorch carlaviruses by a papain-like proteinase.";
RL Virology 207:127-135(1995).
DR EMBL; L25658; AAA68984.1; -
DR MEROPS; C23.001; -
SQ SEQUENCE 1967 AA; 223428 MW; 4CEDD6AF14980188 CRC64;

Query Match 67.9%; Score 36; DB 12; Length 1967;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTFLSYDM 9
Db 1823 FTFLQYDL 1830

RESULT 9
ID Q64962 PRELIMINARY; PRT; 2183 AA.
AC Q64962;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE VIRAL RNA-DEPENDENT RNA POLYMERASE.
OS apple stem pitting virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Foveavirus.
OX NCBI_TaxID=35350;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ASPV;
RX MEDLINE=94292903; PubMed=8021584;
RA Telkmann W.;
RT "Nucleotide sequences of apple stem pitting virus and of the coat protein gene of a similar virus from pear associated with vein yellows disease and their relationship with potex- and carlaviruses.";
RL J. Gen. Virol. 75:1535-1542(1994).
DR EMBL; D21829; BAA04853.1; -
DR MEROPS; C23.001; -
DR INTERPRO; IPR000606; -
DR PFAM; PF01443; Viral_helicase1; 1.
DR RNA-directed RNA polymerase.
SQ SEQUENCE 2183 AA; 247259 MW; 2156D7A75A548CC5 CRC64;

Query Match 67.9%; Score 36; DB 12; Length 2183;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTFLSYDMS 10
Db 2036 FTFLRYDLN 2044

RESULT 10
Q90L93

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ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig: 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 66.0%; Score 35; DB 4; Length 116;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
Db 25 GFTFSSYAM 33
|||||
|

RESULT 11
Q9ZQR7 PRELIMINARY; PRT; 314 AA.
ID Q9ZQR7;
AC Q9ZQR7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PUTATIVE SPLICEOSOMAL ASSOCIATED PROTEIN.
GN T13P21.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006067; AAD15475.1; -
DR HSSP; P09651; 1HA1.
DR INTERPRO; IPR000504; -
DR PFAM; PF00076; rtm: 2.
DR PROSITE; PS00030; RNP_1; UNKNOWN_1.
SQ SEQUENCE 314 AA; 35267 MW; 4C73056D0D6D0F47 CRC64;

Query Match 66.0%; Score 35; DB 10; Length 314;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
Db 128 GFGFISYD 135
|||||
|

RESULT 12
Q9ZU66 PRELIMINARY; PRT; 363 AA.
ID Q9ZU66;
AC Q9ZU66;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PUTATIVE SPLICEOSOMAL PROTEIN (RNA BINDING PROTEIN).
GN F24H14.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006135; AAD12222.1; -
DR HSSP; P09651; 1HA1.
DR INTERPRO; IPR000504; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00076; rtm: 2.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00030; RNP_1; UNKNOWN_1.
SQ SEQUENCE 363 AA; 39888 MW; 62F71DC136A7DFCE CRC64;

Query Match 66.0%; Score 35; DB 10; Length 363;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
Db 155 GFGFISYD 162
|||||
|

RESULT 13
P91823 PRELIMINARY; PRT; 577 AA.
ID P91823;
AC P91823;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE T22A3.6 PROTEIN.
GN T22A3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81125; CAB03383.2; -
DR HSSP; P00749; 1KDU.
DR INTERPRO; IPR000001; -
DR PFAM; PF00051; kringle; 1.
DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
DR PROSITE; PS50070; KRINGLE_2; 1.

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SQ SEQUENCE 577 AA; 66610 MW; 7A6E06364BF2C149 CRC64;

Query Match 66.0%; Score 35; DB 5; Length 577;
Best Local Similarity 60.0%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
II : IIII
Db 292 GFTFLSYDMS 301

RESULT 14

Q92U04 PRELIMINARY; PRT; 289 AA.
AC Q92U04;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PUTATIVE RNA BINDING PROTEIN.
GN F3G5.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005896; AAC98043.1; -
DR HSP; P09651; I0P1.
DR MENDEL; 35355; Arath; 2406; 35355.
DR INTERPRO; IPR000504; -
DR PFAM; PF00076; rrm; 2.
DR PROSITE; PS00030; RNP_1; 2.
KW RNA-binding.
SQ SEQUENCE 289 AA; 30718 MW; E500C3C0518369AD CRC64;

Query Match 64.2%; Score 34; DB 10; Length 289;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
II : IIII
Db 246 GFTFLSYDMS 255

RESULT 15

Q34096 PRELIMINARY; PRT; 347 AA.
AC Q34096;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MURF2 PROTEIN.
OS Crithidia fasciculata.
OG Mitochondrion.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
OX NCBI_TaxID=5656;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89315227; PubMed=2748342;
RT van der Spek H., Arts G.J., Van Den Burg J., Sloof P., Benne R.;
RT "The nucleotide sequence of mitochondrial maxicircle genes of
RT Crithidia fasciculata."
RL Nucleic Acids Res. 17:4876-4876(1989).
DR EMBL; X15081; CAA33190.1; -
KW Mitochondrion.

SQ SEQUENCE 347 AA; 42540 MW; 60291958B1FC711A CRC64;

Query Match 64.2%; Score 34; DB 8; Length 347;
Best Local Similarity 60.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
II : IIII
Db 238 GFTFLSYGLA 247

Search completed: March 28, 2001, 07:27:37
Job time: 1650 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:32 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT:*
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- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	19	W76016
2	47	88.7	10	19	W76007
3	47	88.7	117	19	W76001
4	45	84.9	117	20	W86141
5	44	83.0	117	20	W86137
6	44	83.0	128	19	W54000
7	44	83.0	134	13	R24713
8	44	83.0	225	11	R05710
9	44	83.0	225	11	R06478
10	44	83.0	225	14	R43675
11	44	83.0	225	17	R99645
12	44	83.0	236	11	R06479
					LM609 grafted anti
					Vitaxin antibody h
					protein sequence o
					Anti-CD4 antibody
					Sequence encoded b
					TRY40. Mus muscul
					Single chain polyp
					Single chain bindi
					TRY61. Mus muscul

13	44	83.0	236	14	R43676	Single chain polyp
14	44	83.0	236	17	W02188	TRY61 single chain
15	44	83.0	236	17	R99646	Single chain bindi
16	44	83.0	246	11	R06480	TRY59. Mus muscul
17	44	83.0	246	11	R43677	Single chain polyp
18	44	83.0	246	17	W02189	TRY59 single chain
19	44	83.0	246	17	R99647	Single chain bindi
20	44	83.0	250	11	R06481	TRY104b. Mus musc
21	44	83.0	250	14	R43678	Single chain polyp
22	44	83.0	250	17	W02190	TRY104b single cha
23	44	83.0	250	17	R99648	Single chain bindi
24	44	83.0	448	11	R06476	Heavy chain of ant
25	44	83.0	448	14	R43673	Mouse anti-bovine
26	44	83.0	448	17	R97376	Murine anti-RGH MA
27	44	83.0	448	17	R99643	Anti-BGH monoclon
28	44	83.0	466	13	R24812	Sequence encoded b
29	43	81.1	139	18	W21652	Humanised reshaped
30	42	79.2	10	19	W76015	LM609 grafted anti
31	42	79.2	117	19	W76003	LM609 antibody hea
32	42	79.2	117	20	Y06381	Murine monoclonal
33	42	79.2	121	20	W86122	Protein sequence o
34	42	79.2	130	20	Y06379	Murine monoclonal
35	42	79.2	239	14	R34511	Fv(TU25). Homo sa
36	42	79.2	247	16	W11917	Murine MAb SK48-E2
37	41	77.4	10	21	Y78322	Anti-zeta-chain an
38	41	77.4	119	16	W11919	Humanised MAb SK48
39	41	77.4	123	19	W53998	Anti-CD4 antibody
40	41	77.4	123	21	Y78325	Anti-zeta-chain an
41	41	77.4	532	21	Y78328	Bispecific anti-ze
42	40	75.5	98	19	W59614	Anti-RSV F protein
43	40	75.5	116	16	R66307	Human immunoglobul
44	40	75.5	116	18	W13529	Anti-melanoma anti
45	40	75.5	118	19	W57591	Chimeric antibody

ALIGNMENTS

RESULT 1

W76016
ID W76016 standard; Protein; 10 AA.
XX
AC W76016;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR1 protein fragment #4.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN W09833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49853.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 60; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA:
 Query Match 100.0%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTFLSYDMS 10
 Db | | | | | | | | | |
 1 gftflsydms 10
 RESULT 2
 ID W76007 standard; Protein; 10 AA.
 XX
 AC W76007;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR1 protein fragment #1.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49844.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA:
 Query Match 88.7%; Score 47; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTFLSYDMS 10
 Db | | | | | | | | | |
 1 gftflsydms 10
 RESULT 3
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49820.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC So are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 88.7%; Score 47; DB 19; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.017; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 1 GFTFLSYDMS 10

Db 26 gftfssyds 35

RESULT 4

W86141
 ID W86141 standard; Protein; 117 AA.

AC W86141;

XX 03-MAR-1999 (first entry)

XX Protein sequence of de-immunised murine A33 Vh.

DE Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunogl bulin; therapeutic; streptokinase; murine; de-immunised.

XX Mus sp.

XX WO9852976-A1.

XX 26-NOV-1998.

XX 21-MAY-1998; 98WO-GB01473.

XX 14-APR-1998; 98GB-0007751.

XX 21-MAY-1997; 97GB-0010480.

XX 31-JUL-1997; 97GB-0016197.

XX 28-NOV-1997; 97GB-0025270.

XX 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FJ;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species

XX Example 6; Fig 27; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.

XX Sequence 117 AA;

Query Match 84.9%; Score 45; DB 20; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.044;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 gftftsydms 35

RESULT 5

W86137
 ID W86137 standard; Protein; 117 AA.

XX W86137;

XX 03-MAR-1999 (first entry)

XX Protein sequence of de-immunised humanised A33 Vh.

XX Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.

XX Homo sapiens.

XX WO9852976-A1.

XX 26-NOV-1998.

XX 21-MAY-1998; 98WO-GB01473.

XX 14-APR-1998; 98GB-0007751.

XX 21-MAY-1997; 97GB-0010480.

XX 31-JUL-1997; 97GB-0016197.

XX 28-NOV-1997; 97GB-0025270.

XX 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FJ;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species

XX Example 5; Fig 25; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.

XX Sequence 117 AA;

Query Match 83.0%; Score 44; DB 20; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.07;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 gftftsydms 35

RESULT 6

W54000
ID W54000 standard; Protein; 128 AA.

XX AC
XX W54000;

XX DT 29-JUL-1998 (first entry)

XX DE Anti-CD4 antibody VH3 monkey clone 3-40.

XX KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW Old World monkey; constant domain; eczema; immuno-modulated disease;
KW rheumatoid arthritis.

XX OS Primate sp.

XX FH Key Location/Qualifiers

FT Misc-difference 1..128
FT /note= "Xaa= unspecified amino acid"

XX US5750105-A.

XX PD 12-MAY-1998.

XX PF 07-JUN-1995; 95US-0476349.

XX PR 10-JUL-1992; 92US-0912292.

XX PR 25-JUL-1991; 91US-0735064.

XX PR 23-MAR-1992; 92US-0856281.

XX PR 05-DEC-1995; 95US-0379072.

XX PR 07-JUN-1995; 95US-0476349.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Hanna N, Newman RA, Raab RW;

XX DR WPI; 1998-296690/26.

XX PT Improved method for antibody treatment - uses an antibody comprising
XX an Old World monkey variable region and a human constant domain

XX PS Example 1; Fig 9c; 84pp; English.

XX CC This sequence represents the VH3 domain of an anti-CD4 antibody
CC (Ab). This sequence can be used in the method of the invention for
CC treating a subject, where the treatment comprises administration of an
CC Ab. The method comprises the administration of an antibody which has an
CC Old World monkey (e.g. baboon or macaque) variable region which binds to
CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
CC method is useful for the treatment of eczema and immuno-modulated
CC diseases and especially rheumatoid arthritis. The recombinant antibodies
CC used are sufficiently different from native monkey antibodies to allow
CC human antigens to raise these antibodies, but similar enough to human
CC antibody so there is no immune response to the antibodies in humans.
CC Compared to antibodies used in therapy in prior art, these antibodies do
CC not induce human anti-antibodies on repeated administration. They also
CC have longer half-lives and do not have a lack of effector function with
CC human cells.

XX SQ Sequence 128 AA;

Query Match 83.0%; Score 44; DB 19; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.077;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 26 gftfssydmn 35

RESULT 7

R24713
ID R24713 standard; Protein; 134 AA.

XX R24713;

XX 28-DEC-1992 (first entry)

XX DE Sequence encoded by the genomic chimeric heavy chain variable region
XX (VFH) gene.

XX KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
XX antithrombotic agent; myocardial infarction therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide

FT /label= leader

FT Region

FT /label= Framework Region (FR) 1

FT Region

FT /label= 50..54

FT Region

FT /label= 55..68

FT Region

FT /label= FR-2

FT Region

FT /label= CDR-2

FT Region

FT /label= 85..114

FT Region

FT /label= FR-3

FT Region

FT /label= 115..123

FT Region

FT /label= CDR-3

FT Region

FT /label= 124..134

FT Region

FT /label= FR-4

XX EP491351-A.

XX PD 24-JUN-1992.

XX PF 17-DEC-1991; 91EP-0121591.

XX PR 18-DEC-1990; 90JP-0413829.

XX PR 11-NOV-1991; 91JP-0294464.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Iwasa S, Taka H, Watanabe T, Tada H;

XX DR WPI; 1992-209528/26.

XX DR N-PSDP; Q25666.

XX PT Chimeric monoclonal antibodies - contain anti-human fibrin
XX antibody light and heavy chain variable and constant for treating
XX thrombotic conditions e.g. myocardial infarction

XX PS Example; Figure 4; 87pp; English.

XX CC PCR primers 5'mvH and 3'mvH were used to produce a VH gene-contg.
XX fragment of about 330bp. The fragment was isolated and subcloned in
XX pUC119. The fragment was found to be a functional VH structural
XX gene, referred to as VFH, comprising a VH gene belonging to the
XX subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
XX analysis using the whole RNA of FIB1-11 cells confirmed that VFH
XX was the gene expressed in FIB1-11 cells. The sequence is given in
XX Q25666.

XX SQ Sequence 134 AA;

Query Match 83.0%; Score 44; DB 13; Length 134;
Best Local Similarity 80.0%; Pred. No. 0.081;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Db 45 gftfssydmn 54

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RESULT 8
R05710
XX R05710 standard; protein; 225 AA.
AC AC R05710;
XX
DT 07-JAN-1991 (first entry)
XX
DE TRY40.
XX
KW Monoclonal antibody; variable chain anti-bovine growth hormone.
XX
OS Mus musculus.
XX
FH Key Location/Qualifier
FT Region 4..126
FT Peptide /label= LCVR(1-41)
FT 127..147
FT /label= linker
FT Region 148..471
FT Peptide /label= HCVR(8-115)
FT 472..483
FT /label= linker
FT Region 484..678
FT /label= LCVR(45-109)
XX
XX US4946778-A.
XX
XX PN
XX
XX PD 07-AUG-1990.
XX
XX PF 19-JAN-1989; 89US-0299617.
XX
XX PR 19-JAN-1989; 89US-0299617.
XX
XX PR 02-SEP-1986; 86US-0902971.
XX
XX PR 02-SEP-1987; 87US-0092110.
XX
XX (GENE-) GENEX CORP.
XX
XX PA
XX
XX PI Ladner RC, Bird RE, Hardman K;
XX
XX WPI; 1990-260350/34.
XX
XX DR N-PSDB; Q05710.
XX
XX Single polypeptide chain binding molecules - having light chain
PT variable region of antibody linked by peptide to heavy chain
PT variable region.
XX
XX PS Disclosure; Fig 24; 68pp; English.
XX
XX CC The sequence was constructed from the variable regions of a MAB
CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
CC and kappa light chain. The sequence encodes a single chain binding
CC molecule comprising the variable regions of heavy and light chains
CC linked by a peptides. The variable region of each DNA chain was
CC prep'd. by introducing a ClaI site and an initiation codon (atcgatg)
CC prior to the first codon of the mature sequence and a HindIII site
CC and termination codon (taagctt) after codon 123 (heavy chain) or
CC 109 (light chain). The plasmids constructed to contain these
CC portions were pGX3772 and pGX3773 (heavy and light resp.). TRY40
CC has the following polypeptide structure:
CC Met-[LCVR(1-41)]-I-A-K-A-F-K-N-[HCVR(8-115)]-P-G-S-[LCVR(45-109)].
XX See also Q05708-19.
XX
XX SQ Sequence 225 AA;

Query Match 83.0%; Score 44; DB 11; Length 225;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:||||

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Db 68 gftflsygms 77

RESULT 9
R06478
ID R06478 standard; protein; 225 AA.
XX
AC AC R06478;
XX
DT 07-JAN-1991 (first entry)
XX
DE TRY40.
XX
KW Monoclonal antibody; variable chain anti-bovine growth hormone.
XX
OS Mus musculus.
XX
FH Key Location/Qualifier
FT misc_RNA 2..42
FT Peptide /label= LCVR(1-41)
FT 43..49
FT /label= linker
FT misc_RNA 50..157
FT Peptide /label= HCVR(8-115)
FT 158..160
FT /label= linker
FT misc_RNA 161..225
FT /*tag= e
FT /label= LCVR(45-109)
XX
XX US4946778-A.
XX
XX PN
XX
XX PD 07-AUG-1990.
XX
XX PF 19-JAN-1989; 89US-0299617.
XX
XX PR 19-JAN-1989; 89US-0299617.
XX
XX PR 02-SEP-1986; 86US-0902971.
XX
XX PR 02-SEP-1987; 87US-0092110.
XX
XX (GENE-) GENEX CORP.
XX
XX PA
XX
XX PI Ladner RC, Bird RE, Hardman K;
XX
XX WPI; 1990-260350/34.
XX
XX DR N-PSDB; Q05710.
XX
XX Single polypeptide chain binding molecules - having light chain
PT variable region of antibody linked by peptide to heavy chain
PT variable region.
XX
XX PS Disclosure; Fig 24; 68pp; English.
XX
XX CC The sequence was constructed from the variable regions of a MAB
CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
CC and kappa light chain. The sequence encodes a single chain binding
CC molecule comprising the variable regions of heavy and light chains
CC linked by a peptides. The variable region of each DNA chain was
CC prep'd. by introducing a ClaI site and an initiation codon (atcgatg)
CC prior to the first codon of the mature sequence and a HindIII site
CC and termination codon (taagctt) after codon 123 (heavy chain) or
CC 109 (light chain). The plasmids constructed to contain these
CC portions were pGX3772 and pGX3773 (heavy and light resp.). TRY40
CC has the following polypeptide structure:
CC Met-[LCVR(1-41)]-I-A-K-A-F-K-N-[HCVR(8-115)]-P-G-S-[LCVR(45-109)].
XX See also R06476-R06484.
XX
XX SQ Sequence 225 AA;

Query Match 83.0%; Score 44; DB 11; Length 225;
Best Local Similarity 80.0%; Pred. No. 0.14;

```

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:| | |
Db 68 gftfisygms 77

RESULT 10

R43675
ID R43675 standard; Protein: 225 AA.

XX R43675;

DT 23-MAY-1994 (first entry)

DE Single chain polypeptide with affinity for bovine growth hormone.

XX Monoclonal antibody; MAb; affinity; binding; antigen; diagnostics;
KW therapy; imaging; purification; biosensors.

XX Synthetic.

XX US5260203-A.

PN 09-NOV-1993.

XX 02-SEP-1986; 86US-0902971.

PR 02-SEP-1986; 86US-0902971.

PR 02-SEP-1987; 87US-0092110.

PR 19-JAN-1989; 89US-0299617.

PR 25-APR-1990; 90US-0512910.

XX (ENZO-) ENZON INC.

PA Bird RE, Hardman K, Ladner RC;

DR WPI: 1993-367875/46.

DR N-PSDB; Q51536.

XX Single chain poly:peptide for binding antigen - comprising light

PT and heavy chain antigen binding portions linked by peptide linker

XX Example 1; Figure 24; 78pp; English.

CC The single chain polypeptide is derived from the mature light and
CC heavy chains of a mouse monoclonal antibody (MAb) and has affinity
CC for a given antigen (Bovine growth hormone). It comprises a first
CC polypeptide comprising the antigen binding portion of of the light
CC chain variable region of an antibody and a second polypeptide
CC comprising the antigen binding portion of the heavy chain variable
CC region of an antibody and at least one peptide linker linking the
CC first and second polypeptide chains. The resulting single chain
CC polypeptide can be used in diagnostics, therapy
CC (in vivo and in vitro), imaging, purifications and biosensors.
CC This particular single chain binding molecule was designated TRV40
CC and contains two linker peptides.

XX Sequence 225 AA;

Query Match 83.0%; Score 44; DB 14; Length 225;
Best Local Similarity 80.0%; Pred. No. 0.14;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:| | |
Db 68 gftfisygms 77

RESULT 11

R99645
ID R99645 standard; Protein: 225 AA.

XX R99645;
AC 11-OCT-1996 (first entry)
DT Single chain binding molecule TRV40.
DE
XX
KW Antibody engineering; single polypeptide chain binding molecule;
KW heavy chain; light chain; monoclonal antibody; MAb;
KW bovine growth hormone; bGH; immunoaffinity purification; TRV40.
XX
OS Chimeric Mus sp.;
OS Chimeric synthetic.
XX
XX Key Location/Qualifiers
FT Domain 2..42
FT /label= L-chain
FT /note= "MAB 3C2 VL amino acids 1-41"
FT Region 43..49
FT /label= Linker
FT /note= "linker derived from MCPC-603"
FT Domain 50..157
FT /label= H-chain
FT /note= "MAB 3C2 VH amino acids 8-105"
FT Region 158..160
FT /label= Linker
FT /note= "linker derived from MCPC-603 Fv region"
FT Domain 161..225
FT /label= L-chain
FT /note= "MAB 3C2 VL amino acids 45-109"
XX
XX US5534621-A.
XX
XX 09-JUL-1996.
XX
XX 02-SEP-1986; 86US-0902971.
XX
XX 19-JAN-1989; 89US-0299617.
XX 02-SEP-1986; 86US-0902971.
XX 02-SEP-1987; 87US-0092110.
XX 25-APR-1990; 90US-0512910.
XX 01-APR-1993; 93US-0040440.
XX 06-JUN-1995; 95US-0468992.
XX (ENZO-) ENZON LABS INC.
XX
XX Bird RE, Hardman K, Ladner RC;
XX
XX WPI: 1996-333309/33.
XX N-PSDB; T13735.
XX
XX Immuno:purific. using single binding chain molecule including
XX antigen-binding parts of antibody light and heavy chain variable
XX regions connected by a linker - is smaller, stabler and less
XX expensive than complete antibodies
XX
XX Example 1; Fig 24; 78pp; English.
XX
XX A novel single chain binding molecule (R99645), designated TRV40,
XX is a 2-linker construction incorporating VL and VH regions from
XX 19G1 anti-bovine growth hormone mouse IgG1 monoclonal antibody 3C2,
XX and peptide linkers from the Fv region of the IgA anti-phosphoryl
XX choline myeloma antibody MCPC-603. The single chain binding
XX molecule was expressed in E.coli transformants carrying pGX3776,
XX which incorporates encoding DNA (T13735), at a level of 7-2% of total
XX cell protein. Single chain binding molecules (see also R99646-51)
XX retain the binding specificity and affinity of the light and heavy
XX chain aggregate variable region of the native antibody but have the
XX advantages of smaller size, greater stability and reduced cost.
XX
XX Sequence 225 AA;

Query Match 83.0%; Score 44; DB 17; Length 225;

Best Local Similarity 80.0%; Pred. No. 0.14; Length 225;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
| | | | : | | |
DB 68 gftflsygms 77

RESULT 12

R06479
ID R06479 standard; protein; 236 AA.

XX
AC R06479;

XX 07-JAN-1991 (first entry)

XX TRY61.

KW Monoclonal antibody; variable chain anti-bovine growth hormone; ss.

XX Mus musculus.

XX Key Location/Qualifier
XX Region 2..105
XX FT /label= LCVR(1-104)
XX FT 106..119
XX FT /label= linker
XX FT 120..235
XX FT /label= HCVR(7-123)

XX US4946778-A.

XX 07-AUG-1990.

XX 19-JAN-1989; 89US-0299617.

XX 19-JAN-1989; 89US-0299617.

XX 02-SEP-1986; 86US-0902971.

XX 02-SEP-1987; 87US-0092110.

XX (GENE-) GENEX CORP.

XX Ladner RC, Bird RE, Hardman K;

XX WPI: 1990-260350/34.

XX N-PSDB; Q05711.

XX Single polypeptide chain binding molecules - having light chain variable region of antibody linked by peptide to heavy chain variable region.

XX Disclosure; Fig 26; 68pp; English.

XX The sequence was constructed from the variable regions of a MAB produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain and kappa light chain. The sequence encodes a single chain binding molecule comprising the variable regions of heavy and light chains linked by a peptides. The variable region of each DNA chain was prep'd. by introducing a ClaI site and an initiation codon (atcgatg) prior to the first codon of the mature sequence and a HindIII site and termination codon (taagctt) after codon 123 (heavy chain) or 109 (light chain). The plasmids constructed to contain these portions were pGX3772 and pGX3773 (heavy and light resp.). TRY61 was carried on plasmid pGX4904. The polypeptide has the following polypeptide structure:
Met-[LCVR(1-104)]-V-R-G-S-P-A-I-N-V-A-V-H-V-F-[HCVR(7-123)]
See also R06476-84.

XX Sequence 236 AA;

Query Match

83.0%; Score 44; DB 11; Length 236;

Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
| | | | : | | |
DB 139 gftflsygms 148

RESULT 13

R43676

ID R43676 standard; Protein; 236 AA.

XX AC R43676;

XX 23-MAY-1994 (first entry)

XX Single chain polypeptide with affinity for bovine growth hormone.

XX Monoclonal antibody; MAB; affinity; binding; antigen; diagnostics; therapy; imaging; purification; biosensors.

XX OS Synthetic.

XX US5260203-A.

XX 09-NOV-1993.

XX 02-SEP-1986; 86US-0902971.

XX 02-SEP-1986; 86US-0902971.

XX 02-SEP-1987; 87US-0092110.

XX 19-JAN-1989; 89US-0299617.

XX 25-APR-1990; 90US-0512910.

XX (ENZO-) ENZON INC.

XX Bird RE, Hardman K, Ladner RC;

XX WPI: 1993-367875/46.

XX N-PSDB; Q51537.

XX Single chain polypeptide for binding antigen - comprising light and heavy chain antigen binding portions linked by peptide linker

XX Example 2; Figure 26; 78pp; English.

XX The single chain polypeptide is derived from the mature light and heavy chains of a mouse monoclonal antibody (MAB) and has affinity for a given antigen (Bovine growth hormone). It comprises a first polypeptide comprising the antigen binding portion of of the light chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable region of an antibody and at least one peptide linker linking the first and second polypeptide chains. The resulting single chain polypeptide can be used in diagnostics, therapy (in vivo and in vitro), imaging, purifications and biosensors. This particular single chain binding molecule was designated TRY61 and contains one linker peptide.

XX Sequence 236 AA;

Query Match

83.0%; Score 44; DB 14; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
| | | | : | | |
DB 139 gftflsygms 148

RESULT 14

W02188

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ID W02188 standard; Protein; 236 AA.
XX AC W02188;
XX DT 13-NOV-1996 (first entry)
XX DE TRY61 single chain binding protein.
XX KW Antibody engineering; monoclonal antibody; MAB;
KW single chain antibody; immunoassay; bovine growth hormone; BGH;
KW TRY61; single chain binding protein.
XX OS Chimeric Mus musculus;
OS Chimeric synthetic.
XX FH Key Location/Qualifiers
FT Domain 2..105
FT /label= L-chain
FT /note= "MAB light chain aal-104"
FT Region 106..119
FT /label= Linker
FT Domain 120..236
FT /label= H-chain
FT /note= "MAB heavy chain aa7-123"
XX PN US518889-A.
XX PD 21-MAY-1996.
XX PF 02-SEP-1986; 86US-0902971.
XX PR 19-JAN-1989; 89US-0299617.
XX PR 02-SEP-1986; 86US-0902971.
XX PR 02-SEP-1987; 87US-0092110.
XX PR 25-APR-1990; 90US-0512910.
XX PR 01-APR-1993; 93US-0040440.
XX PR 06-JUN-1995; 95US-0468988.
XX PA (ENZO-) ENZON LABS INC.
XX PI Bird RE, Hardman K, Ladner RC;
XX N-PSDB; T36460.
XX PT Immunoassay using single chain antigen binding mol. - as replacement
PT for labelled or immobilised antibody, are less immunogenic, easier
PT to engineer, more stable and less expensive
XX PS Example 2; Fig 26; 78pp;
XX CC Computer-designed single chain antigen binding molecule TRY61
CC (W02188), encoded by the DNA sequence given in T36460, has the
CC formula Met-(L-chain 1-104)-linker-(H-chain 7-123). The L (light)
CC and H (heavy) chains are from a murine monoclonal antibody (see also
CC R97377 and R97376) specific for bovine growth hormone (BGH). Plasmid
CC PGX3772 (contg. the heavy chain variable region) was cloned into
CC PGX3773 (contg. the light chain sequence) with 2 synthetic
CC oligonucleotides that encoded the linker. The resulting plasmid was
CC inserted into vector PGX3703 and introduced into E. coli. TRY61 was
CC expressed at over 2% of total cellular protein. It was able to
CC bind BGH as effectively as the original monoclonal antibody.
XX SQ Sequence 236 AA;

Query Match 83.0%; Score 44; DB 17; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 139 gftflsydms 148

```

```

RESULT 15
R99646
ID R99646 standard; Protein; 236 AA.
XX AC R99646;
XX DT 11-OCT-1996 (first entry)
XX DE Single chain binding molecule TRY61.
XX KW Antibody engineering; single polypeptide chain binding molecule;
KW heavy chain; light chain; monoclonal antibody; MAB;
KW bovine growth hormone; BGH; immunoaffinity purification; TRY61.
XX OS Chimeric Mus sp.
OS Chimeric synthetic.
XX FH Key Location/Qualifiers
FT Domain 2..105
FT /label= L-chain
FT /note= "MAB 3C2 VL amino acids 1-104"
FT Region 106..119
FT /label= Linker
FT /note= "linker derived from MCPC-603"
FT Domain 120..236
FT /label= H-chain
FT /note= "MAB 3C2 VH amino acids 7-123"
XX PN US534621-A.
XX PD 09-JUL-1996.
XX PF 02-SEP-1986; 86US-0902971.
XX PR 19-JAN-1989; 89US-0299617.
XX PR 02-SEP-1986; 86US-0902971.
XX PR 02-SEP-1987; 87US-0092110.
XX PR 25-APR-1990; 90US-0512910.
XX PR 01-APR-1993; 93US-0040440.
XX PR 06-JUN-1995; 95US-0468992.
XX PA (ENZO-) ENZON LABS INC.
XX PI Bird RE, Hardman K, Ladner RC;
XX N-PSDB; T13736.
XX PT Immuno:purificn. using single binding chain molecule including
PT antigen-binding parts of antibody light and heavy chain variable
PT regions connected by a linker - is smaller, stabler and less
XX expensive than complete antibodies
XX PS Example 2; Fig 26; 78pp; English.
XX CC A novel single chain binding molecule (R99646), designated TRY61,
CC incorporates VL and VH regions from IgG1 anti-bovine growth hormone
CC mouse IgG1 monoclonal antibody 3C2, and a peptide linker from the Fv
CC region of the IgA anti-phosphorylcholine myeloma antibody MCPC-603.
CC The single chain binding molecule was expressed in E.coli transformants
CC carrying pGX4904, which incorporates encoding DNA (T13736), at a level
CC of below 2.0% of total cell protein. Single chain binding molecules
CC (see also R99645 and R99647-51) retain the binding specificity and
CC affinity of the aggregate of the original light and heavy chains of
CC the variable region of the antibody but have the advantages of
XX smaller size, greater stability and reduced cost.
XX SQ Sequence 236 AA;

Query Match 83.0%; Score 44; DB 17; Length 236;

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Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFTFLSYDMS 10
 ||||:||||
Db 139 gftflsygms 148

Search completed: March 28, 2001, 06:34:32
Job time: 512 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:09 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GPTFLSYDMS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	83.0	128	1	US-08-478-039-73
2	44	83.0	128	1	US-08-478-039-73
3	44	83.0	128	1	US-08-476-349A-73
4	44	83.0	128	1	US-08-476-349A-102
5	44	83.0	225	5	5455030-5
6	44	83.0	236	5	5455030-7
7	44	83.0	247	5	5455030-9
8	44	83.0	447	5	5455030-1
9	42	79.2	239	2	US-07-956-399-4
10	42	79.2	247	4	PCT-US94-07659-2
11	41	77.4	119	4	PCT-US94-07659-6
12	41	77.4	123	1	US-08-478-039-71
13	41	77.4	123	1	US-08-478-039-104
14	41	77.4	123	1	US-08-476-349A-71
15	41	77.4	123	1	US-08-476-349A-104
16	40	75.5	98	2	US-08-665-202-31
17	40	75.5	116	3	US-08-545-809A-101
18	40	75.5	116	3	US-08-983-607-36
19	40	75.5	122	1	US-08-276-852-80
20	40	75.5	122	1	US-08-899-575-80
21	40	75.5	122	1	US-08-899-575-80
22	40	75.5	122	4	PCT-US95-08743-80
23	40	75.5	123	2	US-08-665-202-30
24	40	75.5	124	3	US-08-983-607-47
25	40	75.5	239	2	US-08-553-497A-18
26	39	73.6	35	2	US-08-765-179B-1
27	39	73.6	98	2	US-08-428-197-48
28	39	73.6	98	4	PCT-US93-10555-48

Sequence 65, Appl
Sequence 117, App
Sequence 6, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 109, App
Sequence 46, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 43, Appl
Sequence 38, Appl

29 39 73.6 102 2 US-08-273-146-65
30 39 73.6 110 1 US-08-211-202-117
31 39 73.6 113 3 US-08-974-899-6
32 39 73.6 116 4 US-08-428-197-2
33 39 73.6 116 4 PCT-US93-10555-2
34 39 73.6 117 3 US-08-545-809A-109
35 39 73.6 117 3 US-08-983-607-46
36 39 73.6 118 2 US-08-652-816A-12
37 39 73.6 118 4 PCT-US93-08435-10
38 39 73.6 121 1 US-08-339-582-2
39 39 73.6 122 2 US-07-934-373C-21
40 39 73.6 122 3 US-08-437-642B-21
41 39 73.6 122 4 PCT-US93-07832-21
42 39 73.6 122 4 PCT-US93-08435-12
43 39 73.6 122 4 PCT-US93-08435-14
44 39 73.6 122 4 PCT-US93-08435-43
45 39 73.6 123 2 US-08-428-197-38

ALIGNMENTS

RESULT 1
US-08-478-039-73
; Sequence 73, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 26 GFTFSSYDMN 35

RESULT 2
US-08-478-039-102
; Sequence 102, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

COMPUTER READABLE FORM:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #40

US-08-478-039-102

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 26 GFTFSSYDMN 35

RESULT 3
US-08-476-349A-73
; Sequence 73, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

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SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.19;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
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Db 26 GFTFSSYDMN 35

RESULT 4
US-08-476-349A-102
; Sequence 102, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40

Query Match 83.0%; Score 44; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
 |||||
Db 26 GFTFSSYDMN 35

RESULT 5
5455030-5
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 5:
; LENGTH: 225
5455030-5

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Best Local Similarity 80.0%; Pred. No. 0.34;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
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Db 68 GFTFISYGMS 77

RESULT 6
5455030-7
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 7:
; LENGTH: 236
5455030-7

Query Match 83.0%; Score 44; DB 5; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.36;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
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Db 138 GFTFISYGMS 147

RESULT 7
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; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN

; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 9:
; LENGTH: 247
5455030-9

Query Match 83.0%; Score 44; DB 5; Length 247;
Best Local Similarity 80.0%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||:||||
Db 150 GFTFISYGMS 159

RESULT 8
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; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 1:
; LENGTH: 447
5455030-1

Query Match 83.0%; Score 44; DB 5; Length 447;
Best Local Similarity 80.0%; Pred. No. 0.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||:||||
Db 25 GFTFISYGMS 34

RESULT 9
US-07-956-399-4
; Sequence 4, Application US/07956399
; Patent No. 5876717
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: TAKI, SHINSUKE
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
; CHAINS OF IL-2 RECEPTORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,399
; FILING DATE: 19921005
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5876717man P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-586-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-956-399-4

Query Match 79.2%; Score 42; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
|||:||||
Db 148 GFAFSSYDMS 157

RESULT 10
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/090,534
;; FILING DATE: 09-JUL-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50171-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610) 270-5024
;; TELEFAX: (610) 270-5090
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 247 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 79.28; Score 42; DB 4; Length 247;
Best Local Similarity 80.08; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||| |
Db 45 GFAFSSYDMS 54

RESULT 11
PCT-US94-07659-6
;; Sequence 6, Application PC/TUS9407659
;; GENERAL INFORMATION:
;; APPLICANT: Young, Peter
;; APPLICANT: Gross, Mitchell
;; APPLICANT: Jonak, Zdenka L.
;; APPLICANT: Theisen, Timothy
;; APPLICANT: Hurlie, Mark
;; APPLICANT: Jackson, Jeffrey R.
;; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
;; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
;; TITLE OF INVENTION: Disorders in Man
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation - Corp.
;; ADDRESSEE: Intellectual Property
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-2799
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/07659
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/090,534
;; FILING DATE: 09-JUL-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50171-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610) 270-5024
;; TELEFAX: (610) 270-5090
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid

;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 77.4%; Score 41; DB 4; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||| |
Db 26 GFISSYDMS 35

RESULT 12
US-08-478-039-71
;; Sequence 71, Application US/08478039
;; Patent No. 5681722
;; GENERAL INFORMATION:
;; APPLICANT: Newman, Roland A.
;; APPLICANT: Hanna, Nabil
;; APPLICANT: Raab, Ronald W.
;; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
;; NUMBER OF SEQUENCES: 114
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;; STREET: 699 Prince St.
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/478,039
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/379,072
;; FILING DATE: 25-JAN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/912,292
;; FILING DATE: 10-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/856,281
;; FILING DATE: 23-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/735,064
;; FILING DATE: 25-JUL-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin Esq., Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-160
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 123 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; ORIGINAL SOURCE:
;; ORGANISM: Monkey
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT: VH3 clone 3-34
US-08-478-039-71

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFSTDYDMT 35

RESULT 13
US-08-478-039-104
; Sequence 104, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFSTDYDMT 35

RESULT 14
US-08-476-349A-71
; Sequence 71, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH3 clone 3-34

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFSTDYDMT 35

RESULT 15

US-08-476-349A-104
; Sequence 104, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newnan, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #34
US-08-476-349A-104

Query Match 77.4%; Score 41; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
| | | | : | | |
Db 26 GFTFTYDMT 35

Search completed: March 28, 2001, 06:39:09
Job time: 763 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:49 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-54

Perfect score: 55

Sequence: 1 WVAKVSGGG 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	80.0	118	2 S20641	Ig heavy chain V r
2	43	78.2	108	2 PL0248	Ig heavy chain V r
3	43	78.2	138	2 S09258	Ig heavy chain V r
4	42	76.4	111	2 S40090	Ig heavy chain - m
5	42	76.4	111	2 PH1007	Ig heavy chain V r
6	42	76.4	113	2 S26468	Ig heavy chain V r
7	42	76.4	117	1 HVM534	Ig heavy chain pre
8	40	72.7	254	2 B31790	Ig heavy chain V r
9	39	70.9	108	2 PH1006	Ig heavy chain V r
10	39	70.9	117	1 HVM584	Ig heavy chain pre
11	39	70.9	121	2 H27888	Ig heavy chain V r
12	39	70.9	123	2 G27888	Ig heavy chain V r
13	39	70.9	391	2 B83203	arginate o-acetyl
14	39	70.9	408	2 D70549	hypothetical prote
15	38	69.1	92	2 S56009	Ig heavy chain var
16	38	69.1	92	2 S56008	Ig heavy chain var
17	38	69.1	97	1 HVM591	Ig heavy chain V r
18	38	69.1	112	2 S26327	Ig heavy chain V r
19	38	69.1	121	2 H27887	Ig heavy chain V r
20	38	69.1	128	2 PH0094	Ig heavy chain V r
21	38	69.1	128	2 PH0095	Ig kappa chain V r
22	38	69.1	194	2 H83060	peptidyl-trRNA hydr
23	38	69.1	509	2 C49094	methylmalonyl-CoA
24	37	67.3	83	2 C25913	Ig heavy chain V r
25	37	67.3	108	2 PH1010	Ig heavy chain V r
26	37	67.3	108	2 PH1011	Ig heavy chain V r
27	37	67.3	114	2 PH1009	Ig heavy chain V r
28	37	67.3	117	1 HVM557	Ig heavy chain pre
29	37	67.3	118	2 PH0096	Ig heavy chain V r

30	37	67.3	118	2 PH0097	Ig heavy chain V r
31	37	67.3	119	2 F27888	Ig heavy chain V r
32	37	67.3	120	2 S55536	Ig heavy chain V r
33	37	67.3	120	2 S55537	Ig heavy chain V r
34	37	67.3	121	2 B27888	Ig heavy chain V r
35	37	67.3	121	2 I27887	Ig heavy chain V r
36	37	67.3	121	2 D27888	Ig heavy chain V r
37	37	67.3	121	2 A27888	Ig heavy chain V r
38	37	67.3	122	2 E27888	Ig heavy chain V r
39	37	67.3	123	2 S63597	Ig heavy chain, v
40	37	67.3	124	2 C27888	Ig heavy chain V r
41	37	67.3	124	2 I27888	Ig heavy chain V r
42	37	67.3	137	2 S78054	Ig heavy chain pre
43	37	67.3	186	2 T29117	hypothetical prote
44	37	67.3	238	2 T04166	thamatin-like pro
45	37	67.3	256	2 S11878	chlorophyll a/b-b1

ALIGNMENTS

RESULT 1

S20641

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20641

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re

A:Reference number: S20639

A:Accession: S20641

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <LOS>

A:Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 44; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. NO. 0.76;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

DB 47 WVAIISSGGG 56

RESULT 2

PL0248

Ig heavy chain V region (anti-DNA, Dp12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0248

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0248

A:Molecule type: mRNA

A:Residues: 1-108 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-24/Region: framework 1

F:9-92/Domain: immunoglobulin homology <IMM>

F:25-29/Region: complementarity-determining 1

F:30-43/Region: framework 2

F:44-60/Region: complementarity-determining 2

F:61-92/Region: framework 3

F:93-99/Region: complementarity-determining 3

F:100-108/Region: framework 4

Query Match 78.2%; Score 43; DB 2; Length 108;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 41 WVAITSSGGG 50

RESULT 3

S09258
 Ig heavy chain V region precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
 C:Accession: S09258

R:Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK
 A:Reference number: S09258; MUID:90245594

A:Accession: S09258

A:Molecule type: DNA

A:Residues: 1-138 <HAM>

A:Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 43; DB 2; Length 138;
 Best Local Similarity 70.0%; Pred. No. 1.3;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 66 WVAITSSGGG 75

RESULT 4

S40090
 Ig heavy chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S40090

R:Water, C.C.; Galin, F.S.; Jarpe, M.A.; Jackson, P.; Krishna, N.R.; Gautam, A.M.; Zhou,
 submitted to the EMBL Data Library, December 1993

A:Description: A V-lambda x-bearing monoclonal antibody with similar specificity and seq

A:Reference number: S40090

A:Accession: S40090

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-111 <MAI>

A:Cross-references: EMBL:X76751; NID:g435680; PIDN:CAA54154.1; PID:g1334154

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 111;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 39 WVAATKSNNGG 48

RESULT 5

PH1007

Ig heavy chain V region (clone 163-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1007

R:Tillman, D.M.; Joo, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1007

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 111;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 47 WVAITSSGGG 56

RESULT 6

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 1.7;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 ||| : ||||
 Db 43 WVAITSSGGG 52

RESULT 7

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A>Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 42; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 66 WVAISSGGG 75

RESULT 8

Ig heavy chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C:Accession: B31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Willson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an anti-
A:Reference number: A92886; MUID:89034213
A:Accession: B31790
A:Molecule type: mRNA
A:Residues: 1-254 <SCH>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 40; DB 2; Length 254;
Best Local Similarity 60.0%; Pred. No. 8.1;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 47 WVAISSGGG 56

RESULT 9

PH1006
Ig heavy chain V region (clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1006
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 108;
Best Local Similarity 60.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 42 WVAISSGGG 51

RESULT 10

HVMS84
Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0505
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
A:Reference number: JT0501; MUID:89279149
A:Accession: JT0505
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 70.9%; Score 39; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 66 WVAISSGGG 75

RESULT 11

H27888
Ig heavy chain V region (H37-40) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: H27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: H27888
A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 121;
Best Local Similarity 66.7%; Pred. No. 6.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 9
||| : ||||
Db 47 WVAISSGGG 55

RESULT 12

G27888
Ig heavy chain V region (H28-A2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: G27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: G27888
A:Molecule type: DNA
A:Residues: 1-123 <CAT>

A:Experimental source: strain Balb/c
 A:Note: this sequence was determined from the germline gene
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 123;

Best Local Similarity 66.7%; Pred. No. 6.3;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
 |||: |||
 DB 47 WVAEISSG 55

RESULT 13

B83203
 arginate o-acetyltransferase AlgJ PA3549 [imported] - Pseudomonas aeruginosa (strain PA
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
 C:Accession: B83203
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, K.R.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950
 A:Accession: B83203
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <STO>
 A:Cross-references: GB:AE004775; GB:AE004091; NID:g9949692; PIDN:AAG06937.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: algJ; PA3549

Query Match 70.9%; Score 39; DB 2; Length 391;

Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
 |||: |||
 DB 371 WVAQLKASG 380

RESULT 14

D70549
 hypothetical protein Rv0561c - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: D70549
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 .; Connor, R.; Davies, R.; Devlin, K.; Beltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: D70549
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-408 <COL>
 A:Cross-references: GB:Z95558; GB:AL123456; NID:g3261781; PIDN:CAB08972.1; PID:g2114023
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: Rv0561c
 C:Superfamily: fixC protein

Query Match 70.9%; Score 39; DB 2; Length 408;

Best Local Similarity 70.0%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
 |||: |||
 DB 386 WVARWRGGG 395

RESULT 15

S56009
 Ig heavy chain variable region against dystrophin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S56009
 R:Morris, G.E.; Nguyen, C.; Man, N.T.
 Biochem. J. 309, 355-359, 1995
 A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-ter
 A:Reference number: S56008; MUID:95344393
 A:Accession: S56009
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <MOR>
 A:Cross-references: EMBL:Z46661
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:6-86/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 38; DB 2; Length 92;

Best Local Similarity 66.7%; Pred. No. 7.3;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
 |||: |||
 DB 38 WVASISSG 46

Search completed: March 28, 2001, 06:41:50
 Job time: 873 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:46 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WVAKVSGGG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	76.4	117	1 HV55_MOUSE	P18526 mus musculus
2	40	72.7	438	1 TRPE_AERPE	Q9Y8T0 aeropyrum p
3	39	70.9	117	1 HV54_MOUSE	P18525 mus musculus
4	39	70.9	188	1 YLAI_LACAC	P29470 lactobacill
5	38	69.1	97	1 HV56_MOUSE	P18527 mus musculus
6	37	67.3	117	1 HV58_MOUSE	P18529 mus musculus
7	37	67.3	256	1 CB4B_LYCES	P27525 lycopersico
8	36	65.5	37	1 THHS_HORVU	P33045 hordeum vul
9	36	65.5	247	1 HS77_HUMAN	P48741 homo sapien
10	35.5	64.5	196	1 SODE_TETPY	P19666 tetrahymena
11	35	63.6	593	1 CSG_METFE	P27373 methanother
12	35	63.6	593	1 CSG_METSC	P27374 methanother
13	35	63.6	3432	1 POLG_JAEV1	P27395 j genome po
14	35	63.6	3432	1 POLG_JAEV5	P19110 j genome po
15	35	63.6	3432	1 POLG_JAEVJ	P32886 j genome po
16	34	61.8	121	1 NLTP_BOVIN	P07857 bos taurus
17	34	61.8	135	1 RM16_PROWI	P46751 prototheca
18	34	61.8	202	1 P21_SOYBN	P25096 glycine max
19	34	61.8	206	1 IAAT_MAIZE	P13867 zea mays (m
20	34	61.8	227	1 ZEAM_MAIZE	P33679 zea mays (m
21	34	61.8	301	1 YFE4_YEAST	P43558 saccharomyc
22	34	61.8	311	1 BLAC_STRAU	P10509 streptomyce
23	34	61.8	311	1 BLAC_STRCE	Q06650 streptomyce
24	34	61.8	547	1 NLTP_CHICK	Q07598 gallus gall
25	34	61.8	547	1 NLTP_HUMAN	P22307 homo sapien
26	34	61.8	547	1 NLTP_MOUSE	P32020 mus musculus
27	34	61.8	547	1 NLTP_RAT	P11915 rattus norv
28	34	61.8	621	1 TRPX_ARATH	P32069 arabidopsis
29	34	61.8	867	1 NIA_ASPNG	P36858 aspergillus
30	34	61.8	893	1 NIA_LEPMC	P36842 leptosphaer
31	34	61.8	905	1 NIA_FUSOX	P39863 fusarium ox
32	34	61.8	3411	1 POLG_YEFV1	P03314 y genome po
33	34	61.8	3411	1 POLG_YEFV2	P19901 y genome po

34 34 61.8 3430 1 POLG_MNVV p06935 w genome po
35 34 61.8 3433 1 POLG_KUNJM p14335 k genome po
36 33 60.0 98 1 HV57_MOUSE p18528 mus musculus
37 33 60.0 122 1 MPP2_PHLPR p43214 phleum prat
38 33 60.0 137 1 RL16_SPICI o31162 spiroplasma
39 33 60.0 138 1 RL16_MYCBO o06049 mycobacteri
40 33 60.0 138 1 RL16_MYCTU p95036 mycobacteri
41 33 60.0 194 1 PTH_ECOLI p23932 escherichia
42 33 60.0 194 1 PTH_HAETN p44692 haemophilus
43 33 60.0 194 1 PTH_SALTI o60001 salmonella
44 33 60.0 234 1 RL6_MESCR p34091 mesembryant
45 33 60.0 261 1 CB4_SPIOL p36494 spinacia ol

ALIGNMENTS

RESULT 1.
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J70502; HVM534.
DR INTERPRO: IPR003006; -.
DR PFM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 345.
FT CHAIN 20 117 FRAMEWORK 1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 50 54 FRAMEWORK 2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 76.4%; Score 42; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 0.38;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 WVAKVSGGG 10
Db 66 WVAIVSGGG 75

RESULT 2
TRPE_AERPE STANDARD; PRT; 438 AA.
ID TRPE_AERPE
AC Q9Y8T0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN TRPE OR APE2553.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;

OC Aeropyrum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1;
 RX MEDLINE: 99310339.
 RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyana A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.:
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
 CC PYRUVATE + L-GLUTAMATE.
 CC -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
 CC -!- SUBUNIT: Tetramer of two components I and two components II (by
 CC similarity).
 CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
 CC USING AMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
 CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AP000064; BAA81570.1; ALT_INIT.
 DR INTERPRO: IPR000350; -;
 DR PFAM: PF00425; chorismate_bind; 1.
 DR PRINTS: PR00095; ANTSNTHASE1.
 KW Tryptophan biosynthesis; Lysase.
 SQ SEQUENCE 438 AA; 48309 MW; 16559013EFDFAED CRC64;

Query Match 72.7%; Score 40; DB 1; Length 438;
 Best Local Similarity 60.0%; Pred. No. 3.5;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WVAKVSGGG 10
 I : : : : :
 DB 39 WIALESGGG 48

RESULT 3
 HV54_MOUSE
 ID HV54_MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC [1]
 RP SEQUENCE FROM N.A.
 RN STRAIN-BALB/CJ;
 RC MEDLINE: 89279149.
 RX Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RA "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J70505; HVMS84.
 DR INTERPRO: IPR003006; -;
 DR PFAM: PF00047; Ig; 1.

Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 1.4;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 I : : : : :
 DB 66 WVAISNGGG 75

RESULT 4
 YLAI_LACAC
 ID YLAI_LACAC STANDARD; PRT; 188 AA.
 AC P29470;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN IAF 5'REGION (ORF1) (FRAGMENT).
 OS Lactobacillus acidophilus.
 OG Plasmid pTRK160.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 CC Lactobacillus.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-11088;
 RC MEDLINE: 94113718.
 RA Fremaux C., Ahn C., Kjaerhammer T.R.;
 RT "Molecular analysis of the lactacin F operon.";
 RL Appl. Environ. Microbiol. 59:3906-3915(1993).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M57961; AAA16635.1; -;
 DR Hypothetical protein; Plasmid.
 KW NON_TER 1 1
 FT SEQUENCE 188 AA; 21073 MW; D7A1FABE073C1081 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 188;
 Best Local Similarity 70.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 I : : : : :
 DB 70 WVAHVDOGGG 79

RESULT 5
 HV56_MOUSE
 ID HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 914.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0504; HVM591.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 KW Immunoglobulin V region.
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33PF55DA893 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 97;
 Best Local Similarity 66.7%; Pred. No. 1.8;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
 ||| : |||
 Db 47 WVASISSGG 55

RESULT 6
 HV58_MOUSE
 ID HV58_MOUSE STANDARD; PRT; 117 AA.
 AC P18529;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JT0506; HVM557.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 67.3%; Score 37; DB 1; Length 117;
 Best Local Similarity 66.7%; Pred. No. 3.4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
 ||| : |||
 Db 66 WVASISSGG 74

RESULT 7
 CB4B_LYCES
 ID CB4B_LYCES STANDARD; PRT; 256 AA.
 AC P27525;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR (CAB-10B)
 DE (LHCP).
 GN CAB10B.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Solanum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91355849.
 RA Schwartz E., Pichersky E.;
 RT "Sequence of two tomato nuclear genes encoding chlorophyll
 a/b-binding proteins of CP24, a PSII antenna component.";
 RL Plant Mol. Biol. 15:157-160(1990).
 CC -1- SIMILARITY: TO A FAMILY OF PROTEINS INCLUDING THE CP24/CP29, THE
 CAB I/II AND ELIP (EARLY LIGHT-INDUCIBLE PROTEINS) PROTEINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M32606; AAA34146.1; -.
 DR PIR: S11878; S11878.
 DR INTERPRO: IPR001344; -.
 DR PFAM: PF00504; chloroa_b-bind; 1.
 KW Chlorophyll; Photosynthesis; Photosystem II; Thylakoid membrane;
 KW Chloroplast; Transit peptide; Transmembrane.
 FT TRANSIT 1 45 CHLOROPLAST (POTENTIAL).
 FT CHAIN 46 256 CHLOROPHYLL A-B BINDING PROTEIN CP24 10B.
 SQ SEQUENCE 256 AA; 27470 MW; 3332556486496726 CRC64;

Query Match 67.3%; Score 37; DB 1; Length 256;
 Best Local Similarity 66.7%; Pred. No. 7.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
 | : |||||
 Db 55 WIPAVKSGG 63

RESULT 8
 THHS_HORVU
 ID THHS_HORVU STANDARD; PRT; 37 AA.
 AC P33045;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE ANTIFUNGAL PROTEIN S (FRAGMENT).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. BOMI RISO 1508;
 RX MEDLINE; 92037994.
 RA Hejgaard J., Jacobsen S., Svendsen I.;
 RT "Two antifungal thaumatin-like proteins from barley grain.";
 RL FEBS Lett. 291:127-131(1991).
 CC -1- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS THE GROWTH OF
 TRICHODERMA VIRIDAE AND CANDIDA ALBICANS.

CC -1- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.

DR PIR; S17684; S17684.

DR HSP; P25871; 1AUN.

DR INTERPRO; IPR001938; -

DR PRAM; PF00314; thaumat; 1. PARTIAL.

DR PROSITE; PS00316; THAUMATIN; PARTIAL.

KW Fungicide.

FT NON_TER 37 37

SQ SEQUENCE 37 AA; 3871 MW; 7BE164CCB8A9881 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 37;

Best Local Similarity 60.0%; Pred. No. 1.6;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAVKSGGG 10

Db 14 WAAAVPAGGG 23

RESULT 9

HS77_HUMAN

ID HS77_HUMAN STANDARD; PRT; 247 AA.

AC P48741; P19790;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE HEAT SHOCK 70 KDA PROTEIN 7 (HEAT SHOCK 70 KDA PROTEIN B) (FRAGMENT).

GN HSPA7 OR HSP70B.

OS Homo sapiens (HUMAN).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

RN [1]

RX SEQUENCE FROM N.A.

RX MEDLINE; 85270444.

RA Voellmy R., Ahmed A., Schiller P., Bromley P., Rungger D.;

RT "Isolation and functional analysis of a human 70,000-dalton heat

shock protein gene segment.";

RL Proc Natl. Acad. Sci. U.S.A. 82:4949-4953(1985).

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

CC -----

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CC -----

DR EMBL; M11236; AAA52696.1; -

DR PIR; A25773; A25773.

DR HSP; P19120; IMG1.

DR MIM; 140556; -

DR INTERPRO; IPR001023; -

DR PRAM; PF00012; HSP70.1;

DR PROSITE; PS00297; HSP70.1; 1.

DR PROSITE; PS00329; HSP70.2; 1.

DR PROSITE; PS01036; HSP70.3; PARTIAL.

KW ATP-binding; Heat shock; Multigene family.

FT NON_TER 247 247

SQ SEQUENCE 247 AA; 26906 MW; 354EE237F6750DD7 CRC64;

Query Match

Best Local Similarity 65.5%; Score 36; DB 1; Length 247;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAVKSGGG 10

Db 92 WPFVVS GGG 101

RESULT 10

SODF_TETPY

ID SODF_TETPY STANDARD; PRT; 196 AA.

AC P19666;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE SUPEROXIDE DISMUTASE [FE] (EC 1.15.1.1).

OS Tetrahymena pyriformis.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;

OC Tetrahymenina; Tetrahymena.

RN [1]

RX SEQUENCE.

RX MEDLINE; 91009226.

RA Barra D., Schinina M.E., Bossa F., Puget K., Durosay P., Guissani A.,

RA Michelson A.M.;

RT "A tetrameric iron superoxide dismutase from the eucaryote

Tetrahymena pyriformis.";

RL J. Biol. Chem. 265:17680-17687(1990).

CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE

CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.

CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).

CC -1- COFACTOR: THE TETRAMER CONTAINS 2.5 G ATOMS OF FERRIC IRON.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE

FAMILY.

DR PIR; A39223; A39223.

DR HSP; P04179; 1MSD.

DR INTERPRO; IPR001189; -

DR PFAM; PF00081; sodfe; 1.

DR PROSITE; PS00088; SOD_MN; 1.

KW Oxidoreductase; Iron.

FT METAL 20 20

FT METAL 68 68

FT METAL 157 157

FT METAL 161 161

FT SEQUENCE 196 AA; 22657 MW; FC1F2F67893D8DC7 CRC64;

Query Match

Best Local Similarity 53.3%; Score 35.5; DB 1; Length 196;

Matches 8; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

Qy 1 WV-----AKVKSGGG 10

Db 69 WYWDNLAPVKSGGG 83

RESULT 11

CSG_METFE

ID CSG_METFE STANDARD; PRT; 593 AA.

AC P27373;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CELL SURFACE GLYCOPROTEIN PRECURSOR (S-LAYER PROTEIN).

GN SLGA.

OS Methanothermus fervidus.

OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;

OC Methanothermus.

RN [1]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 23-42.

RC STRAIN-DSM 2088 / V24S;

RX MEDLINE; 91293115.

RA Broeckl G., Behr M., Fabry S., Hensel R., Kaudewitz H., Biendl E.,

RA Koenig H.;

RT "Analysis and nucleotide sequence of the genes encoding the surface-

layer glycoproteins of the hyperthermophilic methanogens

Methanothermus fervidus and Methanothermus sociabilis.";

RL Eur. J. Biochem. 199:147-152(1991).

RN [2]

RP CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE; 94086483

RA Karcher U., Schroder H., Haslinger E., Allmaier G., Schreiner R.,

RA *Leland F., Haselbeck A., Konig H.;
 RT "Primary structure of the heterosaccharide of the surface glycoprotein
 of Methanothermobacter ferrooxidans";
 RL J. Biol. Chem. 268:26821-26826(1993).
 CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
 OF PROTEINS WHICH COAT THE SURFACE OF THE CELL.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS ARCHAEA IS COVERED BY A
 S-LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- PTM: PROTEIN CONTAINS ABOUT 10 N-LINKED GLYCANS WHICH CONSIST OF
 METHYL-MAN, MAN AND GALNAC RESIDUES IN A MOLAR RATIO OF 2:3:1.
 CC -----
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 CC -----
 DR EMBL; X58297; CAAM1230.1; -
 DR PIR; S16225; S16225.
 KW Glycoprotein; Cell wall; S-layer; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 593 CELL SURFACE GLYCOPROTEIN.
 FT CARBOHYD 29 29 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 58 58 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 326 326 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 500 500 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT CARBOHYD 516 516 N-LINKED (GALNAC. . .) (POTENTIAL).
 FT SEQUENCE 593 AA; 65481 MW; E064669967B7611C CRC64;

Query Match 63.6%; Score 35; DB 1; Length 593;
 Best Local Similarity 60.0%; Pred. No. 42;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVSGGG 10
 : : | | | |
 DB 228 YIANVSSGGG 237

RESULT 12
 CSG_METSC

ID CSG_METSC STANDARD; PRT; 593 AA.
 AC P27374;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELL SURFACE GLYCOPROTEIN PRECURSOR (S-LAYER PROTEIN).
 GN SLGA.
 OS Methanothermobacter sociabilis.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;
 OC Methanothermobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 3496 / KF1-FL;
 RX MEDLINE: 91293115
 RA Broeckl G., Behr M., Fabry S., Hensel R., Kaudewitz H., Blendl E.,
 RA Koenig H.;

RT "Analysis and nucleotide sequence of the genes encoding the surface-
 layer glycoproteins of the hyperthermophilic methanogens
 Methanothermobacter ferrooxidans and Methanothermobacter sociabilis";
 RL Eur. J. Biochem. 199;147-152(1991).
 CC -1- SUBUNIT: ASSEMBLE INTO MONO-LAYERED CRYSTALLINE ARRAYS.
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -----
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 CC -----
 DR EMBL; X58296; CAAM1229.1; -
 DR PIR; S16375; S16375.
 KW Glycoprotein; Cell wall; S-layer; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 593 CELL SURFACE GLYCOPROTEIN.
 FT CARBOHYD 29 29 N-LINKED (POTENTIAL).
 FT CARBOHYD 58 58 N-LINKED (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (POTENTIAL).
 FT CARBOHYD 326 326 N-LINKED (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (POTENTIAL).
 FT CARBOHYD 500 500 N-LINKED (POTENTIAL).
 FT CARBOHYD 516 516 N-LINKED (POTENTIAL).
 FT SEQUENCE 593 AA; 65503 MW; DFCDFB357E10F2EB CRC64;

Query Match 63.6%; Score 35; DB 1; Length 593;
 Best Local Similarity 60.0%; Pred. No. 42;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVSGGG 10
 : : | | | |
 DB 228 YIANVSSGGG 237

RESULT 13
 POLG_JAEV1 STANDARD; PRT; 3432 AA.
 ID POLG_JAEV1 STANDARD; PRT; 3432 AA.
 AC P27395; Q82920; Q82921; Q82922; Q82923; Q82924; Q82925; Q82926;
 AC Q82927; Q82928;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
 PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
 DE PROTEINS NS1, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
 DE RNA POLYMERASE (EC 2.7.7.48) (NS5)].
 OS Japanese encephalitis virus (strain SA-14).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OC [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90320126.
 RA Nitayaphan S., Grant J.A., Chang G.J.J., Trent D.W.;
 RT "Nucleotide sequence of the virulent SA-14 strain of Japanese
 encephalitis virus and its attenuated vaccine derivative,
 SA-14-14-2.";

RL Virology 177:541-552(1990).

CC -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE

CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A

CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF

CC PROTEIN C AND MRNA.

CC -----

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CC -----

DR EMBL; M55506; AAA46248.1; -

DR EMBL; M55506; AAA46249.1; ALT_INIT.

DR PIR; A35519; GNVVJS.

DR HSSP; P14336; 1SVB.

DR INTERPRO; IPR000069; -

DR INTERPRO; IPR000208; -

DR INTERPRO; IPR000336; -

DR INTERPRO; IPR000404; -

DR INTERPRO; IPR000487; -

DR INTERPRO; IPR000752; -

DR INTERPRO; IPR001122; -

DR INTERPRO; IPR001157; -

DR INTERPRO; IPR001528; -

DR INTERPRO; IPR001850; -

DR INTERPRO; IPR002535; -

DR PFAM; PF01004; Flavi_M; 1.

DR PFAM; PF00948; Flavi_NSL; 1.

DR PFAM; PF01005; Flavi_NS2A; 1.

DR PFAM; PF01002; Flavi_NS2B; 1.

DR PFAM; PF01350; Flavi_NS4A; 1.

DR PFAM; PF01349; Flavi_NS4B; 1.

DR PFAM; PF00972; Flavi_NS5; 1.

DR PFAM; PF01003; Flavi_capsid; 1.

DR PFAM; PF00869; Flavi_glycoprot; 1.

DR PFAM; PF00949; Flavi_helicase; 1.

DR PFAM; PF01570; Flavi_propep; 1.

DR PFAM; PF01570; Flavi_helicase; 1.

KW Polypeptide; Glycoprotein; Transferase; RNA-directed RNA polymerase;

KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;

KW Transmembrane; Nonstructural

KW INIT_MET 1

FT CHAIN 1 127

FT PROPEP 128 219

FT CHAIN 220 294

FT CHAIN 295 794

FT CHAIN 795 1206

FT CHAIN 1207 1373

FT CHAIN 1374 1504

FT CHAIN 1505 2123

FT CHAIN 2124 2412

FT CHAIN 2413 2527

FT CHAIN 2528 3432

FT NP_BIND 1698 1705

FT SITE 1789 1792

FT TRANSMEM 44 60

FT TRANSMEM 112 127

FT TRANSMEM 280 294

FT TRANSMEM 774 790

FT DISULFID 297 324

FT DISULFID 354 410

FT DISULFID 368 399

FT DISULFID 386 415

FT DISULFID 484 581

FT DISULFID 598 629

FT CARBOHYD 142 142

FT CARBOHYD 448 448

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 924 924 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1001 1001 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1594 1594 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2463 2463 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2491 2491 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2761 2761 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2866 2866 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2904 2904 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 3432 AA; 380205 MW; 11B9423735B1B5FE CRC64;

Query Match 63.6%; Score 35; DB 1; Length 3432;

Best Local Similarity 50.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

DB 3026 WLSRENSGGG 3035

RESULT 14

POLG_JAEV5 STANDARD; PRT; 3432 AA;

ID POLG_JAEV5

AC P19110;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX

DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL

DE PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED

DE RNA POLYMERASE (EC 2.7.7.48) (NS5)].

OS Japanese encephalitis virus (strain SA(V)).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OC [1]

RN SEQUENCE FROM N.A.

RP MEDLINE; 91280801.

RX Aihara S., Rao C., Yu Y.X., Lee T., Watanabe K., Komiya T.,

RA Sumiyoshi H., Hashimoto H., Nomoto A.;

RT "Identification of mutations that occurred on the genome of Japanese

RL encephalitis virus during the attenuation process."

RL Virus Genes 5:95-109(1991).

CC -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE

CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A

CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF

CC PROTEIN C AND MRNA.

CC -----

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CC -----

DR EMBL; D90194; BAA14218.1; -

DR HSSP; P14336; 1SVB.

DR INTERPRO; IPR000069; -

DR INTERPRO; IPR000208; -

DR INTERPRO; IPR000336; -

DR INTERPRO; IPR000404; -

DR INTERPRO; IPR000487; -

DR INTERPRO; IPR000752; -

DR INTERPRO; IPR001122; -

DR INTERPRO; IPR001157; -

DR INTERPRO; IPR001528; -

DR INTERPRO; IPR001850; -

DR INTERPRO; IPR002535; -

DR PFAM; PF01004; Flavi_M; 1.

DR PFAM; PF00948; Flavi_NSL; 1.

DR PFAM; PF01005; Flavi_NS2A; 1.
 DR PFAM; PF01002; Flavi_NS2B; 1.
 DR PFAM; PF01350; Flavi_NS4A; 1.
 DR PFAM; PF01349; Flavi_NS4B; 1.
 DR PFAM; PF00972; Flavi_NS5; 1.
 DR PFAM; PF01003; Flavi_capsid; 1.
 DR PFAM; PF00869; Flavi_glycoprot; 1.
 DR PFAM; PF00949; Flavi_helicase; 1.
 DR PFAM; PF01570; Flavi_propep; 1.
 KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
 KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
 KW Transmembrane; Nonstructural protein.
 FT INIT_MET 1 1
 FT CHAIN 1 127
 FT PROPEP 128 219
 FT CHAIN 220 294
 FT CHAIN 295 794
 FT CHAIN 795 1206
 FT CHAIN 1207 1373
 FT CHAIN 1374 1504
 FT CHAIN 1505 2123
 FT CHAIN 2124 2412
 FT CHAIN 2413 2527
 FT CHAIN 2528 3432
 FT NP_BIND 1698 1705
 FT SITE 1789 1792
 FT TRANSMEM 44 60
 FT TRANSMEM 112 127
 FT TRANSMEM 280 294
 FT TRANSMEM 774 790
 FT DISULFID 297 324
 FT DISULFID 354 410
 FT DISULFID 368 399
 FT DISULFID 386 415
 FT DISULFID 484 581
 FT DISULFID 598 629
 FT CARBOHYD 142 142
 FT CARBOHYD 448 448
 FT CARBOHYD 924 924
 FT CARBOHYD 1001 1001
 FT CARBOHYD 2463 2463
 FT CARBOHYD 2491 2491
 SQ SEQUENCE 3432 AA; 380176 MW; AB8A63E0C00C4674 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 3432;
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
 Db 3026 WLSRENSGGG 3035
 RESULT 15
 POLG_JAEVJ STANDARD; PRT; 3432 AA.
 AC P32886; P08769;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
 DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
 DE PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
 DE RNA POLYMERASE (EC 2.7.7.48) (NS5)].
 OS Japanese encephalitis virus (strain Jaoc8982).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 88072090.
 RA Sumiyoshi H., Mori C., Fuke I., Morita K., Kuhara S., Kondou J.,

RA Kikuchi Y., Nagamatsu H., Igarashi A.,
 RT "Complete nucleotide sequence of the Japanese encephalitis virus
 RL genome RNA.";
 RN Virology 161:497-510(1987).
 RP [2].
 RP SEQUENCE OF 1-969 FROM N.A.
 RX MEDLINE; 87163522.
 RA Sumiyoshi H., Morita K., Mori C., Fuke I., Shiba T., Sakaki Y.,
 RA Igarashi A.,
 RT "Sequence of 3000 nucleotides at the 5' end of Japanese encephalitis
 RT virus RNA.";
 RL Gene 48:195-201(1986).
 CC -I- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
 CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
 CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 CC -I- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
 CC PROTEIN C AND MRNA.
 CC -----
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 CC -----
 DR EMBL; M15337; AAA46247.1; -;
 DR EMBL; M18370; AAA81554.1; -;
 DR PIR; A27403; GNVVJE.
 DR HSP; P14336; LSVB.
 DR INTERPRO; IPR000069; -;
 DR INTERPRO; IPR000208; -;
 DR INTERPRO; IPR000336; -;
 DR INTERPRO; IPR000404; -;
 DR INTERPRO; IPR000487; -;
 DR INTERPRO; IPR001122; -;
 DR INTERPRO; IPR001157; -;
 DR INTERPRO; IPR001528; -;
 DR INTERPRO; IPR001850; -;
 DR INTERPRO; IPR002535; -;
 DR PFAM; PF01004; Flavi_M; 1.
 DR PFAM; PF00948; Flavi_NS1; 1.
 DR PFAM; PF01005; Flavi_NS2A; 1.
 DR PFAM; PF01002; Flavi_NS2B; 1.
 DR PFAM; PF01350; Flavi_NS4A; 1.
 DR PFAM; PF01349; Flavi_NS4B; 1.
 DR PFAM; PF00972; Flavi_NS5; 1.
 DR PFAM; PF01003; Flavi_capsid; 1.
 DR PFAM; PF00869; Flavi_glycoprot; 1.
 DR PFAM; PF00949; Flavi_helicase; 1.
 DR PFAM; PF01570; Flavi_propep; 1.
 KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
 KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
 KW Transmembrane; Nonstructural protein.
 FT INIT_MET 1 1
 FT CHAIN 1 127
 FT PROPEP 128 219
 FT CHAIN 220 294
 FT CHAIN 295 794
 FT CHAIN 795 1206
 FT CHAIN 1207 1373
 FT CHAIN 1374 1504
 FT CHAIN 1505 2123
 FT CHAIN 2124 2412
 FT CHAIN 2413 2527
 FT CHAIN 2528 3432
 FT NP_BIND 1698 1705
 FT SITE 1789 1792
 FT TRANSMEM 44 60
 FT TRANSMEM 112 127
 FT TRANSMEM 280 294
 FT TRANSMEM 774 790
 FT DISULFID 297 324
 FT DISULFID 354 410
 FT DISULFID 368 399
 FT DISULFID 386 415
 FT DISULFID 484 581
 FT DISULFID 598 629
 FT CARBOHYD 142 142
 FT CARBOHYD 448 448
 FT CARBOHYD 924 924
 FT CARBOHYD 1001 1001
 FT CARBOHYD 2463 2463
 FT CARBOHYD 2491 2491
 SQ SEQUENCE 3432 AA; 380176 MW; AB8A63E0C00C4674 CRC64;

FT	TRANSMEM	44	60	POTENTIAL.
FT	TRANSMEM	112	127	POTENTIAL.
FT	TRANSMEM	280	294	POTENTIAL.
FT	TRANSMEM	774	790	POTENTIAL.
FT	DISULFID	297	324	BY SIMILARITY.
FT	DISULFID	354	410	BY SIMILARITY.
FT	DISULFID	368	399	BY SIMILARITY.
FT	DISULFID	386	415	BY SIMILARITY.
FT	DISULFID	484	581	BY SIMILARITY.
FT	DISULFID	598	629	BY SIMILARITY.
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	448	448	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	924	924	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1001	1001	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2463	2463	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2491	2491	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	3432 AA;	380160 MW;	EEFA26DBF54BF991 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 3432;
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 |::: ||||
 Db 3026 WLSRENSGGG 3035

Search completed: March 28, 2001, 07:29:48
 Job time: 1655 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:37 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WVAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues 374700
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	74.5	352	12 Q9IR97	Q9IR97 Japanese ir
2	39	70.9	134	8 Q9T232	Q9T232 phytophthor
3	39	70.9	342	12 Q55810	Q55810 meaban viru
4	39	70.9	391	2 Q51393	Q51393 pseudomonas
5	39	70.9	408	2 Q06427	Q06427 mycobacteri
6	38	69.1	509	2 Q57079	Q57079 vellionella
7	38	69.1	691	12 Q72120	Q72120 canine cali
8	38	69.1	907	3 Q00303	Q00303 botrytis ci
9	37	67.3	186	2 Q86545	Q86545 streptomyce
10	37	67.3	238	10 Q04364	Q04364 oryza sativ
11	37	67.3	289	2 Q9X2P4	Q9X2P4 mycobacteri
12	37	67.3	345	12 Q55828	Q55828 sepiak virus
13	37	67.3	409	2 Q54496	Q54496 streptomyce
14	37	67.3	1008	2 Q9X082	Q9X082 thermotoga
15	37	67.3	1350	10 Q04013	Q04013 volvox cart
16	37	67.3	1765	11 Q88457	Q88457 rattus norv
17	36.5	66.4	375	10 Q9XH01	Q9XH01 arabidopsis
18	36	65.5	71	10 P93234	P93234 lycopersico
19	36	65.5	171	2 Q9PMU1	Q9PMU1 campylobact

20	36	65.5	175	10	O81927	O81927 cicer ariet
21	36	65.5	225	5	P92048	P92048 periplaneta
22	36	65.5	235	5	P92047	P92047 periplaneta
23	36	65.5	303	2	Q9LCJ1	Q9LCJ1 photobacter
24	36	65.5	303	2	Q9LCJ0	Q9LCJ0 vibrio para
25	36	65.5	303	2	Q9LCI9	Q9LCI9 vibrio mari
26	36	65.5	386	5	Q9VNY4	Q9VNY4 drosophila
27	36	65.5	407	2	Q56584	Q56584 vibrio algi
28	36	65.5	411	2	O05012	O05012 haemophilus
29	36	65.5	443	10	Q9SB43	Q9SB43 arabidopsis
30	36	65.5	521	5	Q9ULN6	Q9ULN6 caenorhabdi
31	36	65.5	616	10	O81533	O81533 nicotiana t
32	36	65.5	639	2	Q9RB48	Q9RB48 clostridium
33	36	65.5	683	12	Q9JE42	Q9JE42 rhizoctonia
34	36	65.5	1244	2	Q55576	Q55576 synecocyst
35	36	65.5	1376	5	Q9W5D0	Q9W5D0 drosophila
36	36	65.5	1765	11	Q9R053	Q9R053 mus musculu
37	36	65.5	1765	11	Q9JMD4	Q9JMD4 mus musculu
38	35	63.6	140	8	Q9TLT9	Q9TLT9 cyanidium c
39	35	63.6	163	1	Q9YBA8	Q9YBA8 aeropyrum p
40	35	63.6	196	2	Q9KQ21	Q9KQ21 vibrio chol
41	35	63.6	301	2	Q9LCI7	Q9LCI7 shevanella
42	35	63.6	303	10	Q42912	Q42912 malus domes
43	35	63.6	303	10	Q9SX52	Q9SX52 arabidopsis
44	35	63.6	303	10	Q9LHE7	Q9LHE7 arabidopsis
45	35	63.6	343	12	O55830	O55830 spondweni v

ALIGNMENTS

RESULT 1
Q9IR97 PRELIMINARY; PRT; 352 AA.
AC Q9IR97;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CAPSID PROTEIN (P38).
OS Japanese iris necrotic ring virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
OC Carnovirus.
OX NCBI_TaxID=77344;
RN [1]
RP SEQUENCE FROM N.A.
RA Takemoto Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Takemoto Y., Kanehira T., Shinohara M., Yamashita S., Hibi T.;
RT "The nucleotide sequence and genome organization of Japanese iris
RT necrotic ring virus, a new species in the genus Carnovirus.";
RL Arch. Virol. 145:651-657(2000).
DR EMBL; D86123; BAA92796.1;
SQ SEQUENCE 352 AA; 37682 MW; 7A34087A0AEFF2CE8 CRC64;

Query Match 74.5%; Score 41; DB 12; Length 352;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
DB 19 WVAKVSGGG 28

RESULT 2
Q9T232 PRELIMINARY; PRT; 134 AA.
ID Q9T232;
AC Q9T232;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE RIBOSOMAL PROTEIN L16 (RPL16 PROTEIN).
GN RPL16.
OS Phytophthora infestans (Potato late blight fungus).
OC Mitochondrion.
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WEST VIRGINIA 4;
RA Lang B.F., Forget L.;
RT "The mitochondrial genome of Phytophthora infestans."; (In) O'Brien S.J. (eds.);
RL Genetic Maps, pp.133-135, Cold Spring Harbor Laboratory Press, NY (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WEST VIRGINIA 4;
RA Paquin B., Roewer I., Wang Z., Lang B.F.;
RT "A robust fungal phylogeny using the mitochondrially encoded nad5 protein sequence."; (In) O'Brien S.J. (eds.);
RL Can. J. Bot. 73: S180-S185 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-WEST VIRGINIA 4;
RX MEDLINE=97306266; PubMed=9162109;
RA Paquin B., Laforest M.J., Forget L., Roewer I., Wang Z., Longcore J., Lang B.F.;
RT "The fungal mitochondrial genome project: evolution of fungal mitochondrial genomes and their gene expression."; Curr. Genet. 31:380-395 (1997).
RL EMBL: U17009; AAF24799.1;
DR INTERPRO: IPR000114;
DR PFAM: PF00252; Ribosomal_L16; 1.
DR PRINTS: PR00060; RibosomalL16.
DR PROSITE: PS00701; RIBOSOMAL_L16_2; 1.
DR Ribosomal protein; Mitochondrion.
KW RIBOSOMAL
SQ SEQUENCE 134 AA; 15364 MW; 63CC5239B51095EA CRC64;

Query Match 70.9%; Score 39; DB 8; Length 134;

Best Local Similarity 87.5%; Pred. No. 9.6;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVAKVKG 8
||| ||| |
DB 93 WVAKVKG 100

RESULT 3
ID O55810 PRELIMINARY; PRT; 342 AA.
AC O55810;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE NS5 PROTEIN (FRAGMENT).
GN NS5.
OS Meaban virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=35279;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREST ART707;
RX MEDLINE=98080391; PubMed=9420202;
RA Kuno G., Chang G.-J., Tsuchiya K.R., Karabatsos N., Cropp C.B.;
RT "Phylogeny of the genus Flavivirus."; (In) J. Virol. 72:73-83 (1998).
RL EMBL: AF013386; AAC58774.1;
DR INTERPRO: IPR000208;
DR PFAM: PF00972; Flavi_NS5; 1.
FT NON_TER 1

FT NON_TER 342 342
SQ SEQUENCE 342 AA; 38615 MW; D06D642B4CFEE7CC CRC64;
Query Match 70.9%; Score 39; DB 12; Length 342;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 WVAKVKG 10
| : : | | | | |
DB 37 WASREKSGG 46
RESULT 4
Q51393 PRELIMINARY; PRT; 391 AA.
ID Q51393
AC Q51393;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE ALGJ.
GN ALGJ.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRD1;
RA Franklin M.J., Ohman D.E.;
RL J. Bacteriol. 178:0-0(0).
DR EMBL: U50202; AAB09782.1;
SQ SEQUENCE 391 AA; 43106 MW; AE048823947D5503 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 391;

Best Local Similarity 60.0%; Pred. No. 31;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVAKVKG 10
||| : | : | |
DB 371 WVAQLKASGG 380

RESULT 5
ID O06427 PRELIMINARY; PRT; 408 AA.
AC O06427;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 43.8 KDA PROTEIN.
GN RV0561C OR MTCY25D10.40C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E., Taylor K., Whitehead S., Barrrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544 (1998).
RL EMBL: Z95558; CAB08972.1;
DR

DR TUBERCULIST; RV0561c; -
 DR INTERPRO; IPR000205; -
 DR EMBL; AF053720; AAC16446.1; -
 DR PFAM; PF01494; FAD_binding_3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 408 AA; 43869 MW; B2F61E46A656EA8C CRC64;

Query Match 70.9%; Score 39; DB 2; Length 408;
 Best Local Similarity 70.0%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 0; Indels 2; Gaps 0;

QY 1 WVAKVSGGG 10
 :||:| |||
 Db 386 WVARVRRGG 395

RESULT 6

Q57079 PRELIMINARY; PRT; 509 AA.
 AC Q57079;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE ALPHA-SUBUNIT, METHYLMALONYL-CoA DECARBOXYLASE.
 OS Veillonella parvula.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Sporomusa subbranch;
 OC Veillonella.
 OX NCBI_TaxID=29466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huder J.B., Dimroth P.;
 RL J. Biol. Chem. 0:0-0(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94043308; PubMed=8227015;
 RA Huder J.B., Dimroth P.;
 RT "Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from
 Veillonella parvula."
 RL J. Biol. Chem. 268:24564-24571(1993).
 DR EMBL; Z24754; CAA80872.1; -
 DR EMBL; L22208; AAC36820.1; -
 DR INTERPRO; IPR00022; -
 DR INTERPRO; IPR002203; -
 DR PFAM; PF01039; Carboxyl_trans; 1.
 DR PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.
 SQ SEQUENCE 509 AA; 55100 MW; B9F85266A422B03B CRC64;

Query Match 69.1%; Score 38; DB 2; Length 509;
 Best Local Similarity 77.8%; Pred. No. 62;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAKVSGGG 10
 :|||:| |||
 Db 15 LAKVKAGGG 23

RESULT 7

O72120 PRELIMINARY; PRT; 691 AA.
 AC O72120;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE CAPSID PROTEIN PRECURSOR.
 OS Canine calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 OX NCBI_TaxID=74724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NO. 48;

RA Roerink F., Hashimoto M., Tohya Y., Mochizuki M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053720; AAC16446.1; -
 DR INTERPRO; IPR001643; -
 DR PFAM; PF00915; Calici_coat; 2.
 SQ SEQUENCE 691 AA; 76181 MW; FLC9774C9217AEF4 CRC64;

Query Match 69.1%; Score 38; DB 12; Length 691;
 Best Local Similarity 60.0%; Pred. No. 87;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 :||:| |||
 Db 549 WIAKEQAGG 558

RESULT 8

Q00303 PRELIMINARY; PRT; 907 AA.
 AC Q00303;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE NITRATE REDUCTASE.
 OS NIAD.
 GN Botrytis cinerea (Botryotinia fuckelliana).
 OC Eukaryota; Fungi; Ascomycota; Leotiales; Sclerotiniaceae; Botryotinia.
 OX NCBI_TaxID=40359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=T4;
 RA Lewis C., Dutertre M., Fortini D., Brygoo Y.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U43783; AAC02633.1; -
 DR HSP; P17571; 2CND.
 DR INTERPRO; IPR000572; -
 DR INTERPRO; IPR001199; -
 DR INTERPRO; IPR001433; -
 DR INTERPRO; IPR001834; -
 DR PFAM; PF00173; heme_1; 1.
 DR PFAM; PF00174; oxidored_molyb; 1.
 DR PFAM; PF00175; oxidored_fad; 1.
 DR PFAM; PF00970; Cyt_reductase; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR PRINTS; PR00406; CYTH5RDTASE.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PROSITE; PS00191; CYTOCHROME B5_1; UNKNOWN_1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 SQ SEQUENCE 907 AA; 101896 MW; 9E04BA54B5084FAD CRC64;

Query Match 69.1%; Score 38; DB 3; Length 907;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 :||:| |||
 Db 494 WMERVKSAGG 503

RESULT 9

O86545 PRELIMINARY; PRT; 186 AA.
 AC O86545;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE HYPOTHETICAL 19.9 KDA PROTEIN.
 OS SCIF2.08C.
 GN Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL031350; CAA20499.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 186 AA; 19874 MW; A32B4FE734D48FB2 CRC64;

Query Match 67.3%; Score 37; DB 2; Length 186;
 Best Local Similarity 60.0%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 || | |||
 DB 51 WVTVRPGG 60

RESULT 10
 ID 004364 PRELIMINARY; PRT; 238 AA.
 AC 004364;
 DT 01-JUL-1997 (TEMBLrel. 04, Created)
 DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
 DE PATHOGENESIS-RELATED THAUMATIN-LIKE PROTEIN.
 GN YPR5.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cole K.C., Velazhahan R., Anuratha C.S., Muthukrishnan S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77657; AAB53368.1; -;
 DR HSSP; P33679; IDU5.
 DR MENDEL; 13787; Oryza.Ypr5;13787.
 DR INTERPRO; IPR001938; -;
 DR PFAM; PF00314; thaumatin; 1.
 DR PROSITE; PS00316; THAUMATIN; 1.
 DR PRODOM; PD001321; -; 1.
 SQ SEQUENCE 238 AA; 24779 MW; EF8BF22F7F6B53E CRC64;

Query Match 67.3%; Score 37; DB 10; Length 238;
 Best Local Similarity 70.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 | | | ||||
 DB 45 WPAVPSGG 54

RESULT 11
 Q9X2P4 PRELIMINARY; PRT; 289 AA.
 ID Q9X2P4

AC Q9X2P4;
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
 DE ALKANAL MONOOXYGENASE-LIKE HYPOTHETICAL PROTEIN.
 GN AMLP.
 OS Mycobacterium smegmatis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC2155;
 RA Kim B.-K., Choi K.-P., Daniels L.;
 RT "The gene for F420-dependent glucose-6-phosphate dehydrogenase (fgd)
 RT and a conserved upstream gene coding for a beta-lactamase-like protein
 RT in Mycobacterium species."
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC2155;
 RA Purwanti E., Daniels L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF041061; AAD31326.1; -;
 KW Monooxygenase.
 SQ SEQUENCE 289 AA; 31630 MW; 28776602C9BEFA1E CRC64;

Query Match 67.3%; Score 37; DB 2; Length 289;
 Best Local Similarity 50.0%; Pred. No. 52;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 || : ||||
 DB 203 WYISIRAGG 212

RESULT 12
 ID 055828 PRELIMINARY; PRT; 345 AA.
 AC 055828;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
 DE NS5 PROTEIN (FRAGMENT).
 GN NS5.
 OS Sepik virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=44026;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MK7148;
 RX MEDLINE=98080391; PubMed=9420202;
 RA Kuno G., Chang G.-J., Tsuchiya K.R., Karabatsos N., Cropp C.B.;
 RT "Phylogeny of the genus Flavivirus."
 RL J. Virol. 72:73-83(1998).
 DR EMBL; AF013404; AAC58792.1; -;
 DR INTERPRO; IPR000208; -;
 DR PFAM; PF00972; Flavi_NS5; 1.
 FT NON_TER 1.
 FT NON_TER 345 345
 SQ SEQUENCE 345 AA; 39170 MW; E2A274071CF8AA16 CRC64;

Query Match 67.3%; Score 37; DB 12; Length 345;
 Best Local Similarity 60.0%; Pred. No. 63;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 || : ||||
 DB 37 WVSRRNSGG 46

```

RESULT 13
Q54496          PRELIMINARY;          PRT;    409 AA.
ID   Q54496
AC   Q54496;
DT   01-NOV-1996 (TRENBLrel. 01, Created)
DT   01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT   01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE   SNO2 PROTEIN.
GN   SNO2.
OS   Streptomyces nogalater.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX   NCBI_TaxID=38314;
[1]
RN   SEQUENCE FROM N.A.
RP   STRAIN=ATCC 27451.
RC   MEDLINE=96242142; PubMed=8668120;
RA   Ylihanko K., Tuikka J., Jussila S., Cong L., Mantsala P.;
RX   Ylihanko K., Tuikka J., Jussila S., Cong L., Mantsala P.;
RT   "A gene cluster involved in nogalmycin biosynthesis from Streptomyces
RT   nogalater: sequence analysis and complementation of early-block
RT   mutations in the anthracycline pathway.";
RL   Mol. Gen. Genet. 251:113-120(1996).
[3]
RN   SEQUENCE FROM N.A.
RP   STRAIN=ATCC 27451.
RC   MEDLINE=96349102; PubMed=8760909;
RA   Ylihanko K., Hakala J., Kunnari T., Mantsala P.;
RX   Ylihanko K., Hakala J., Kunnari T., Mantsala P.;
RT   "Production of hybrid anthracycline antibiotics by heterologous
RT   expression of Streptomyces nogalater nogalmycin biosynthesis genes.";
RL   Microbiology 142:1965-1972(1996).
[4]
RN   SEQUENCE FROM N.A.
RP   STRAIN=ATCC 27451.
RC   MEDLINE=98007868; PubMed=9349712;
RA   Tokkell S., Ylihanko K., Hakala J., Skurnik M., Mantsala P.;
RX   Tokkell S., Ylihanko K., Hakala J., Skurnik M., Mantsala P.;
RT   "Characterization of Streptomyces nogalater genes encoding enzymes
RT   involved in glycosylation steps in nogalmycin biosynthesis.";
RL   Mol. Gen. Genet. 256:203-209(1997).
DR   EMBL; AJ224512; CAA12018.1;
DR   HSSP; P39435; 1KAS.
DR   INTERPRO; IPR000794;
DR   PFAM; PF00109; ketoacyl-synt; 1.
SQ   SEQUENCE 409 AA; 42583 MW; 93A8784508E15717 CRC64;

Query Match          67.3%; Score 37; DB 2; Length 409;
Best Local Similarity 56.7%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WVAKVKSQG 9
Db 198 WVAQLSSGG 206
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RESULT 14
O9X082          PRELIMINARY;          PRT;    1008 AA.
ID   O9X082
AC   O9X082;
DT   01-NOV-1999 (TRENBLrel. 12, Created)
DT   01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT   01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE   CONSERVED HYPOTHETICAL PROTEIN.
GN   TM0987.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogales; Thermotoga.
OX   NCBI_TaxID=2336;
[1]

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RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
DR   EMBL; AE001760; AAD36066.1;
DR   TIGR; TM0987;
DR   INTERPRO; IPR002052;
DR   PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ   SEQUENCE 1008 AA; 115760 MW; 4D640F610123B614 CRC64;

Query Match          67.3%; Score 37; DB 2; Length 1008;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WVAKVKSQG 10
Db 196 WLARVKDGG 205
|||::|||

RESULT 15
O04013          PRELIMINARY;          PRT;    1350 AA.
ID   O04013
AC   O04013;
DT   01-JUL-1997 (TRENBLrel. 04, Created)
DT   01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT   01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE   REVERSE TRANSCRIPTASE, GAG, POLYPROTEIN.
OS   Volvox carteri.
OC   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC   Volvocaceae; Volvox.
OX   NCBI_TaxID=3067;
[1]
RN   SEQUENCE FROM N.A.
RC   STRAIN=HK10; TRANSPOSON=LUECKENBUESSE;
RA   Koehl G., Putz E., Schmitt R.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR   EMBL; U90320; AAB51275.1;
DR   MENDEL; 15899; Voica; 2432:15899.
DR   INTERPRO; IPR001584;
DR   INTERPRO; IPR001878;
DR   PFAM; PF000098; zf-CCHC; 1.
DR   PFAM; PF000665; rve; 1.
KW   Polyprotein; RNA-directed DNA polymerase.
SQ   SEQUENCE 1350 AA; 149847 MW; BE7299C85BFFFA013 CRC64;

Query Match          67.3%; Score 37; DB 10; Length 1350;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WVAKVKSQG 8
Db 892 WYKVKSG 899
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Search completed: March 28, 2001, 07:27:42
Job time: 1655 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:32 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WYAKVKSOGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 segs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	19	W76017
2	50	90.9	10	19	W76008
3	50	90.9	117	19	W76001
4	50	90.9	117	19	W76003
5	50	90.9	117	20	Y06381
6	50	90.9	130	20	Y06379
7	43	78.2	119	19	W69322
8	43	78.2	119	20	I32832
9	43	78.2	119	20	W73503
10	43	78.2	138	13	R20064
11	42	76.4	119	16	W11919
12	42	76.4	123	19	W66099

13	42	76.4	247	16	W11917
14	41	74.5	110	18	W06207
15	41	74.5	118	18	W06208
16	41	74.5	140	18	W06205
17	39	70.9	119	14	R32240
18	39	70.9	119	14	R32243
19	39	70.9	119	14	R32244
20	39	70.9	119	18	W27144
21	39	70.9	119	21	Y87570
22	39	70.9	120	17	W00240
23	39	70.9	122	13	R25722
24	39	70.9	131	16	R70466
25	39	70.9	138	14	R32242
26	39	70.9	138	14	R32246
27	39	70.9	139	14	R31588
28	39	70.9	139	15	R52773
29	39	70.9	139	15	R52791
30	39	70.9	139	15	R52823
31	39	70.9	139	16	R70471
32	39	70.9	141	21	Y43869
33	39	70.9	623	17	W02284
34	38	69.1	115	11	R04939
35	38	69.1	115	11	R05039
36	38	69.1	115	15	R54137
37	37	67.3	13	20	W86105
38	37	67.3	13	20	W86092
39	37	67.3	13	20	W86100
40	37	67.3	98	16	R72075
41	37	67.3	98	21	Y56664
42	37	67.3	108	17	R95283
43	37	67.3	108	17	R91364
44	37	67.3	116	16	R79245
45	37	67.3	116	16	R79246

ALIGNMENTS

RESULT 1

W76017 ID W76017 standard; Protein: 10 AA.

XX W76017;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR2 protein fragment #3.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

PN 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49854.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 PS Claim 61; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC vitaxin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
 |||||

Db 1 wvakvsggg 10

RESULT 2

ID W76008 standard; Protein; 10 AA.

XX W76008;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR2 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49845.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.009;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10

|||||

Db 1 wvakvsggg 10

RESULT 3

ID W76001 standard; Protein; 117 AA.

XX W76001;

XX 02-NOV-1998 (first entry)

DE Vitaxin antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49820.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 1; Fig 1a; 129pp; English.

XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVAKVSGGG 10
 ||||| ||||
 Db 47 wvakvsggg 56

RESULT 4

W76003
 ID W76003 standard; Protein; 117 AA.

XX AC W76003;

XX 02-NOV-1998 (first entry)

XX LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI: 1998-437472/37.

XX N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVAKVSGGG 10
 ||||| ||||
 Db 47 wvakvsggg 56

RESULT 5

Y06381
 ID Y06381 standard; Protein; 117 AA.

XX AC Y06381;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VII region.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI: 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 90.9%; Score 50; DB 20; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVAKVSGGG 10
 ||||| ||||
 Db 47 wvakvsggg 56

RESULT 6

Y06379
 ID Y06379 standard; Protein; 130 AA.

XX AC Y06379;

XX

DT 06-SEP-1999 (first entry)
DE Murine monoclonal antibody LM609 V kappa.
XX
DE Humanised antibody; antibody humanisation; antibody engineering;
XX LM609; monoclonal antibody; complementarity determining region;
XX CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX cancer; therapy; diagnosis.
XX
XX Mus musculus.
XX
XX
XX Key Location/Qualifiers
FH Peptide 1..2
FT /note= "vector-encoded residues"
FT Region 28..32
FT /note= "CDR1"
FT Region 47..63
FT /note= "CDR2"
FT Region 96..103
FT /note= "CDR3"
FT
FT
PN W09929888-A1.
XX
XX 17-JUN-1999.
PD
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPT; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 49-50; 55pp; English.
XX
XX This sequence represents the light chain V kappa region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
XX Sequence 130 AA;
SQ
Query Match 90.9%; Score 50; DB 20; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 WVAVKVSGGG 10
DB 44 wvakvsgggg 53
RESULT 7
ID W69322 standard; Protein; 119 AA.
XX
XX W69322;
AC
XX
XX 19-NOV-1998 (first entry)
DT
XX

DE 15D3 antibody heavy chain.
XX
XX Hybridoma 15D3; 15D3 antibody; complementarity-determining region; scFv;
KW single-chain antibody molecule; multidrug-resistant human tumour cell;
KW MDR tumour; CDR; therapy; heavy chain.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..30
FT /note= "HFR1"
FT Region 31..35
FT /note= "HCDR1"
FT Region 36..49
FT /note= "HFR2"
FT Region 50..66
FT /note= "HCDR2"
FT Region 67..98
FT /note= "HFR3"
FT Region 99..108
FT /note= "HCDR3"
FT Region 109..119
FT /note= "HFR4"
FT
XX US5811267-A.
XX
XX 22-SEP-1998.
XX
XX 07-JUN-1995; 95US-0475000.
XX
XX 07-JUN-1995; 95US-0475000.
PR 29-OCT-1990; 90US-0605399.
PR 22-OCT-1993; 93US-0141375.
PR 17-OCT-1994; 94US-0323566.
XX
XX (CHIR) CHIRON CORP.
XX
XX Ring DB;
XX
XX WPI; 1998-530873/45.
XX N-PSDB; V44997.
XX
XX DNA encoding single-chain antibody molecule - specific for
PT multidrug-resistant tumour cells, useful in diagnosis or therapy
XX
XX Disclosure; Fig 1; 26pp; English.
XX
XX This sequence represents the VH chain of the antibody
CC produced by hybridoma cell line 15D3. It is part of the nucleic acid of
CC the invention which encodes a single-chain antibody molecule (scFv)
CC comprising the heavy-chain complementarity-determining regions (CDRs) of
CC the monoclonal antibody produced by hybridoma cell line 15D3, where the
CC monoclonal antibody and scFv are capable of binding to
CC multidrug-resistant (MDR) human tumour cells. The CDR sequences from both
CC the heavy and light chains (HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3)
CC are all used in an expression cassette that can be used in a method for
CC inducing the production of a polypeptide. The method is useful for
CC producing recombinant scFv, which can be used for diagnosis or therapy
CC (e.g. in the form of an immunotoxin) for MDR tumours.
XX
XX Sequence 119 AA;
SQ

Query Match 78.2%; Score 43; DB 19; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 WVAVKVSGGG 10
DB 47 wvatissggg 56
RESULT 8

Y32832
ID Y32832 standard; Protein; 119 AA.
XX AC Y32832;
XX DT 27-OCT-1999 (first entry)
XX DE 15D3 VH chain protein sequence.
XX KW Complementarity determining region; CDR; framework region; FR; antibody;
KW 15D3; immunoglobulin; human tumour cell; multiple drug resistance;
KW MDR phenotype; cancer; retroviral vector development; gene therapy;
KW murine antigen binding site.
XX OS Mus sp.
XX PN US5948647-A.
XX PD 07-SEP-1999.
XX PF 07-JUN-1995; 95US-0484508.
XX PR 07-JUN-1995; 95US-0484508.
XX PR 29-OCT-1990; 90US-0605399.
XX PR 22-OCT-1993; 93US-0141375.
XX PR 17-OCT-1994; 94US-0323566.
XX PA (CHIR) CHIRON CORP.
XX PI Ring DB;
XX WPI; 1999-517953/43.
XX DR N-PSDB; Z10957.
XX PT Nucleic acids encoding antibody binding sites of immunoglobulins
PT with affinity for cancer antigens useful in cancer therapy
XX PS Disclosure; Fig 1; 27pp; English.
XX CC This sequence is the antibody 15D3 VH chain. The invention relates
CC to isolated nucleic acid molecules comprising complementarity determining
CC regions (CDRs) and framework regions (FRs) from humans and mice encoding
CC a monomeric polypeptide that exhibits the immunological binding
CC properties of an immunoglobulin which binds to a human tumour cell
CC displaying the multiple drug resistance (MDR) phenotype. The recombinant
CC nucleotide sequences can be used to transfect mammalian cells for the
CC expression of recombinant human antibodies which exhibit the antigen
CC specificity of the murine antibody molecule. The polypeptides produced
CC can be used in specific binding assays, affinity purification schemes,
CC drug or toxin targeting, imaging and genetic or immunological
CC therapeutics for various cancers. The CDRs can be used in single chain Fv
CC (scFv) molecules which can be used in the development of retroviral
CC vectors that target human cancer cells expressing the MDR phenotype for
CC gene therapy. The recombinantly veneered murine antigen binding sites
CC consist of the selective replacement of FR residues from a rodent light
CC or heavy chain V region with human FR residues to provide a xenogeneic
CC molecule comprising an antigen binding site which retains substantially
CC all of the native FR polypeptide folding structure. The nucleic acids
CC encode molecules with altered or enhanced antigen-binding capabilities
CC and/or reduced immunogenicity.
XX SQ Sequence 119 AA;

Query Match 78.2%; Score 43; DB 20; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WVAKVSGGG 10
III : IIII
DB 47 wvatissggg 56

RESULT 9
W73503
ID W73503 standard; Protein; 119 AA.
XX AC W73503;
XX DT 26-FEB-1999 (first entry)
XX DE Antibody 15D3 heavy chain protein sequence.
XX KW Antibody; 15D3; human; tumour cell; multiple drug resistance; cancer;
KW immunotherapy; heavy chain.
XX OS Homo sapiens.
XX PN US5849877-A.
XX PD 15-DEC-1998.
XX PF 07-JUN-1995; 95US-0483199.
XX PR 07-JUN-1995; 95US-0483199.
XX PR 29-OCT-1990; 90US-0605399.
XX PR 22-OCT-1993; 93US-0141375.
XX PR 17-OCT-1994; 94US-0323566.
XX PA (CHIR) CHIRON CORP.
XX PI Ring DB;
XX WPI; 1999-069806/06.
XX DR N-PSDB; V08933.
XX PT Monomeric and dimeric poly:peptide(s) - which bind to human tumour
PT cell displaying multiple drug resistance
XX PS Claim 1; Fig 1; 26pp; English.
XX CC This sequence represents the heavy chain of the antibody produced by
CC the hybridoma 15D3. The protein is an example of a monomeric
CC polypeptide of the invention that binds to a human tumour cell displaying
CC multiple drug resistance. The polypeptides are used in specific binding
CC assays, affinity purification, drug or toxin targeting, imaging or
CC immunotherapy of various cancers.
XX SQ Sequence 119 AA;
Query Match 78.2%; Score 43; DB 20; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WVAKVSGGG 10
III : IIII
DB 47 wvatissggg 56
RESULT 10
R20064
ID R20064 standard; Protein; 138 AA.
XX AC R20064;
XX DT 27-MAR-1992 (first entry)
XX DE MRK16-H chain.
XX KW Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
XX OS Chimeric Homo sapiens;
XX OS Chimeric Mus musculus.
XX PN JP03254691-A.

XX 13-NOV-1991.
 XX
 XX 02-MAR-1990; 90JP-0051563.
 PF
 XX 02-MAR-1990; 90JP-0051563.
 PR
 XX (GANK-) 2H GAN KENYUKAI.
 PA (FUJI-) FUJITA GAKUEN GH.
 PA
 XX WPI; 1992-002461/01.
 XX N-PSDB; Q20070.
 DR
 XX Chimera antibody against drug resistant cancer - comprises
 XX variable region homologous to region in mouse monoclonal antibody
 PT and constant region homologous to region in human immunoglobulin
 PT
 XX Disclosure; Fig 4; 20pp; Japanese.
 PS
 XX A chimeric antibody against drug-resistant cancer consists of
 CC (1) a variable region having an amino acid sequence homologous to
 CC a variable region in the mouse monoclonal antibody against drug-
 CC resistance and (2) a constant region having an amino acid sequence
 CC homologous to the constant region in human immunoglobulin.
 CC The chimeric antibody selectively inhibits the growth of cancer
 CC cells showing drug resistance or enhances the sensitivity to the
 CC drug. The antibody is very low in immunogenicity.
 CC The MRK16-L chain is shown in Q20071.
 XX
 XX Sequence 138 AA;
 SQ

Query Match 78.2%; Score 43; DB 13; Length 138;
 Best Local Similarity 70.0%; Pred. No. 2;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
 Db 66 wvatissggg 75

RESULT 11
 W11919
 ID W11919 standard; Protein; 119 AA.
 AC
 AC W11919;
 XX
 XX 24-JUN-1997 (first entry)
 DT
 XX Humanised MAB SK48-E26 heavy chain.
 XX
 XX Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAB; SK48-E26; inflammation; therapy.
 KW
 XX Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 OS
 XX
 XX Key Location/Qualifiers
 FH
 FT Region 1..30
 FT /label= FR1
 FT /note= "framework region 1"
 FT 31..35
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 (Claim 10, page 48)"
 FT
 FT Region 36..49
 FT /label= FR2
 FT /note= "framework region 2"
 FT 50..66
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 (Claim 10, page 48)"
 FT
 FT

FT Region 67..98
 FT /label= FR3
 FT /note= "framework region 3"
 FT 99..108
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 (Claim 10, page 48)"
 FT
 FT Region 109..119
 FT /label= FR4
 FT /note= "framework region 4"
 XX
 XX WO9501997-A1.
 XX
 XX 19-JAN-1995.
 PD
 XX
 XX 07-JUL-1994; 94WO-US07659.
 PF
 XX
 XX 09-JUL-1993; 93US-0090534.
 PR
 XX 04-MAR-1994; 94US-0206190.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Gross MS, Hurler MR, Jackson JR, Jonak ZL, Theisen TW;
 PI Young PR;
 PI
 XX WPI; 1995-066868/09.
 DR N-PSDB; T51438.
 DR
 XX Recombinant and humanised chimeric antibodies against human
 PT interleukin-1-beta - for preventing and treating
 PT interleukin-mediated inflammatory disorders
 PT
 XX Claim 39; Page 40-41; 62pp; English.
 PS
 XX The heavy chain variable region (W11919) and light chain variable
 CC region (W11920) of humanised anti-human interleukin-1 beta (IL-1
 CC beta) murine monoclonal antibody (MAB) SK48-E26 comprise the
 CC complementarity determining regions from MAB SK48-E26 (see also
 CC W11917-18) grafted into human frameworks. The humanised antibody
 CC can be produced in e.g. COS cells transfected with vectors carrying
 CC humanised heavy and light chain nucleic acids (T51437-39) for use
 CC in the treatment and prevention of IL-1 mediated inflammatory
 CC disorders.
 CC
 XX Sequence 119 AA;
 SQ

Query Match 76.4%; Score 42; DB 16; Length 119;
 Best Local Similarity 70.0%; Pred. No. 2.5;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
 Db 47 wwayissggg 56

RESULT 12
 W66099
 ID W66099 standard; Protein; 123 AA.
 AC
 AC W66099;
 XX
 XX 10-DEC-1998 (first entry)
 DT
 XX anti-CD22 monoclonal antibody heavy chain variable region.
 DE
 XX anti-CD22 monoclonal antibody heavy chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; immunodiagnosis; RFBA IgG.
 KW
 XX Mammalia.
 OS
 XX Key Location/Qualifiers
 FH

FT Misc-difference 121 /note= "Encoded by gtc"
 FT XX WO9841641-A1.
 FT PN 24-SEP-1998.
 FT PD 19-MAR-1998; 98WO-US05453.
 FT XX 20-MAR-1997; 97US-0041437.
 FT PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 FT PA Fitzgerald D, Kreitman R, Mansfield E, Pastan I;
 FT XX WPI; 1998-521227/44.
 FT DR N-PSDB; V07642.
 FT XX Recombinant anti-CD22 antibodies and immuno-conjugates - of
 FT PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
 FT PT or a label; for inhibiting malignant B-cells
 FT XX Claim 6; Fig 1; 71pp; English.
 FT XX The invention claims for a recombinant immunoconjugate comprising
 CC of a therapeutic agent (e.g Pseudomonas exotoxin) or a detectable
 CC label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)
 CC having the present variable heavy (VH) chain with a cysteine residue
 CC at amino acid 44 and a variable light (VL; W66098) chain with a
 CC cysteine residue at amino acid 100. The immunoconjugate is claimed
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and
 CC can be used in diagnostic kits.
 FT XX Sequence 123 AA;
 FT SQ

Query Match 76.4%; Score 42; DB 19; Length 123;
 Best Local Similarity 70.0%; Pred. No. 2.6;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVKGSGG 10
 III : IIII
 Db 47 wwayissggg 56

RESULT 13
 ID W11917
 ID W11917 standard; Protein; 247 AA.
 AC W11917;
 XX 24-JUN-1997 (first entry)
 DE Murine MAb SK48-E26 heavy chain.
 XX Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Sig_peptide
 FT Region 20..49
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 FT (Claim 10, page 48)"

FT Region 55..68
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 FT (Claim 10, page 48)"
 FT Region 86..117
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 118..127
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 FT (Claim 10, page 48)"
 FT Region 128..138
 FT /label= FR4
 FT /note= "framework region 4"
 FT Region 139..247
 FT /label= Constant_region
 FT PN WO9501997-A1.
 FT XX 19-JAN-1995.
 FT PD 07-JUL-1994; 94WO-US07659.
 FT XX 09-JUL-1993; 93US-0090534.
 FT PR 04-MAR-1994; 94US-0206190.
 FT XX (SMIK) SMITHKLINE BEECHAM CORP.
 FT XX Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;
 FT PI Young PR;
 FT XX WPI; 1995-066868/09.
 FT DR N-PSDB; T51436.
 FT XX Recombinant and humanised chimeric antibodies against human
 FT PT interleukin-1-beta - for preventing and treating
 FT PT interleukin-mediated inflammatory disorders
 FT XX Claim 5; Page 36-37; 62pp; English.
 FT XX Amino acid sequences of the heavy chain (W11917) and light chain
 CC (W11918) of anti-human interleukin-1 beta (IL-1 beta) murine
 CC monoclonal antibody (MAb) SK48-E26 were deduced from nucleic acids
 CC (T51436-37) derived from hybridoma SK48-E26. The heavy and light
 CC chains, esp. the complementarity determining region sequences,
 CC can be utilised in novel recombinant chimeric and humanised
 CC antibodies (see also W11919-20) useful for the treatment and
 CC prevention of IL-1 mediated inflammatory disorders.
 FT XX Sequence 247 AA;
 FT SQ

Query Match 76.4%; Score 42; DB 16; Length 247;
 Best Local Similarity 70.0%; Pred. No. 5.3;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVKGSGG 10
 III : IIII
 Db 66 wwayissggg 75

RESULT 14
 W06207
 ID W06207 standard; Protein; 110 AA.
 XX W06207;
 AC
 XX 17-FEB-1997 (first entry)
 FT DE Rat antibody heavy chain variable region.

XX Xenograft rejection; xenotransplantation; organ transplant;
 KW animal model; hamster; monoclonal antibody; HAR-1.
 XX
 XX Rattus sp.
 XX
 FH Location/Qualifiers
 FT Region 1..19
 FT /label= Leader
 FT Misc-difference 11
 FT /note= "amino acid 11 is Leu in HAR-1 VH encoded
 FT by a cDNA clone"
 FT Region 20..49
 FT /label= FR-1
 FT /note= "framework region 1"
 FT Region 50..54
 FT /label= CDR-1
 FT /note= "complementarity determining region 1"
 FT Region 55..68
 FT /label= FR-2
 FT /note= "framework region 2"
 FT Region 69..85
 FT /label= CDR-2
 FT /note= "complementarity determining region 2"
 FT Region 86..110
 FT /label= FR-3
 FT /note= "framework region 3"
 PN W09636358-A1.
 XX 21-NOV-1996.
 XX 14-MAY-1996; 96WO-US06804.
 XX 15-MAY-1995; 95US-0440621.
 XX (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX Cramer DV, Makowka L, Wu G;
 XX WPI; 1997-011852/01.
 DR N-PSDB; T43416.
 XX
 XX Inhibiting xenograft rejection by modifying antigen expression of
 PT the graft - prevents binding of anti-donor antibody and prolongs
 PT graft survival
 XX
 XX Disclosure; Page 102-103; 135pp; English.
 XX
 XX A polypeptide (W06207) comprises the variable heavy chain segment
 CC of a LEW rat antibody, and is encoded by a genomic DNA clone
 CC (T43416) obtd. from a newborn LEW rat. It differs in 1 position
 CC from the VH region of LEW rat anti-hamster xenograft antibody
 CC HAR-1 (W06205). Evidence is provided that the hyperacute
 CC rejection of xenografts is mediated by polyreactive anti-donor
 CC xenograft antibodies having VH germline configurations.
 XX
 XX Sequence 110 AA;
 SQ
 Query Match 74.5%; Score 41; DB 18; Length 110;
 Best Local Similarity 60.0%; Pred. No. 3.5;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 WVAKVSGGG 10
 Db 66 wvasistggg 75
 III : III
 RESULT 15
 W06208
 ID W06208 standard; Protein; 118 AA.
 XX

AC W06208;
 XX 17-FEB-1997 (first entry)
 XX
 XX Xenograft antibody ID12BF3 heavy chain variable region.
 DE
 XX Xenograft rejection; xenotransplantation; organ transplant;
 KW animal model; hamster; monoclonal antibody; ID12BF3.
 XX
 XX Rattus sp.
 XX
 FH Location/Qualifiers
 FT Region 1..98
 FT /label= VH-Segment
 FT /note= "variable segment of heavy chain variable
 FT region"
 FT Region 99..103
 FT /label= D-Segment
 FT /note= "diversity segment of heavy chain variable
 FT region"
 FT Region 104..118
 FT /label= JH-Segment
 FT /note= "joining segment of heavy chain variable
 FT region"
 FT Region 1..30
 FT /label= FR-1
 FT /note= "framework region 1"
 FT Region 31..35
 FT /label= CDR-1
 FT /note= "complementarity determining region 1"
 FT Region 36..49
 FT /label= FR-2
 FT /note= "framework region 2"
 FT Region 50..66
 FT /label= CDR-2
 FT /note= "complementarity determining region 2"
 FT Region 67..98
 FT /label= FR-3
 FT /note= "framework region 3"
 FT Region 99..107
 FT /label= CDR-3
 FT /note= "complementarity determining region 3"
 FT Region 108..118
 FT /label= FR-4
 FT /note= "framework region 4"
 XX
 PN W09636358-A1.
 XX 21-NOV-1996.
 XX 14-MAY-1996; 96WO-US06804.
 XX 15-MAY-1995; 95US-0440621.
 XX (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX Cramer DV, Makowka L, Wu G;
 XX WPI; 1997-011852/01.
 DR N-PSDB; T43417.
 XX
 XX Inhibiting xenograft rejection by modifying antigen expression of
 PT the graft - prevents binding of anti-donor antibody and prolongs
 PT graft survival
 XX
 XX Claim 13; Page 96; 135pp; English.
 XX
 XX A polypeptide (W06208) comprises the variable heavy chain segment
 CC of the LEW rat anti-hamster xenograft monoclonal antibody ID12BF3.
 CC It is encoded by a cDNA clone (T43417) obtd. from a ID12BF3
 CC hybridoma heavy chain cDNA library; the hybridoma was produced by
 CC fusing spleen cells of a LEW rat that had received a hamster heart
 CC transplant, with rat myeloma cells. Recombinant fragments, e.g.

CC Fab'12 and Fab', of the antibody block binding of preformed
CC anti-donor xenograft antibodies in a recipient animal serum to
CC antigen expressed by endothelial cells of the xenograft, i.e. they
CC inhibit antibody-mediated rejection, thereby prolonging the
CC survival of the hamster xenograft in the recipient.

xx

SQ Sequence 118 AA;

Query Match 74.5%; Score 41; DB 18; Length 118;
Best Local Similarity 60.0%; Pred. No. 3.7;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVAKVKS GGG 10
||| : |||
Db 47 wvasistggg 56

Search completed: March 28, 2001, 06:34:33
Job time: 513 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:09 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WVAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep:*
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep:*
3: /cgnl_7/ptodata/1/iaa/6_COMB.pep:*
4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	78.2	119	2	US-08-475-000-16
2	43	78.2	119	2	US-08-483-199-16
3	43	78.2	119	2	US-08-484-508-16
4	42	76.4	119	4	PCT-US94-07659-6
5	42	76.4	247	4	PCT-US94-07659-2
6	39	70.9	119	1	US-08-053-171-12
7	39	70.9	119	1	US-08-053-171-13
8	39	70.9	119	1	US-08-053-171-14
9	39	70.9	119	1	US-08-053-171-17
10	39	70.9	119	3	US-08-815-190A-13
11	39	70.9	122	1	US-07-634-278-48
12	39	70.9	122	1	US-07-634-278-49
13	39	70.9	122	1	US-08-477-728-48
14	39	70.9	122	1	US-08-477-728-49
15	39	70.9	122	1	US-08-474-040-48
16	39	70.9	122	1	US-08-474-040-49
17	39	70.9	122	1	US-08-487-200-48
18	39	70.9	122	1	US-08-487-200-49
19	39	70.9	125	1	US-08-331-398A-65
20	39	70.9	125	2	US-08-331-397B-65
21	39	70.9	125	2	US-08-759-804A-64
22	39	70.9	138	1	US-08-053-171-7
23	39	70.9	138	1	US-08-053-171-11
24	39	70.9	139	1	US-08-129-930B-96
25	39	70.9	623	1	US-08-332-838-2
26	37	67.3	109	2	US-08-793-490-6
27	37	67.3	116	2	US-08-888-366-10
28	37	67.3	116	2	US-08-888-366-12

29	37	67.3	116	3	US-09-184-658-48	Sequence 48, Appl
30	37	67.3	119	1	US-08-207-996-18	Sequence 18, Appl
31	37	67.3	119	1	US-08-207-996-19	Sequence 19, Appl
32	37	67.3	119	1	US-08-207-996-20	Sequence 20, Appl
33	37	67.3	119	1	US-08-207-996-21	Sequence 21, Appl
34	37	67.3	119	1	US-08-207-996-22	Sequence 22, Appl
35	37	67.3	119	1	US-08-207-996-27	Sequence 27, Appl
36	37	67.3	119	1	US-08-497-312-20	Sequence 20, Appl
37	37	67.3	119	2	US-08-760-840A-18	Sequence 18, Appl
38	37	67.3	119	2	US-08-760-840A-19	Sequence 19, Appl
39	37	67.3	119	2	US-08-760-840A-20	Sequence 20, Appl
40	37	67.3	119	2	US-08-760-840A-21	Sequence 21, Appl
41	37	67.3	119	2	US-08-760-840A-22	Sequence 22, Appl
42	37	67.3	119	2	US-08-760-840A-28	Sequence 28, Appl
43	37	67.3	119	3	US-09-266-119-18	Sequence 18, Appl
44	37	67.3	119	3	US-09-266-119-19	Sequence 19, Appl
45	37	67.3	119	3	US-09-266-119-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-475-000-16
; Sequence 16, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-000-16

Query Match 78.2%; Score 43; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

Db 47 WVAITSSGGG 56

RESULT 2

US-08-483-199-16
; Sequence 16, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-199-16

Query Match 78.2%; Score 43; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVKSGG 10
Db 47 WVAISSGGG 56

RESULT 3
US-08-484-508-16
; Sequence 16, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-385
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-508-16

Query Match 78.2%; Score 43; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVKSGG 10
Db 47 WVAISSGGG 56

RESULT 4
PCT-US94-07659-6
; Sequence 6, Application PC/US9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US94-07659-6

Query Match 76.4%; Score 42; DB 4; Length 119;

Best Local Similarity 70.0%; Pred. No. 1.7;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

||| : ||||

Db 47 WWAYISSGGG 56

RESULT 5

PCT-US94-07659-2

; Sequence 2, Application PC/TUS9407659

; GENERAL INFORMATION:

; APPLICANT: Young, Peter

; APPLICANT: Gross, Mitchell

; APPLICANT: Jonak, Zdenka L.

; APPLICANT: Theisen, Timothy

; APPLICANT: Hurler, Mark

; APPLICANT: Jackson, Jeffrey R.

; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta

; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation - Corp.

; ADDRESSEE: Intellectual Property

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-2799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07659

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/090,534

; FILING DATE: 09-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P50171-1

; TELEPHONE: (610) 270-5024

; TELEFAX: (610) 270-5090

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-07659-2

Query Match

76.4%; Score 42; DB 4; Length 247;

Best Local Similarity 70.0%; Pred. No. 3.5;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

||| : ||||

Db 66 WWAYISSGGG 75

RESULT 6

US-08-053-171-12

; Sequence 12, Application US/08053171

; Patent No. 5562903

; GENERAL INFORMATION:

; APPLICANT: Co. Loibner

; TITLE OF INVENTION: Antibody Derivatives

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourile and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-54-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; NAME/KEY: Peptide

; LOCATION: 1..119

; OTHER INFORMATION: /note= "Sequence of Humanized

; Patent No. 5562903

; OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant

; OTHER INFORMATION: H-hu-BR55-2/1"

; FEATURE:

; NAME/KEY: Region

; LOCATION: 31..35

; OTHER INFORMATION: /note= "Complementarity-determining

; OTHER INFORMATION: region"

; FEATURE:

; NAME/KEY: Region

; LOCATION: 50..66

; OTHER INFORMATION: /note= "Complementarity-determining

; OTHER INFORMATION: region"

; FEATURE:

; NAME/KEY: Region

; LOCATION: 99..108

; OTHER INFORMATION: /note= "Complementarity-determining

; OTHER INFORMATION: region"

; US-08-053-171-12

Query Match

70.9%; Score 39; DB 1; Length 119;

Best Local Similarity 60.0%; Pred. No. 5.6;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

||| : ||||

Db 47 WWAYISSGGG 56

RESULT 7

US-08-053-171-13

; Sequence 13, Application US/08053171

Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..119
OTHER INFORMATION: /note= "Sequence of Humanized
Patent No. 5562903
OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant H-hu-BR5-2/2"
FEATURE:
NAME/KEY: Region
LOCATION: 31..35
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 50..66
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 99..108
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
US-08-053-171-13

Query Match 70.9%; Score 39; DB 1; Length 119;
Best Local Similarity 60.0%; Pred. No. 5,6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WYAKVSGGG 10
DB 47 WYATISNGGG 56

RESULT 8
US-08-053-171-14
Sequence 14, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:

APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..119
OTHER INFORMATION: /note= "Sequence of Humanized
Patent No. 5562903
OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant H-hu-BR55-2/3"
FEATURE:
NAME/KEY: Region
LOCATION: 31..35
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 50..66
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 99..108
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
US-08-053-171-14

Query Match 70.9%; Score 39; DB 1; Length 119;
Best Local Similarity 60.0%; Pred. No. 5,6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WYAKVSGGG 10
DB 47 WYATISNGGG 56

RESULT 9
US-08-053-171-17
Sequence 17, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner

;; TITLE OF INVENTION: Antibody Derivatives
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: 22-APR-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-54-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..119
;; OTHER INFORMATION: /note= "Sequence of the heavy chain
;; Patent No. 5562903
;; OTHER INFORMATION: of humanized BR55-2/3 antibody."
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 31..35
;; OTHER INFORMATION: /note= "Complementarity-determining
;; OTHER INFORMATION: region"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 50..66
;; OTHER INFORMATION: /note= "Complementarity-determining
;; OTHER INFORMATION: region"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 99..108
;; OTHER INFORMATION: /note= "Complementarity-determining
;; OTHER INFORMATION: region"
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 42
;; OTHER INFORMATION: /note= "Residue in the framework
;; OTHER INFORMATION: replaced with mouse amino acid in the humanized
;; OTHER INFORMATION: antibody."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 44
;; OTHER INFORMATION: /note= "Residue replaced with mouse
;; OTHER INFORMATION: amino acid in humanized antibody."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 73..75
;; OTHER INFORMATION: /note= "Residues replaced with
;; OTHER INFORMATION: mouse amino acids in humanized antibody."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 82
;; OTHER INFORMATION: /note= "Residue replaced with mouse

;; OTHER INFORMATION: amino acids in humanized antibody."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 87
;; OTHER INFORMATION: /note= "Residue replaced with mouse
;; OTHER INFORMATION: amino acid in humanized antibody."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 109
;; OTHER INFORMATION: /note= "Residue replaced with mouse
;; OTHER INFORMATION: amino acid in humanized antibody."
;; US-08-053-171-17
;;
;; Query Match 70.9%; Score 39; DB 1; Length 119;
;; Best Local Similarity 60.0%; Pred. No. 5.6;
;; Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
;;
;; Qy 1 WYAKVSGGG 10
;; III : III
;; Db 47 WYAYISNGG 56
;;
;; RESULT 10
;; US-08-815-190A-13
;; Sequence 13, Application US/08815190A
;; Patent No. 6046310
;; GENERAL INFORMATION:
;; APPLICANT: Queen, Cary L.
;; APPLICANT: Schneider, William P.
;; APPLICANT: Vasquez, Maximiliano
;; TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
;; TITLE OF INVENTION: Uses
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/815,190A
;; FILING DATE: 11-MAR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/614,584
;; FILING DATE: 13-MAR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 011823-006710US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..119
;; OTHER INFORMATION: /note= "mature heavy chain variable
;; OTHER INFORMATION: region of humanized ABL 364 antibody"
;; US-08-815-190A-13

Query Match 70.9%; Score 39; DB 3; Length 119;
Best Local Similarity 60.0%; Pred. No. 5.6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : |||
Db 47 WWAYISGGG 56

RESULT 11
US-07-634-278-48
; Sequence 48, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-48

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : |||
Db 47 WWAYISGGG 56

RESULT 12
US-07-634-278-49
; Sequence 49, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-49

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : |||
Db 47 WWAYISGGG 56

RESULT 13
US-08-477-728-48
; Sequence 48, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.

APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-48

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
Db 47 WVASIRGGG 56

RESULT 14
US-08-477-728-49
Sequence 49, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-49

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
Db 47 WVASIRGGG 56

RESULT 15
US-08-474-040-48
Sequence 48, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/474,040
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-474-040-48

Query Match 70.9%; Score 39; DB 1; Length 122;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 WVAKVKGSGG 10
Db 47 WVASISRGSGG 56
||| : |||

Search completed: March 28, 2001, 06:39:10
Job time: 764 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:50 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVOG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	92.9	111	2 S51211	Ig heavy chain V r
2	52	92.9	113	2 S02717	Ig heavy chain V r
3	52	92.9	113	2 S26468	Ig heavy chain V r
4	52	92.9	115	2 PH1538	Ig H chain V regio
5	52	92.9	117	1 HVMSRF	Ig heavy chain pre
6	52	92.9	117	1 HVMS84	Ig heavy chain pre
7	52	92.9	117	1 HVMS34	Ig heavy chain pre
8	52	92.9	117	2 PH1552	Ig H chain V regio
9	52	92.9	119	2 PH1548	Ig H chain V regio
10	52	92.9	119	2 PH1549	Ig H chain V regio
11	49	87.5	108	2 PH1006	Ig heavy chain V r
12	49	87.5	118	2 PH1532	Ig H chain V regio
13	49	87.5	118	2 PH1550	Ig H chain V regio
14	49	87.5	119	2 PH1544	Ig H chain V regio
15	49	87.5	119	2 PH1551	Ig H chain V regio
16	49	87.5	119	2 PH1547	Ig H chain V regio
17	49	87.5	119	2 PH1555	Ig H chain V regio
18	49	87.5	119	2 PH1531	Ig H chain V regio
19	49	87.5	119	2 PH1533	Ig H chain V regio
20	49	87.5	120	2 PH1534	Ig H chain V regio
21	49	87.5	122	2 PH1537	Ig H chain V regio
22	48	85.7	70	2 PL0250	Ig heavy chain V r
23	48	85.7	97	1 HVMS91	Ig heavy chain V r
24	48	85.7	108	2 PL0248	Ig heavy chain V r
25	48	85.7	111	2 PH1007	Ig heavy chain V r
26	48	85.7	112	2 S26327	Ig heavy chain V r
27	48	85.7	117	2 PH1535	Ig H chain V regio
28	48	85.7	117	2 PH1553	Ig H chain V regio
29	48	85.7	117	2 PH1542	Ig H chain V regio

30	48	85.7	117	2 PL0249	Ig heavy chain V r
31	48	85.7	117	2 PL0252	Ig heavy chain V r
32	48	85.7	118	2 PH1539	Ig H chain V regio
33	48	85.7	119	2 PH1554	Ig H chain V regio
34	48	85.7	119	2 PH0098	Ig heavy chain V r
35	48	85.7	120	2 B49715	Ig heavy chain V r
36	46	82.1	108	2 PH1011	Ig heavy chain V r
37	46	82.1	111	2 S40090	Ig heavy chain - m
38	46	82.1	112	2 A27889	Ig heavy chain V r
39	46	82.1	119	2 PH1541	Ig H chain V regio
40	46	82.1	119	2 PH1546	Ig H chain V regio
41	46	82.1	121	2 H27888	Ig heavy chain V r
42	46	82.1	123	2 G27888	Ig heavy chain V r
43	46	82.1	124	2 I27888	Ig heavy chain V r
44	45	80.4	103	2 PH1528	Ig H chain V regio
45	45	80.4	114	2 PH1009	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S51211
Ig heavy chain V region (AC7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S51211; S58929
R:Jarvin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.
FEBS Lett. 354; 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an ant
A:Reference number: S51210; MUID:95046326
A:Accession: S51211
A:Molecule type: mRNA
A:Residues: 9-111 <JAR>
A:Accession: S58929
A:Molecule type: protein
A:Residues: 1-20 <JAR2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVOG 10
|||||||:1
Db 57 STYYPDTVKG 66

RESULT 2

S02717
Ig heavy chain V region (clone pH62) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.
submitted to the EMBL Data Library, February 1989
C:Accession: S02717
A:Reference number: S02717
A:Accession: S02717
A:Molecule type: DNA
A:Residues: 1-113 <SOL>
A:Cross-references: EMBL:Y00744; NID:g52472; PIDN:CAA68713.1; PID:g1334095
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 113;
Best Local Similarity 90.0%; Pred. No. 0.017;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 DB 57 STYYPDTVKG 66

RESULT 3

Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26468
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26468
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <KAV>
 A:Cross-references: EMBL:X59107; NID:g51944; PDB:CAA41833.1; PID:g51945
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 113;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 DB 53 STYYPDTVKG 62

RESULT 4

Ig H chain V region (clone 13G12) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
 C:Accession: PH1538
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1538
 A:Molecule type: mRNA
 A:Residues: 1-115 <MUK>
 A:Note: the stop codons X appear in residues 82, 85 and 106
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 115;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 DB 56 STYYPDTVKG 65

RESULT 5

Ig heavy chain precursor V region (RF) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0503
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0503

A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; hybridoma; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 DB 76 STYYPDTVKG 85

RESULT 6

Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0505
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0505

A:Status: translation not shown

A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 DB 76 STYYPDTVKG 85

RESULT 7

Ig heavy chain precursor V region (345) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0502
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0502

A:Status: translation not shown

A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 |||||:|
 Db 76 STYYPDTVKG 85

RESULT 8

PH1552
 Ig H chain V region (clone 16E4) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
 C:Accession: PH1552
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1552
 A:Molecule type: mRNA
 A:Residues: 1-117 <MUK>
 A:Note: the stop codon X appears in residue 87
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 |||||:|
 Db 57 STYYPDTVKG 66

RESULT 9

PH1548
 Ig H chain V region (clone 12F4) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1548
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1548
 A:Molecule type: mRNA
 A:Residues: 1-119 <MUK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 119;
 Best Local Similarity 90.0%; Pred. No. 0.018;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 |||||:|
 Db 57 STYYPDTVKG 66

RESULT 10

PH1549
 Ig H chain V region (clone 13F1) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1549
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1549
 A:Molecule type: mRNA
 A:Residues: 1-119 <MUK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 119;
 Best Local Similarity 90.0%; Pred. No. 0.018;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 |||||:|
 Db 57 STYYPDTVKG 66

RESULT 11

PH1006

Ig heavy chain V region (clone 202.33) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1006
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1006
 A:Molecule type: mRNA
 A:Status: nucleic acid sequence not shown
 A:Residues: 1-108 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 0.057;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 :|||:|
 Db 52 NTYYPDTVKG 61

RESULT 12

PH1532

Ig H chain V region (clone 4B4) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1532
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1532
 A:Molecule type: mRNA
 A:Residues: 1-118 <MUK>
 A:Note: the stop codons X appear in residues 82 and 85
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 118;
 Best Local Similarity 80.0%; Pred. No. 0.062;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
:|||||:|
Db 56 NTYYPDTVKG 65

RESULT 13

PH1550
Ig H chain V region (clone 14E1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1550
J. Exp. Med. 177, 1105-1116, 1993
R: Mukherjee, J.; Casadevall, A.; Scharff, M.D.
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1550
A:Molecule type: mRNA
A:Residues: 1-118 <MUK>
A:Note: the stop codon X appears in residue 30
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.063;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
:|||||:|
Db 56 NTYYPDTVKG 65

RESULT 14

PH1544
Ig H chain V region (clone 9E11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1544
J. Exp. Med. 177, 1105-1116, 1993
R: Mukherjee, J.; Casadevall, A.; Scharff, M.D.
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1544
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
A:Note: the stop codons X appear in residues 83, 86 and 107
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.063;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
:|||||:|
Db 57 NTYYPDTVKG 66

RESULT 15

PH1551
Ig H chain V region (clone 15E8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1551
J. Exp. Med. 177, 1105-1116, 1993
R: Mukherjee, J.; Casadevall, A.; Scharff, M.D.
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1551
A:Molecule type: mRNA

A:Residues: 1-119 <MUK>
A:Note: the stop codons X appear in residues 88, 100 and 107
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.063;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
:|||||:|
Db 57 NTYYPDTVKG 66

Search completed: March 28, 2001, 06:41:50
Job time: 873 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:48 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues 87993
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	Description
1	52	92.9	117	1 HV53_MOUSE
2	52	92.9	117	1 HV54_MOUSE
3	52	92.9	117	1 HV55_MOUSE
4	48	85.7	97	1 HV56_MOUSE
5	44	78.6	98	1 HV57_MOUSE
6	44	78.6	117	1 HV58_MOUSE
7	44	78.6	117	1 HV59_MOUSE
8	40	71.4	116	1 HV05_CARAU
9	39	69.6	117	1 HV3C_HUMAN
10	39	69.6	706	1 HDAL_YEAST
11	37	66.1	115	1 HV3F_HUMAN
12	37	66.1	426	1 GUNZ_ERWCH
13	37	66.1	517	1 FGR_MOUSE
14	37	66.1	3433	1 POLG_KUNJM
15	36	64.3	119	1 PV3L_HUMAN
16	36	64.3	329	1 HV22_CAEEL
17	36	64.3	624	1 YE70_METJA
18	36	64.3	889	1 IREB_CHICK
19	35	62.5	117	1 HV02_CANFA
20	35	62.5	121	1 HV3J_HUMAN
21	35	62.5	519	1 ACH4_DROME
22	34	61.6	507	1 VLL_HPV09
23	34	60.7	352	1 GBAL_CORPO
24	34	60.7	358	1 COQ2_SCHPO
25	34	60.7	566	1 Y397_MYCGE
26	34	60.7	763	1 DPOL_HPEVP
27	34	60.7	969	1 MSU1_YEAST
28	33	58.9	214	1 SC14_SCHCO
29	33	58.9	434	1 TRB2_AQUAE
30	33	58.9	477	1 YQ06_CAEEL
31	33	58.9	481	1 MEC2_CAEEL
32	33	58.9	532	1 HEXA_DICDI
33	33	58.9	608	1 YLP5_CAEEL

34	33	58.9	814	1 GUNE_CLOTH	P10477 clostridium
35	33	58.9	870	1 FIMD_SALTY	P37924 salmonella
36	33	58.9	889	1 IRE1_HUMAN	P21399 homo sapien
37	33	58.9	889	1 IRE1_MOUSE	P28271 mus musculus
38	33	58.9	889	1 IRE1_RABIT	Q01059 oryctolagus
39	33	58.9	889	1 IRE1_RAT	Q63270 rattus norv
40	33	58.9	987	1 EPB4_MOUSE	P54761 mus musculus
41	33	58.9	1005	1 MANA_DICDI	P34098 dictyostell
42	33	58.9	3430	1 POLG_WNV	P06935 w genome po
43	32	57.1	96	1 YC4_TYLCV	P27271 tomato yell
44	32	57.1	207	1 RAB7_MESCR	P93267 mesembryant
45	32	57.1	251	1 YRPE_BACSU	O05410 bacillus su

ALIGNMENTS

RESULT 1
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION RF PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
PIR: JT0503; HVMSRF.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; Ig 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CR3295F390F725B CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 76 STYYPDTVKRG 85

RESULT 2
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.

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RN  SEQUENCE FROM N.A.
RC  STRAIN=BALB/CJ;
RX  MEDLINE: 89279149.
RA  Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during
RL  the primary immune response.";
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR  INTERPRO: IPR003006; -.
DR  PFAM: PF00047; Ig: 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 19
FT  CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT  DOMAIN 20 49 FRAMEWORK 1.
FT  DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT  DOMAIN 55 68 FRAMEWORK 2.
FT  DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT  DOMAIN 86 117 FRAMEWORK 3.
FT  DISULFID 41 115 BY SIMILARITY.
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVOG 10
DB 76 STYYPDTVKG 85

RESULT 3
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVOG 10
DB 76 STYYPDTVKG 85

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QY 1 STYYPDTVOG 10
DB 76 STYYPDTVKG 85

RESULT 4
HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J00504; HVMS91.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVOG 10
DB 56 STYYPDSVKG 65

RESULT 5
HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J00501; HVMS96.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7E92FBF95B CRC64;

Query Match 78.6%; Score 44; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.11;

```

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDVTQVG 10
|||||:|

Db 58 TYYPDSVKG 66

RESULT 6

HV58_MOUSE STANDARD; PRT; 117 AA.

AC P18529;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;

RX MEDLINE; 89279149.

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR: JT0506; HVMS57.

DR INTERPRO: IPR003006;

DR PFAM: PF00047; Ig; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.

FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 55 68 FRAMEWORK 2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 86 117 FRAMEWORK 3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12991 MW; 93A04782B7888FA0 CRC64;

Query Match

Best Local Similarity 78.6%; Score 44; DB 1; Length 117;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDVTQVG 10
|||||:|

Db 77 TYYPDSVKG 85

RESULT 7

HV59_MOUSE STANDARD; PRT; 117 AA.

AC P18530;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;

RX MEDLINE; 89279149.

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

the primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

DR PIR: JT0507; HVMS39.

DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.

FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 55 68 FRAMEWORK 2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 86 117 FRAMEWORK 3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match

Best Local Similarity 78.6%; Score 44; DB 1; Length 117;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDVTQVG 10
|||||:|

Db 77 TYYPDSVKG 85

RESULT 8

HV05_CARAU

ID HV05_CARAU STANDARD; PRT; 116 AA.

AC P19181;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION 5A PRECURSOR.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 88144476.

RA Wilson M.R., Middleton D., Warr G.W.;

RT "Immunoglobulin heavy chain variable region gene evolution: structure

and family relationships of two genes and a pseudogene in a teleost

fish.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).

DR PIR: B28966; B28966.

DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.

FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 55 68 FRAMEWORK 2.

FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 85 116 FRAMEWORK 3.

FT DISULFID 41 114 BY SIMILARITY.

FT NON_TER 116 116

SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match

Best Local Similarity 71.4%; Score 40; DB 1; Length 116;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
|||||:|

Db 75 STYYPDSVKG 84

RESULT 9

HV3C_HUMAN

ID HV3C_HUMAN STANDARD; PRT; 117 AA.

AC P01764;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81101090.
 RA Matthysens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 RT heavy chain variable region."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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 CC or send an email to license@isb-sib.ch)
 CC -----
 CC EMBL; J00236; AAA53516.1; -;
 DR EMBL; M35415; AAA58735.1; -;
 DR PIR; A02047; H3HU26.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 12582 MW; E826733FIA3CB0F1 CRC64;
 SQ

 Query Match 69.6%; Score 39; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 STYYPDTVOG 10
 DB 76 STYYGDSVKG 85

 RESULT 10
 HDAL_YEAST
 ID HDAL_YEAST STANDARD; PRT; 706 AA.
 AC P53973;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HISTONE DEACETYLASE HDAL.
 GN HDAL OR YNL021W OR N2819.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andre B., Iraqi Houssaini I., Urrestazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE; 97121415.
 RA Rundlett S.E., Carmen A.A., Kobayashi R., Bavykin S., Turner B.M.,
 RA Grunstein M.;
 RT "HDAL and RPD3 are members of distinct yeast histone deacetylase
 RT complexes that regulate silencing and transcription."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).
 CC -1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
 CC THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
 CC HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
 CC REGULATION AND CELL CYCLE PROGRESSION.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch)
 CC -----
 CC EMBL; 271297; CAA95883.1; -;
 DR SGD; S0004966; HDAL.
 DR INTERPRO; IPR000286; -;
 DR PFAM; PF00850; Hist.deacetyl; 1.
 DR PRINTS; PR01270; HDASUPER.
 KW Hydrolase; Nuclear protein.
 SQ SEQUENCE 706 AA; 80069 MW; 4E7069E66D03264D CRC64;

 Query Match 69.6%; Score 39; DB 1; Length 706;
 Best Local Similarity 75.0%; Pred. No. 8.4;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 3 YYPDTVOG 10
 DB 275 YYPGTIQG 282

 RESULT 11
 HV3F_HUMAN
 ID HV3F_HUMAN STANDARD; PRT; 115 AA.
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION BUT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 78137069.
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 RT IgA2 immunoglobulin of the A2m (2) allotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 DR PIR; A02050; A2HUBU.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 115 115
 FT SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;
 SQ

 Query Match 66.1%; Score 37; DB 1; Length 115;
 Best Local Similarity 60.0%; Pred. No. 2.7;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 QY 1 STYYPDTVOG 10
 DB 56 TTYADSVKG 65

 RESULT 12
 GUNZ_ERWCH
 ID GUNZ_ERWCH STANDARD; PRT; 426 AA.
 AC P07103;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ENDOGLUCANASE Z PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE Z)
 GN (CELLULOSE Z) (EGZ).
 OS CELZ OR CEL5.
 OC Erwinia chrysanthemi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 RN Pectobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3937;
 RX MEDLINE: 88216177.
 RA Guiseppe A., Cami B., Aymeric J.-L., Ball G., Creuzet N.;
 RT "Homology between endoglucanase Z of Erwinia chrysanthemi and
 RT endoglucanases of Bacillus subtilis and alkalophilic Bacillus";
 RL Mol. Microbiol. 2:159-164(1988).
 RN [2]
 RP REVISIONS, AND DISULFIDE BOND.
 RC STRAIN=3937;
 RX MEDLINE: 94203057.
 RA Bortoli-German I., Brun E., Py B., Chippaux M., Barras F.;
 RT "Periplasmic disulphide bond formation is essential for cellulase
 RT secretion by the plant pathogen Erwinia chrysanthemi.";
 RL Mol. Microbiol. 11:545-553(1994).
 RN [3]
 RP MUTAGENESIS, AND DOMAINS.
 RX MEDLINE: 91312880.
 RA Py B., Bortoli-German I., Haiech J., Chippaux M., Barras F.;
 RT "Cellulase EGZ of Erwinia chrysanthemi: structural organization and
 RT importance of His98 and Glu133 residues for catalysis.";
 RL Protein Eng. 4:325-333(1991).
 RN [4]
 RP STEREOCHEMISTRY OF THE REACTION.
 RC MEDLINE: 92225124.
 RA Barras F., Bortoli-German I., Bauzan M., Rouvier J., Gey C.,
 RA Heyraud A., Henrissat B.;
 RT "Stereochemistry of the hydrolysis reaction catalyzed by
 RT endoglucanase Z from Erwinia chrysanthemi.";
 RL FEBS Lett. 300:145-148(1992).
 RN [5]
 RP STRUCTURE BY NMR OF 365-426.
 RX MEDLINE: 98070232.
 RA Brun E., Moriad F., Gans P., Blackledge M.J., Barras F., Marlon D.;
 RT "Solution structure of the cellulose-binding domain of the
 RT endoglucanase Z secreted by Erwinia chrysanthemi.";
 RL Biochemistry 36:16074-16086(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.30 ANGSTROMS) OF 44-335.
 RA Czjzek M., el Hassouni M., Py B., Juy M., Bortoli-German I.,
 RA Barras F.;
 RT "Protein secretion in Gram-negative pathogenic bacteria: the study of
 RT the structure/function relationships of the Erwinia chrysanthemi
 RT cellulase cel5 (former egz).";
 RL Submitted (MAR-1999) to the PDB data bank.
 CC -!- FUNCTION: REPRESENTS 97% OF THE GLOBAL CELLULOSE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF 1,4-BETA-D-GLUCOSIDIC
 CC LINKAGES IN CELLULOSE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC -----
 CC EMBL: Y00540; CAA68604.1; -
 DR PIR: S03767; S03767.
 DR PDB: 1AIW; 06-MAY-98.
 DR PDB: 1EGZ; 26-MAR-99.
 DR INTERPRO: IPR001547; -
 DR PFAM: PF00150; cellulase; 1.

DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
 FT SIGNAL 1 43
 FT CHAIN 44 426 ENDOGLUCANASE Z.
 FT DOMAIN 44 332 CATALYTIC.
 FT DOMAIN 333 366 LINKER.
 FT DOMAIN 367 426 CELLULOSE-BINDING.
 FT ACT_SITE 176 176 PROTON DONOR.
 FT ACT_SITE 263 263 NUCLEOPHILE (BY SIMILARITY).
 FT MUTAGEN 141 141 H->A: LOSS OF ACTIVITY.
 FT MUTAGEN 176 176 E->A: LOSS OF ACTIVITY.
 FT DISULFID 368 425
 FT CONFLICT 293 295
 FT CONFLICT 350 364 SNA -> QLTQ (IN REF. 1).
 FT CONFLICT 388 426 TDTTVDEPTTDTTPA -> MTPPLTNRPQPTHQ (IN
 FT REF. 1).
 FT CONFLICT 426 THNEAGOSIVYKGNLYTANWYTASVPGSDSSKTVGSCN
 FT -> LITQANSSSTKATCIPQTGPHPPRAALPPGRLV
 FT AVTN (IN REF. 1).
 SQ SEQUENCE 426 AA; 46418 MW; E78F2EE021FCA5DA CRC64;
 Query Match 66.18; Score 37; DB 1; Length 426;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYYPDT 7
 Db 307 STYYPDS 313
 RESULT 13
 FGR_MOUSE
 ID FGR_MOUSE STANDARD; PRT; 517 AA.
 AC P14234;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR)
 DE (C-FGR).
 GN FGR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2J;
 RX MEDLINE: 89385605.
 RA Yi T.L., Willman C.L.;
 RT "Cloning of the murine c-fgr proto-oncogene cDNA and induction of
 RT c-fgr expression by proliferation and activation factors in normal
 RT bone marrow-derived monocytic cells.";
 RL Oncogene 4:1081-1087(1989).
 CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X16440; CAA34463.1; -
 DR PIR: A33127; A33127.
 DR PIR: S10072; S10072.
 DR HSP: P00523; 2PTK.
 DR MGD: MGI:95527; FGR.
 DR INTERPRO: IPR000719; -

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DR INTERPRO: IPR000980; -
DR INTERPRO: IPR001245; -
DR INTERPRO: IPR001452; -
DR PFAM: PF00017; SH2; 1.
DR PFAM: PF00018; SH3; 1.
DR PFAM: PF00069; kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00001; SH2; 1.
DR PROSITE: PS00002; SH3; 1.
DR TRANSFERASE: Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain; SH3 domain.
FT DOMAIN 65 126
FT DOMAIN 132 229
FT DOMAIN 251 504
FT NP_BIND 257 265
FT BINDING 279 279
FT ACT_SITE 370 370
FT MOD_RES 400 400
SQ SEQUENCE 517 AA; 5867 MW; F655BDB4510F3076 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 517;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYPDTVQG 10
Db 32 YYPDTQG 39

RESULT 14
POLG_KUNJM STANDARD; PRT; 3433 AA.
AC P14335; Q82983;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA
DE POLYMERASE (EC 2.7.7.48) (NS5)].
OS Kunjin virus (strain MRM61C).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88089524.
RA Cola G., Parker M.D., Byrne M.E., Westaway E.G.;
RT "Nucleotide and complete amino acid sequences of Kunjin virus:
RT definitive gene order and characteristics of the virus-specified
RT proteins";
RL J. Gen. Virol. 69:1-21(1988).
CC -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA.
CC
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CC -----

EMBL: D00246; BAA00176.1; -
PIR: A28697; GNWVKV.
HSSP: P14336; 1SVB.
DR INTERPRO: IPR000069; -
DR INTERPRO: IPR000208; -
DR INTERPRO: IPR000336; -
DR INTERPRO: IPR000404; -
DR INTERPRO: IPR000487; -
DR INTERPRO: IPR000752; -
DR INTERPRO: IPR001122; -
DR INTERPRO: IPR001157; -
DR INTERPRO: IPR001528; -
DR INTERPRO: IPR001850; -
DR INTERPRO: IPR002535; -
DR PFAM: PF01004; Flavi_M; 1.
DR PFAM: PF00948; Flavi_NS1; 1.
DR PFAM: PF01005; Flavi_NS2A; 1.
DR PFAM: PF01002; Flavi_NS2B; 1.
DR PFAM: PF01350; Flavi_NS4; 1.
DR PFAM: PF01349; Flavi_NS4B; 1.
DR PFAM: PF00972; Flavi_NS5; 1.
DR PFAM: PF01003; Flavi_capsid; 1.
DR PFAM: PF00869; Flavi_glycoprot; 1.
DR PFAM: PF00949; Flavi_helicase; 1.
DR PFAM: PF01570; Flavi_propep; 1.
KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
KW Transmembrane; Nonstructural protein.
INIT_MET 1
CHAIN 1 123
FT CHAIN 124 215
FT CHAIN 216 290
FT CHAIN 291 791
FT CHAIN 792 1143
FT CHAIN 1144 1374
FT CHAIN 1375 1505
FT CHAIN 1506 2124
FT CHAIN 2125 2273
FT CHAIN 2274 2528
FT CHAIN 2529 3433
FT NP_BIND 1699 1706
FT SITE 1790 1793
FT DISULFID 293 320
FT DISULFID 350 406
FT DISULFID 364 395
FT DISULFID 382 411
FT DISULFID 480 578
FT DISULFID 595 626
FT CARBOHYD 138 138
FT CARBOHYD 921 921
FT CARBOHYD 966 966
FT CARBOHYD 998 998
SQ SEQUENCE 3433 AA; 381363 MW; EE4B888A7D040B99 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 3433;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYPDTVQG 10
Db 825 YYPETPQG 832

RESULT 15
HV3L_HUMAN STANDARD; PRT; 119 AA.
ID HV3L_HUMAN
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE IG HEAVY CHAIN V-III REGION BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE; 79151016.
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
 RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR; A02056; ALH0BR.
 DR HSSP; P01772; 2IG2.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 119;
 Best Local Similarity 66.7%; Pred. No. 4.3;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYPDPTVOG 10
 ||| |:
 Db 58 TYADSVRG 66

Search completed: March 28, 2001, 07:29:49
 Job time: 1656 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:42 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-56

Perfect score: 56

Sequence: 1 STYPPDTVQG 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	71.4	77	4 075728	075728 homo sapien
2	40	71.4	121	4 09UL71	09UL71 homo sapien
3	40	71.4	426	2 09REW0	09REW0 erwinia chr
4	40	71.4	1151	11 09QVN5	09QVN5 rattus sp.
5	39	69.6	594	8 09T3A0	09T3A0 nephroselimi
6	39	69.6	3839	3 09P421	09P421 neurospora
7	38	67.9	534	5 09VM10	09VM10 drosophila
8	38	67.9	2126	4 09UD02	09UD02 homo sapien
9	38	67.9	3460	4 078509	078509 homo sapien
10	37	66.1	262	13 09PWN6	09PWN6 brachydanio
11	37	66.1	517	11 063206	063206 rattus norv
12	37	66.1	517	11 061404	061404 mus musculus
13	37	66.1	622	5 09NBC7	09NBC7 helisoma tr
14	37	66.1	962	12 089443	089443 african swi
15	37	66.1	3209	13 093574	093574 gallus gall
16	37	66.1	3433	12 09Q6P4	09Q6P4 west nile v
17	37	66.1	3433	12 09Q5I9	09Q5I9 west nile v
18	37	66.1	3433	12 09Q3G9	09Q3G9 west nile v
19	37	66.1	3461	11 060841	060841 mus musculus

20 36 64.3 77 4 075741
21 36 64.3 116 12 Q9JH40
22 36 64.3 116 12 Q9IR73
23 36 64.3 118 4 Q9UL72
24 36 64.3 194 5 016565
25 36 64.3 326 5 017863
26 36 64.3 352 2 005938
27 36 64.3 534 2 Q9K996
28 36 64.3 837 5 Q9W326
29 35 62.5 258 5 09Y0E9
30 35 62.5 331 5 Q9VR49
31 35 62.5 519 5 Q9VC71
32 35 62.5 715 10 Q9SFB8
33 35 62.5 731 3 074693
34 35 62.5 799 4 Q9P0U2
35 35 62.5 807 4 Q9Y2R2
36 35 62.5 808 4 095063
37 35 62.5 1252 2 Q9ZA93
38 35 62.5 1252 2 Q9KUV0
39 35 62.5 3097 5 015943
40 34 60.7 82 4 075732
41 34 60.7 129 2 060111
42 34 60.7 129 12 P89125
43 34 60.7 129 12 P89130
44 34 60.7 141 12 Q9WRV2
45 34 60.7 141 12 Q9WRV1

ALIGNMENTS

RESULT 1
075728 PRELIMINARY; PRT; 77 AA.
AC 075728;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA Fischer M., Kueppers R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily mutated VH region genes";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009525; CAA08732.1;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8925 MW; 08EAEF6F1ECEFB66 CRC64;

Query Match 71.4%; Score 40; DB 4; Length 77;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYPPDTVQG 10
Db 27 TFYPPDSVKG 35

RESULT 2
09UL71 PRELIMINARY; PRT; 121 AA.
ID 09UL71
AC 09UL71;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -;
 DR HSSP; P01772; 2FB4.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; 19; 1.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 71.4%; Score 40; DB 4; Length 121;
 Best Local Similarity 70.0%; Pred. No. 3.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDTVOG 10
 ||||| I:I:I
 Db 57 STYYADSVKG 66

RESULT 3

Q9REWO PRELIMINARY; PRT; 426 AA.
 AC Q9REWO;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE ENDO-1,4-BETA-GLUCANASE PRECURSOR (EC 3.2.1.4).
 GN CEL52.
 OS Erwinia chrysanthemi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PY35;
 RA Park S.R., Yun H.D.;
 RT "Beta-(1,4)-glucan glucanohydrolase precursor (cel52).";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF208495; AAF18152.1; -;
 DR HSSP; P07103; IEGZ.
 DR INTERPRO; IPR001547; -;
 DR PFAM; PF00150; cellulase; 1.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
 KW Hydrolase; Glycosidase.
 SQ SEQUENCE 426 AA; 46501 MW; 60217A1C6C05FE16 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 426;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTV 8
 ||||| I:
 Db 307 STYYPDSI 314

RESULT 4

Q9QVN5 PRELIMINARY; PRT; 1151 AA.
 ID Q9QVN5

AC Q9QVN5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE NEUROFASCIN ISOFORM.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97103184; PubMed=8947556;
 RA Davis J.Q., Lambert S., Bennett V.;
 RT "Molecular composition of the node of Ranvier: identification of
 ankyrin-binding cell adhesion molecules neurofascin (mucin+/third
 FNIII domain-) and NrCAM at nodal axon segments.";
 RL J. Cell Biol. 135:1355-1367(1996).
 DR HSSP; P20241; ICFB.
 DR INTERPRO; IPR001777; -;
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00041; fn3; 4.
 DR PFAM; PF00047; ig; 6.
 SQ SEQUENCE 1151 AA; 129732 MW; 770BD492C4A4ECC5 CRC64;

Query Match 71.4%; Score 40; DB 11; Length 1151;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YPDTVOG 10
 ||||| I:
 Db 823 YPDTVOG 829

RESULT 5

Q9T3A0 PRELIMINARY; PRT; 594 AA.
 ID Q9T3A0;
 AC Q9T3A0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE HYPOTHETICAL 67.7 KDA PROTEIN.
 OS Nephroselmis olivacea.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
 OC Chlorodendreales; Chlorodendraceae; Nephroselmis.
 OX NCBI_TaxID=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Turmel M., Otis C., Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga Nephroselmis
 olivacea: Insights into the architecture of ancestral chloroplast
 genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Turmel M., Otis C., Lemieux C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF137379; AAD54924.1; -;
 DR EMBL; AF137379; AAD54865.1; -;
 KW Hypothetical protein; Chloroplast.
 SQ SEQUENCE 594 AA; 67671 MW; C6AD240A53F19231 CRC64;

Query Match 69.6%; Score 39; DB 8; Length 594;
 Best Local Similarity 70.0%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STYYPDTVOG 10
 I: ||||| I
 Db 223 SSLYPDTVHG 232

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RESULT 6
Q9P4Z1 ID Q9P4Z1 PRELIMINARY; PRT; 3839 AA.
AC Q9P4Z1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE RELATED TO TOM1 PROTEIN.
GN B1B22.10.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL356834; CAB92704.1; -
SQ SEQUENCE 3839 AA; 427187 MW; 6A9E57DEB48A5D9D CRC64;

Query Match 69.6%; Score 39; DB 3; Length 3839;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYPDVTQV 10
DB 286 SYPDVTNG 294

RESULT 7
Q9VM10 ID Q9VM10 PRELIMINARY; PRT; 534 AA.
AC Q9VM10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CG12789 PROTEIN.
GN CG12789.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe W., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegun C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003617; AAF52518.1; -
DR FLYBASE: FBgn0031915; CG12789.
DR INTERPRO: IPR002159; -
DR PFAM: PF01130; CD36; 1.
SQ SEQUENCE 534 AA; 59828 MW; 163A3E2DF27D5CBE CRC64;

Query Match 67.9%; Score 38; DB 5; Length 534;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYPDVTQV 10
DB 338 YYPDQVEG 345

RESULT 8
Q9UDQ2 ID Q9UDQ2 PRELIMINARY; PRT; 2126 AA.
AC Q9UDQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE EXTRACELLULAR MATRIX PROTEIN REELIN (FRAGMENT).
GN RELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Maas J., Bauer C., Sapetti L.;
RT "The sequence of Homo sapiens PAC clone RP4-672Q11.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006316; AAD29127.1; -
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR002860; -
DR PFAM: PF00008; EGF; 3.
DR PFAM: PF02012; BNR; 11.
DR PROSITE: PS00022; EGF_1; UNKNOWN_5.
DR PROSITE: PS01186; EGF_2; 5.
KW Matrix protein.

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FT NON_TER      1      1
SQ SEQUENCE     2126 AA; 238614 MW; 07F73154549C36C5 CRC64;

Query Match      67.9%; Score 38; DB 4; Length 2126;
Best Local Similarity 70.0%; Pred. No. 2;ler+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
||||| |:||
Db 1647 STYYACTWQG 1656

RESULT 9
ID P78509 PRELIMINARY; PRT; 3460 AA.
AC P78509;
DT 01-MAY-1997 (TremBLrel. 03, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE RELIN.
GN RELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA DeSilva U., D'Arcangelo G., Braden V.V., Chen J., Miao G.G.,
RA Curran T., Green E.D.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 194-430 FROM N.A.
RA Lamar B., Wamsley P., Gibson A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79716; AAC51105.1; -.
DR EMBL; AC000121; AAB46357.1; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR002860; -.
DR INTERPRO; IPR002861; -.
DR PFAM; PF00008; EGF; 5.
DR PFAM; PF02012; BNR; 15.
DR PFAM; PF02014; Reeler; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_7.
DR PROSITE; PS01186; EGF_2; 6.
KW Glycoprotein.
SQ SEQUENCE 3460 AA; 388399 MW; BB2C0BA415AB93C1 CRC64;

Query Match      67.9%; Score 38; DB 4; Length 3460;
Best Local Similarity 70.0%; Pred. No. 3;7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
||||| |:||
Db 2077 STYYACTWQG 2086

RESULT 10
ID Q9PWM6 PRELIMINARY; PRT; 262 AA.
AC Q9PWM6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE HOMEBOX PROTEIN.
GN HOXD9A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RT "zebrafish hox clusters and vertebrate genome evolution.";
RL Science 282:1711-1714(1998).
DR EMBL; AF071268; AAD15961.1; -.
DR HSSP; P02834; 1B8I.
DR INTERPRO; IPR000047; -.
DR INTERPRO; IPR001356; -.
DR PFAM; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 262 AA; 29731 MW; 93BC979F8677CA27 CRC64;

Query Match      66.1%; Score 37; DB 13; Length 262;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
||||| |:||
Db 8 SSYYVDITMG 17

RESULT 11
ID Q63206 PRELIMINARY; PRT; 517 AA.
AC Q63206;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE FGR MRNA.
GN FGR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=F344; TISSUE=LEUKEMIA;
RA Yue C.C., Labash J.D., Jaye M.;
RL Nucleic Acids Res. 0:0-0(1990).
DR EMBL; X57018; CAA40337.1; -.
DR HSSP; P12931; 1FMK.
DR INTERPRO; IPR000719; -.
DR INTERPRO; IPR000980; -.
DR INTERPRO; IPR001245; -.
DR INTERPRO; IPR001452; -.
DR PFAM; PF00017; SH2; 1.
DR PFAM; PF00018; SH3; 1.
DR PFAM; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ SEQUENCE 517 AA; 58792 MW; 852F8BF3778C403F CRC64;

Query Match      66.1%; Score 37; DB 11; Length 517;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YYPDTVQG 10

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Db 32 YPDPQTQ 39
|||||
Query Match 66.1%; Score 37; DB 11; Length 517;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YPDPQTQ 10
|||||
Db 32 YPDPQTQ 39

RESULT 13
Q9N8C7
ID Q9N8C7 PRELIMINARY; PRT; 622 AA.
AC Q9N8C7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE FMRFAMIDE-GATED Na+ CHANNEL.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE FROM N.A.
RA Jezlorski M.C., Green K.A., Sommerville J., Cottrell G.A.;
RT "Cloning and expression of a FMRFamide-gated Na+ channel from Helisoma
trivolvis and comparison with the native neuronal channel.";
RL J. Physiol. 526:13-25(2000).
DR EMBL; AF254118; AAF80601.1; -.
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SQ SEQUENCE 622 AA; 70407 MW; 2F995EFA0E98EB13 CRC64;

Query Match 66.1%; Score 37; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDT 7
|||||
Db 601 TYYPDT 606

RESULT 14
Q89443
ID Q89443 PRELIMINARY; PRT; 962 AA.
AC Q89443;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HELICASE.
GN B962L.
OS African swine fever virus (ASFV).
OC Viruses; dsDNA viruses, no RNA stage;
OC African swine fever-like viruses.
OX NCBI_TaxID=10497;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=96036500; PubMed=7483270;
RA Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
RT Rodriguez J.F., Vinuela E.;
RT "Immune protection conferred by the baculovirus-related glycoprotein
of Thogoto virus (Orthomyxoviridae).";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94233765; PubMed=8178480;
RA La Vega I., Gonzalez A., Blasco R., Calvo V., Vinuela E.;
RT "Nucleotide sequence and variability of the inverted terminal
repetitions of African swine fever virus DNA.";
RL Virology 201:152-156(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90219205; PubMed=2325203;
RA Gonzalez A., Calvo V., Almazan F., Almendral J.M., Ramirez J.C.,
RA La Vega I., Blasco R., Vinuela E.;
RT "Multigene families in African swine fever virus: family 360.";
RL J. Virol. 64:2073-2081(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90219204; PubMed=2325202;
RA Almendral J.M., Almazan F., Blasco R., Vinuela E.;
RT "Multigene families in African swine fever virus: family 110.";
RL J. Virol. 64:2064-2072(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=91134988; PubMed=1994575;
RA Camacho A., Vinuela E.;
RT "Protein p22 of African swine fever virus: an early structural protein
that is incorporated into the membrane of infected cells.";
RL Virology 181:251-257(1991).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RA Almazan F., Murguía J.R., Rodriguez J.M., La Vega I., Vinuela E.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBSJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
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RX MEDLINE-94187118; PubMed-8139051;
 RA Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
 RA Vinuela E.;
 RT "Multigene families in African swine fever virus: family 505.";
 RL J. Virol. 68:2746-2751(1994).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93346971; PubMed-8393914;
 RA Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E.;
 RT "African swine fever virus thymidylate kinase gene: sequence and
 RT transcriptional mapping.";
 RL J. Gen. Virol. 74:1633-1638(1993).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-94065656; PubMed-8245848;
 RA Alcami A., Angulo A., Vinuela E.;
 RT "Mapping and sequence of the gene encoding the African swine fever
 RT virion protein of Mr 11500.";
 RL J. Gen. Virol. 74:2317-2324(1993).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93277388; PubMed-8503790;
 RA Munoz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
 RT "Structure and expression in E. coli of the gene coding for protein
 RT p10 of African swine fever virus.";
 RL Arch. Virol. 130:93-107(1993).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-90357780; PubMed-2389555;
 RA Blasco R., Lopez-Otin C., Munoz M., Bockamp E.O., Simon-Mateo C.,
 RA Vinuela E.;
 RT "Sequence and evolutionary relationships of African swine fever virus
 RT thymidine kinase.";
 RL Virology 178:301-304(1990).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93281390; PubMed-8506138;
 RA Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela E.;
 RT "African swine fever virus encodes two genes which share significant
 RT homology with the two largest subunits of DNA-dependent RNA
 RT polymerases.";
 RL Nucleic Acids Res. 21:2423-2427(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93353606; PubMed-8102411;
 RA Rodriguez J.M., Yanez R.J., Almazan F., Vinuela E., Rodriguez J.F.;
 RT "African swine fever virus encodes a CD2 homolog responsible for the
 RT adhesion of erythrocytes to infected cells.";
 RL J. Virol. 67:5312-5320(1993).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-94085774; PubMed-8262374;
 RA Yanez R.J., Rodriguez J.M., Boursnell M., Boursnell M., Vinuela E.;
 RT "Two putative African swine fever virus helicases similar to yeast
 RT 'DBAH' pre-mRNA processing proteins and vaccinia virus ATPases D1L
 RT and D6R.";
 RL Gene 134:161-174(1993).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-90223993; PubMed-2327074;
 RA Lopez-Otin C., Freije J.M., Parra F., Mendez E., Vinuela E.;
 RT "Mapping and sequence of the gene coding for protein p72, the major
 RT capsid protein of African swine fever virus.";
 RL Virology 175:477-484(1990).
 RN [16]

RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-94123986; PubMed-8293992;
 RA Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
 RT "The DNA polymerase-encoding gene of African swine fever virus:
 RT sequence and transcriptional analysis.";
 RL Gene 136:103-110(1993).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93327788; PubMed-8335009;
 RA Simon-Mateo C., Andres G., Vinuela E.;
 RT "Polyprotein processing in African swine fever virus: a novel gene
 RT expression strategy for a DNA virus.";
 RL EMBO J. 12:2977-2987(1993).
 RN [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93233210; PubMed-8474154;
 RA Prados F.J., Vinuela E., Alcami A.;
 RT "Sequence and characterization of the major early phosphoprotein p32
 RT of African swine fever virus.";
 RL J. Virol. 67:2475-2485(1993).
 RN [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-92260660; PubMed-1583732;
 RA Alcami A., Angulo A., Lopez-Otin C., Munoz M., Freije J.M.,
 RA Carrascosa A.L., Vinuela E.;
 RT "Amino acid sequence and structural properties of protein p12, an
 RT African swine fever virus attachment protein.";
 RL J. Virol. 66:3860-3868(1992).
 RN [20]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93174976; PubMed-8438592;
 RA Yanez R.J., Vinuela E.;
 RT "African swine fever virus encodes a DNA ligase.";
 RL Virology 193:531-536(1993).
 RN [21]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-93174941; PubMed-8382399;
 RA Pena L., Yanez R.J., Revilla Y., Vinuela E., Salas M.L.;
 RT "African swine fever virus guanylyltransferase.";
 RL Virology 193:319-328(1993).
 RN [22]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-95159428; PubMed-7856088;
 RA Simon-Mateo C., Freije J.M., Andres G., Lopez-Otin C., Vinuela E.;
 RT "Mapping and sequence of the gene encoding protein p17, a major
 RT African swine fever virus structural protein.";
 RL Virology 206:1140-1144(1995).
 RN [23]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-92263807; PubMed-1316688;
 RA Garcia-Beato R., Freije J.M., Lopez-Otin C., Blasco R., Vinuela E.,
 RA Salas M.L.;
 RT "A gene homologous to topoisomerase II in African swine fever virus.";
 RL Virology 188:938-947(1992).
 RN [24]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE-94091056; PubMed-8266720;
 RA Freije J.M., Lain S., Vinuela E., Lopez-Otin C.;
 RT "Nucleotide sequence of a nucleoside triphosphate phosphohydrolase

Query Match 66.1%; Score 37; DB 12; Length 962;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1-STYYPDTVQG 10
 ||:|||| : |
 Db 110 STHYPMILG 119

RESULT 15

093574 PRELIMINARY; PRT; 3209 AA.
 AC 093574;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE EXTRACELLULAR REELIN (FRAGMENT).
 GN RELN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bernier B., Goffinet A.M.;
 RT "Comparative study of reelin in vertebrates.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF090441; AAC35559.1; -
 DR INTERPRO; IPR000561; -
 DR INTERPRO; IPR002860; -
 DR PFAM; PF00008; EGF; 5
 DR PFAM; PF02012; BNR; 15
 DR PROSITE; PS00022; EGF_1; UNKNOWN_7.
 DR PROSITE; PS01186; EGF_2; 7.
 KW Glycoprotein.
 FT NON_TER 1 1
 SQ SEQUENCE 3209 AA; 361291 MW; 81A7B6675BCAA3D1 CRC64;

Query Match 66.1%; Score 37; DB 13; Length 3209;
 Best Local Similarity 70.0%; Pred. No. 5.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1-STYYPDTVQG 10
 ||||| ||
 Db 1826 STYVTGTQG 1835

Search completed: March 28, 2001, 07:27:48
 Job time: 1661 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:33 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-56

Perfect score: 56

Sequence: 1 STYYPDTVOG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT:*
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- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	19 W76018	LM609 grafted anti
2	52	92.9	17	18 W27342	CDR2 from murine a
3	52	92.9	117	16 W79155	Human IgE receptor
4	52	92.9	117	18 W27357	Heavy chain variab
5	52	92.9	117	18 W27526	Heavy chain variab
6	52	92.9	117	18 W27354	Heavy chain variab
7	52	92.9	118	16 W79161	Human IgE receptor
8	52	92.9	120	17 W00240	Egf receptor chime
9	52	92.9	139	18 W21652	Humanised reshaped
10	52	92.9	139	18 W21656	Chimeric MAB 15 PC
11	52	92.9	140	18 W21654	Mouse MAB 15 heavy
12	52	92.9	158	18 W19577	Mouse anti-idiotyp

13	52	92.9	158	18 W19579	Mouse anti-idiotyp
14	52	92.9	239	20 W73874	Human antiFc epsil
15	52	92.9	242	20 W73876	Human antiFc epsil
16	52	92.9	260	16 R77617	Anti-C5 MAB N19/8
17	50	89.3	117	16 R79157	Human IgE receptor
18	49	87.5	98	14 R36526	Heavy chain VH 718
19	49	87.5	123	19 W66099	Anti-CD22 monoclon
20	49	87.5	136	11 R06251	Variable region of
21	48	85.7	119	16 W11919	Humanised MAB SK48
22	48	85.7	121	15 R60626	ME1-14 heavy chain
23	48	85.7	121	18 W22951	Monoclonal antibod
24	48	85.7	121	18 W16648	Anti-cancer specif
25	48	85.7	121	20 W86124	Protein sequence o
26	48	85.7	121	20 W86125	Protein sequence o
27	48	85.7	121	20 W86122	Protein sequence o
28	48	85.7	121	20 W86120	Protein sequence o
29	48	85.7	121	20 W86118	Murine 340 Vh amin
30	48	85.7	130	16 R86318	Anti-IL-8 MAB 5.12
31	48	85.7	130	18 W42318	Anti IL-8 antibody
32	48	85.7	130	18 W31575	Anti IL-8 monoclon
33	48	85.7	130	18 W23785	Monoclonal antibod
34	48	85.7	130	19 W69306	Murine anti-IL-8 M
35	48	85.7	130	19 W40121	Murine monoclonal
36	48	85.7	130	19 W33740	Anti IL-8 monoclon
37	48	85.7	130	20 Y29438	Murine 5.12.14 ant
38	48	85.7	130	21 Y77743	Murine anti-IL-8 a
39	48	85.7	138	17 W03722	Anti-human gp39 MA
40	48	85.7	139	13 R27053	Anti-CEA specific
41	48	85.7	139	14 R30480	hCEA specific mous
42	48	85.7	144	15 R61239	Monoclonal antibod
43	48	85.7	247	16 W11917	Murine MAB SK48-E2
44	48	85.7	251	16 R86320	Anti-IL-8 MAB 5.12
45	48	85.7	251	18 W42320	Murine variable an

ALIGNMENTS

RESULT 1

W76018 ID W76018 standard; Protein; 10 AA.

XX W76018;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR2 protein fragment #4.

XX Vitaxin; antibody; variable region; heavy chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

OS Mus sp.

XX W09833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSV-) IXSVS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49855.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS
 XX Claim 61; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10

Db 1 STYYPDTVQG 10

RESULT 2

W27342
 ID W27342 standard; peptide; 17 AA.

AC W27342;

DT 12-DEC-1997 (first entry)

DE CDR2 from murine anti-human IgE receptor antibody heavy chain.

XX Complementarity determining region; CDR2; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; Mab; heavy chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy.

XX Mus spp.

XX JP09191886-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

XX (ASAK) ASahi BREWERIES LTD.

XX (NIKK-) NIKKA WHISKEY KK.

XX (TORI) TORII YAKUHIIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human
 PT high-affinity IgE receptor - useful medicinally and have low
 PT antigenicity in humans

XX Claim 1; Page 12; 26pp; Japanese.

XX The present complementarity determining region 2 (CDR2), which is
 CC from a murine, anti-human high affinity immunoglobulin E (IgE)
 CC receptor, monoclonal antibody (Mab) heavy chain variable region,
 CC can be used in the preparation of humanised or semi-chimeric

CC anti-human high affinity IgE receptor Mab. The Mab can be used to
 CC treat or prevent diseases, specifically allergies, associated with
 CC the receptor. The humanised, semi-chimeric or chimeric Mab have
 CC very low antigenicity in humans.

SQ Sequence 17 AA;

Query Match 92.9%; Score 52; DB 18; Length 17;
 Best Local Similarity 90.0%; Pred. No. 0.0012;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10

Db 8 STYYPDTVKG 17

RESULT 3

R79155
 ID R79155 standard; peptide; 117 AA.

XX R79155;

XX 04-MAR-1996 (first entry);

DE Human IgE receptor-binding antibody-related peptide heavy chain.

KW Immunoglobulin E; antibody; receptor; monoclonal; detection;

KW complementarity determining region.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1H

FT /note= "all CDR regions are claimed"

FT Region 50..66

FT /label= CDR2H

FT /note= "all CDR regions are claimed"

FT Region 99..106

FT /label= CDR3H

FT /note= "all CDR regions are claimed"

XX JP07165799-A.

XX 27-JUN-1995.

XX 22-OCT-1993; 93JP-0264792.

XX 22-OCT-1993; 93JP-0264792.

XX (ASAK) ASahi BREWERIES LTD.

XX (NIKK-) NIKKA WHISKEY KK.

XX (TORI) TORII YAKUHIIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1995-261292/34.

XX N-PSDB; Q96282.

XX Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the Mab, for the specific identification
 PT of human Fc-epsilon RI

XX Claim 3; Page 13; 20pp; Japanese.

XX Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
 CC Q96280, Q96282, Q96284, Q96286 and Q96288. FRI is a polypeptide
 CC having 29-35 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is

CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
 CC the light chains have the general formula FR5-CDRL1-FR6-CDRL2L-FR7-
 CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
 CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
 CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
 CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
 CC peptides are derived from mouse hybridoma cells and are useful in
 CC the detection of the human FC-epsilonRI or for the elucidation of
 CC an antigen recognising region of a monoclonal antibody against
 CC human FC-epsilonRI.
 CC
 XX
 SQ Sequence 117 AA;

Query Match 92.9%; Score 52; DB 16; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.01;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTVOG 10
 |||||:|
 Db 57 styyptdvkg 66

RESULT 4

ID W27357 standard; Protein; 117 AA.

XX W27357;

DT 16-DEC-1997 (first entry)

XX Heavy chain variable region of chimeric human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;

KW high affinity; immunoglobulin E; receptor; monoclonal antibody;

KW IGE; MAb; heavy chain; variable region; humanised; semi-chimeric;

KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX Chimeric - Homo sapiens.

OS Chimeric - Mus spp.

OS Synthetic.

XX JP09191886-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

PA (ASAK) ASahi BREWERIES LTD.

PA (NIKK-) NIKKA WHISKEY KK.

PA (TORI) TORII YAKUHIIN KK.

PA (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IGE receptor - useful medicinally and have low

PT antigenicity in humans

PS Claim 8; Page 15; 26pp; Japanese.

XX The present sequence, the heavy chain variable region of a
 CC chimeric human CRA2 antibody (Ab), comprises complementarity
 CC determining regions (CDR) from a murine, anti-human high affinity
 CC immunoglobulin E (IgE) receptor, monoclonal Ab (MAB). The
 CC humanised chimeric MAB can be used to treat or prevent diseases,
 CC specifically allergies, associated with the receptor, and has very
 CC low antigenicity in humans.

XX Sequence 117 AA;

Query Match 92.9%; Score 52; DB 18; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.01;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTVOG 10
 |||||:|
 Db 57 styyptdvkg 66

RESULT 5

ID W27526 standard; Protein; 117 AA.

XX W27526;

DT 16-DEC-1997 (first entry)

XX Heavy chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;

KW high affinity; immunoglobulin E; receptor; monoclonal antibody;

KW IGE; MAB; heavy chain; variable region; humanised; semi-chimeric;

KW chimeric; treatment; prevention; disease; allergy; CRA2.

OS Homo sapiens.

PN JP09191886-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

PR 19-JAN-1996; 96JP-0024816.

PA (ASAK) ASahi BREWERIES LTD.

PA (NIKK-) NIKKA WHISKEY KK.

PA (TORI) TORII YAKUHIIN KK.

PA (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IGE receptor - useful medicinally and have low

PT antigenicity in humans

PS Claim 2; Page 13; 26pp; Japanese.

XX The present sequence, the heavy chain variable region of the human
 CC antibody (Ab) CRA2, was used in the preparation of a humanised or
 CC semi-chimeric monoclonal Ab (MAB), comprising complementarity
 CC determining regions (CDR) from a murine, anti-human high affinity
 CC immunoglobulin E (IgE) receptor, MAB. The humanised, semi-chimeric
 CC or chimeric MAB can be used to treat or prevent diseases,
 CC specifically allergies, associated with the receptor, and has very
 CC low antigenicity in humans.

XX Sequence 117 AA;

Query Match 92.9%; Score 52; DB 18; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.01;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTVOG 10
 |||||:|
 Db 57 styyptdvkg 66

RESULT 6

ID W27354 standard; Protein; 117 AA.

XX

AC W27354;
 XX 16-DEC-1997 (first entry)
 XX Heavy chain variable region of human CRA2 antibody.
 DE
 XX Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy; CRA2.
 XX
 XX Homo sapiens.
 OS
 XX JP09191886-A.
 PN
 XX 29-JUL-1997.
 PD
 XX 19-JAN-1996; 96JP-0024816.
 PF
 XX 19-JAN-1996; 96JP-0024816.
 PR
 XX (ASAK) ASahi BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKOHIN KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1997-429186/40.
 DR
 DR N-PSDB; T90025.
 XX
 PT Humanised, semi-chimeric and chimeric antibodies against human
 PT high-affinity IgE receptor - useful medicinally and have low
 PT antigenicity in humans
 XX
 PS Disclosure; Fig 1; 26pp; Japanese.
 XX
 CC The cDNA encoding the present sequence, the heavy chain variable
 CC region of the human antibody (Ab) CRA2, was used in the preparation
 CC of a humanised or semi-chimeric monoclonal Ab (MAB), comprising
 CC complementarity determining regions (CDR) from a murine, anti-human
 CC high affinity immunoglobulin E (IgE) receptor, MAB. The humanised,
 CC semi-chimeric or chimeric MAB can be used to treat or prevent
 CC diseases, specifically allergies, associated with the receptor, and
 CC has very low antigenicity in humans.
 XX
 SQ Sequence 117 AA;
 Query Match 92.9%; Score 52; DB 18; Length.117;
 Best Local Similarity 90.0%; Pred. No. 0.01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYPPDTVQG 10
 Db 57 styppdtvkg 66
 |||||:|
 RESULT 7
 ID R79161 standard; peptide; 118 AA.
 XX
 AC R79161;
 XX
 XX 04-MAR-1996 (first entry)
 DT
 XX Human IgE receptor-binding antibody-related peptide heavy chain.
 DE
 XX Immunoglobulin E; antibody; receptor; monoclonal; detection;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 29..33

FT /label= CDR1H
 FT /note= "all CDR regions are claimed"
 FT 48..64
 FT /label= CDR2H
 FT /note= "all CDR regions are claimed"
 FT 97..107
 FT /label= CDR3H
 FT /note= "all CDR regions are claimed"
 XX JP07165799-A.
 PN
 XX 27-JUN-1995.
 PD
 XX 22-OCT-1993; 93JP-0264792.
 PF
 XX 22-OCT-1993; 93JP-0264792.
 PR
 XX (ASAK) ASahi BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAHUKIN KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1995-261292/34.
 DR
 DR N-PSDB; Q96288.
 XX
 PT Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the MAb, for the specific identification
 PT of human Fc-epsilon RI
 XX
 PS Claim 9; Page 16; 20pp; Japanese.
 XX
 CC Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
 CC Q96280, Q96282, Q96284, Q96286 and Q96288. FRI is a polypeptide
 CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
 CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
 CC the light chains have the general formula FR5-CDRIL-FR6-CDR2L-FR7-
 CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
 CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
 CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
 CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
 CC peptides are derived from mouse hybridoma cells and are useful in
 CC the detection of the human Fc-epsilon-RI or for the elucidation of
 CC an antigen recognising region of a monoclonal antibody against
 CC human Fc-epsilon-RI.
 XX
 SQ Sequence 118 AA;
 Query Match 92.9%; Score 52; DB 16; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 STYPPDTVQG 10
 Db 55 styppdtvkg 64
 |||||:|
 RESULT 8
 ID W00240 standard; Protein; 120 AA.
 XX
 AC W00240;
 XX
 XX 22-NOV-1996 (first entry)
 DT
 XX EGF receptor chimeric MAB chMint5 VH chain.
 DE
 XX Mouse-human chimeric antibody; monoclonal antibody; chMint5;
 KW

KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
 KW immunotoxin; immunocytokine; tumour; cancer.

XX Mus musculus.

XX Key Location/Qualifiers
 FH Region 31..35
 FT /label= CDR1
 FT Region 51..66
 FT /label= CDR2
 FT Region 99..109
 FT /label= CDR3

XX W09627010-A1.

PN 06-SEP-1996.

XX 01-MAR-1996; 96WO-EP00805.

XX 01-MAR-1995; 95IT-OFI0036.

XX (ITUJ-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;
 PI Ferrer Marsal C, Mele A;

XX WPI; 1996-412776/41.

XX N-PSDB; T33445.

XX Murine/human chimeric monoclonal antibody, chMint5 specific for
 PT EGF-R - shows a lower immunogenicity when administered to humans

XX Claim 7; Page 15; 28pp; English.

XX The amino acid sequence (W00240) of the heavy chain variable region
 CC (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-
 CC human chimeric antibody chMint5 was deduced from a cDNA clone
 CC (T33445) obtd. by PCR amplification of murine Mint5 hybridoma DSM
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
 CC to human C-gamma1 and CK regions. Constructs were expressed in
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than
 CC Mint5 when administered to humans. It can be used in diagnostic
 CC assays or used to produce immunotoxins or immunocytokines useful
 CC for tumour therapy.

XX Sequence 120 AA;

Query Match 92.9%; Score 52; DB 17; Length 120;
 Best Local Similarity 90.0%; Pred. No. 0.01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
 Db 57 styypdvtvg 66
 |||||

RESULT 9

W21652
 ID W21652 standard; Protein; 139 AA.

XX W21652;

XX 03-JAN-1998 (first entry)

XX Humanised reshaped MAb 15 heavy chain variable region.

XX Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy.

XX Chimeric Mus musculus.
 OS Chimeric Homo sapiens.
 OS Chimeric synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..139
 FT /label= Mat_protein
 FT Region 20..49
 FT /label= Framework-1
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 55..68
 FT /label= Framework-2
 FT Region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 86..117
 FT /label= Framework-3
 FT Region 118..128
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 129..138
 FT /label= Framework-4

XX EP781847-A1.

XX 02-JUL-1997.

XX 25-OCT-1996; 96EP-0117154.

XX 06-NOV-1995; 95EP-0117407.

XX (MERE) MERCK PATENT GMBH.

XX Bendig M, Jones T, Saldana J;

XX WPI; 1997-334904/31.
 XX N-PSDB; T72237.

XX Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer

XX Claim 2; Fig 12; 71pp; English.

XX This polypeptide comprises the heavy chain variable region VH
 CC of humanised reshaped monoclonal antibody (MAB) 15 comprising
 CC complementarity determining regions of murine MAB 15 (DSM ACC2117),
 CC and reshaped human 30P1 framework regions. It is expressed by a
 CC cDNA clone (see T72237) prepared using PCR mutagenesis methods. A
 CC claimed process for preparation of humanised reshaped MAB 15
 CC involves: cloning and sequencing murine MAB 15 VL and VH regions
 CC (see W21653 and W21654); constructing, expressing and analysing
 CC chimeric MAB 15 antibody (see W21655-56); modelling the structure
 CC of murine MAB 15 variable regions; designing reshaped human MAB 15
 CC variable regions; preparing an oligonucleotide sequence which codes
 CC for the constant regions of the light and heavy chain of a human
 CC immunoglobulin; and constructing, expressing and analysing the
 CC complete reshaped human MAB 15. The humanised MAB can be used for
 CC treating tumours, especially lung cancer, and for the manufacture
 CC of a drug related to tumours, especially lung cancer.

XX Sequence 139 AA;

Query Match 92.9%; Score 52; DB 18; Length 139;
 Best Local Similarity 90.0%; Pred. No. 0.012;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
 Db 76 styypdvtvg 85
 |||||

RESULT 10

W21656
ID W21656 standard; Protein: 139 AA.

XX AC W21656;

XX DT 03-JAN-1998 (first entry)

XX DE Chimeric MAB 15 PCR-modified heavy chain variable region.

XX KW Humanised antibody; monoclonal antibody; MAB 15; tumour;

XX KW lung cancer; therapy.

XX OS Chimeric Mus musculus.

XX OS Chimeric synthetic.

XX XX Key Location/Qualifiers

XX FT Peptide 1..19

XX FT /label= Sig_peptide

XX FT Protein 25..139

XX FT /label= Mat_protein

XX FT Region 20..49

XX FT /label= Framework-1

XX FT Region 50..54

XX FT /label= CDR1

XX FT /note= "complementarity determining region 1"

XX FT Region 55..68

XX FT /label= Framework-2

XX FT Region 69..86

XX FT /label= CDR2

XX FT /note= "complementarity determining region 2"

XX FT Region 87..117

XX FT /label= Framework-3

XX FT Region 118..128

XX FT /label= CDR3

XX FT /note= "complementarity determining region 3"

XX FT Region 129..138

XX FT /label= Framework-4

XX EP781847-A1.

XX PD 02-JUL-1997.

XX PF 25-OCT-1996; 96EP-0117154.

XX PR 06-NOV-1995; 95EP-0117407.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Bendig M, Jones T, Saldana J;

XX DR WPI; 1997-334904/31.

XX DR N-PSDB; T72269.

XX XX Humanised form of murine monoclonal antibody MAB 15 - useful for

XX PT treating lung cancer

XX PS Disclosure; Fig 5; 71pp; English.

XX XX This polypeptide comprises the heavy chain variable region VH

XX CC region of murine monoclonal antibody (MAB) 15 (DSM ACC2117). It is

XX CC encoded by a MAB 15 VH cDNA sequence (T72269) modified for the

XX CC expression of chimeric antibody. The VL sequence was similarly

XX CC obtained (see W21655). The modified VH and VL sequences were used

XX CC in a claimed process to model and design novel humanised, reshaped

XX CC MAB 15 having humanised, reshaped VH and VL sequences (see W21652

XX CC and W21651), which can be used for treating tumours, especially

XX CC lung cancer, and for the manufacture of a drug related to tumours,

XX CC especially lung cancer.

XX XX Sequence 139 AA;

XX SQ

Query Match

Best Local Similarity 92.9%; Score 52; DB 18; Length 139;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVOG 10

DB 76 styypdtvkg 85

DE Mouse MAB 15 heavy chain variable region.

XX Humanised antibody; monoclonal antibody; MAB 15; tumour;

XX Lung cancer; therapy.

XX Mus musculus.

XX XX Key Location/Qualifiers

XX FT Peptide 1..19

XX FT /label= Sig_peptide

XX FT Protein 20..140

XX FT /label= Mat_protein

XX FT Region 20..49

XX FT /label= Framework-1

XX FT Region 50..53

XX FT /label= CDR1

XX FT /note= "complementarity determining region 1"

XX FT Region 54..68

XX FT /label= Framework-2

XX FT Region 69..86

XX FT /label= CDR2

XX FT /note= "complementarity determining region 2"

XX FT Region 87..117

XX FT /label= Framework-3

XX FT Region 118..128

XX FT /label= CDR3

XX FT /note= "complementarity determining region 3"

XX FT Region 129..139

XX FT /label= Framework-4

XX EP781847-A1.

XX PD 02-JUL-1997.

XX PF 25-OCT-1996; 96EP-0117154.

XX PR 06-NOV-1995; 95EP-0117407.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Bendig M, Jones T, Saldana J;

XX DR WPI; 1997-334904/31.

XX DR N-PSDB; T72267.

XX XX Humanised form of murine monoclonal antibody MAB 15 - useful for

XX PT treating lung cancer

XX PS Example 1; Fig 2; 71pp; English.

XX XX This polypeptide comprises the heavy chain variable region VH

XX CC of murine monoclonal antibody (MAB) 15 (DSM ACC2117), a MAB that

XX CC shows a therapeutic effect on human tumour cells, especially human

XX CC lung cancer. Its sequence was deduced from an isolated cDNA

XX CC clone (see T72267). The MAB 15 VL region sequence (W21653)

XX CC has also been determined. Amplified VH and VL cDNA sequences were

CC used in a claimed process for the production of novel humanised,
 CC reshaped MAB 15 having humanised, reshaped VH and VL regions (see
 CC W21652 and W21651), which can be used for treating tumours, (see
 CC especially lung cancer, and for the manufacture of a drug related
 CC to tumours, especially lung cancer.
 XX
 SQ Sequence 140 AA;

Query Match 92.9%; Score 52; DB 18; Length 140;
 Best Local Similarity 90.0%; Pred. No. 0.012; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;

Qy 1 STYYPDTVQG 10
 |||||:|
 Db 76 styyptvkg 85

RESULT 12
 W19577
 ID W19577 standard; Protein; 158 AA.
 XX
 AC W19577;
 XX
 DT 30-JUL-1997 (first entry)
 DE Mouse anti-idiotypic antibody 386 heavy chain variable region.
 XX
 KW Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;
 KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
 XX
 OS Mus musculus.

Key	Location/Qualifiers
FT Peptide	1..19
FT /label= sig_peptide	20..49
FT Region	/label= FR1
FT /note= "framework region 1"	50..53
FT Region	/label= CDR1
FT /note= "complementarity determining region 1"	54..68
FT Region	/label= FR2
FT /note= "framework region 2"	69..85
FT Region	/label= CDR2
FT /note= "complementarity determining region 2"	86..117
FT Region	/label= FR3
FT /note= "framework region 3"	118..133
FT Region	/label= CDR3
FT /note= "complementarity determining region 3"	134..144
FT Region	/label= FR4
FT /note= "framework region 4"	145..158
FT Region	/note= "mouse constant IgG1 region"

EP745612-A1.
 XX
 PD 04-DEC-1996.
 XX
 PF 14-MAY-1996; 96EP-0107651.
 XX
 PR 26-MAY-1995; 95EP-0107967.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Adan J, Carceller A, Gomez A, Piulats J, Rosell E;
 XX WPI; 1997-013659/02.
 DR

DR N-PSDB: T70808.
 XX Monoclonal anti-idiotypic antibodies mimicking epidermal growth
 PT factor receptor - useful for tumour therapy
 XX Claim 6; Fig 5C; 28pp; English.
 XX Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are
 CC new. They induce an immune response against epidermal growth factor
 CC receptor (EGFR). The sequences of the heavy and light chain variable
 CC regions of these antibodies are given in the specification. The
 CC antibodies are used for the manufacture of drugs directed against
 CC tumours that express EGFR on their surface, including melanomas,
 CC gliomas and carcinomas.
 XX Sequence 158 AA;

Query Match 92.9%; Score 52; DB 18; Length 158;
 Best Local Similarity 90.0%; Pred. No. 0.014;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:|
 Db 76 styyptvkg 85

RESULT 13
 W19579
 ID W19579 standard; Protein; 158 AA.
 XX
 AC W19579;
 XX
 DT 30-JUL-1997 (first entry)
 DE Mouse anti-idiotypic antibody 5A6 heavy chain variable region.
 XX
 KW Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;
 KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
 XX
 OS Mus musculus.

Key	Location/Qualifiers
FT Peptide	1..19
FT /label= sig_peptide	20..49
FT Region	/label= FR1
FT /note= "framework region 1"	50..54
FT Region	/label= CDR1
FT /note= "complementarity determining region 1"	55..68
FT Region	/label= FR2
FT /note= "framework region 2"	69..85
FT Region	/label= CDR2
FT /note= "complementarity determining region 2"	86..117
FT Region	/label= FR3
FT /note= "framework region 3"	118..133
FT Region	/label= CDR3
FT /note= "complementarity determining region 3"	134..144
FT Region	/label= FR4
FT /note= "framework region 4"	145..158
FT Region	/note= "mouse constant IgG1 region"

EP745612-A1.
 XX
 PD 04-DEC-1996.
 XX

PF 14-MAY-1996; 96EP-0107651.
 XX
 PR 26-MAY-1995; 95EP-0107967.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Adan J, Carceller A, Gomez A, Piulats J, Rosell E;
 XX
 DR WPI; 1997-013659/02.
 DR N-PSDB; T70810.
 XX
 XX Monoclonal anti-idiotypic antibodies mimicking epidermal growth
 PT factor receptor - useful for tumour therapy
 PT
 PS Claim 6; Fig 5E; 28pp; English.
 XX
 CC Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are
 CC new. They induce an immune response against epidermal growth factor
 CC receptor (EGFR). The sequences of the heavy and light chain variable
 CC regions of these antibodies are given in the specification. The
 CC antibodies are used for the manufacture of drugs directed against
 CC tumours that express EGFR on their surface, including melanomas,
 CC gliomas and carcinomas.
 CC
 XX Sequence 158 AA;
 SQ

Query Match 92.9%; Score 52; DB 18; Length 158;
 Best Local Similarity 90.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 14
 W73874
 ID W73874 standard; Protein; 239 AA.
 XX
 AC W73874;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #2.
 XX
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19 /note= "signal peptide"
 FT Protein 20..239 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01214.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Query Match 92.9%; Score 52; DB 20; Length 242;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Query Match 92.9%; Score 52; DB 20; Length 242;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
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 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Query Match 92.9%; Score 52; DB 20; Length 242;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
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 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

XX Claim 6; Page 7; 13pp; Japanese.
 PS
 XX This sequence represents a human antiFc epsilon RI alpha chain antibody,
 CC produced using the method of the invention. The method is for preparing
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host
 CC cell. The method can prepare an antibody Fab fragment cost efficiently
 CC and in high yield.
 CC
 XX Sequence 239 AA;
 SQ

Query Match 92.9%; Score 52; DB 20; Length 239;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Query Match 92.9%; Score 52; DB 20; Length 242;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Query Match 92.9%; Score 52; DB 20; Length 242;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Query Match 92.9%; Score 52; DB 20; Length 242;
 Best Local Similarity 90.0%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
 |||||:
 Db 76 stypdvtvk 85

RESULT 15
 W73876
 ID W73876 standard; Protein; 242 AA.
 XX
 AC W73876;
 XX
 XX 31-MAR-1999 (first entry)
 DT
 XX Human antiFc epsilon RI alpha chain antibody #4.
 DE
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT
 FT
 XX JPI1000174-A.
 PN
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 13-JUN-1997; 97JP-0171232.
 PF
 XX 13-JUN-1997; 97JP-0171232.
 XX
 PR (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHI KK.
 PA (TSUR/) TSURA T.
 XX
 XX WPI; 1999-124394/11.
 DR N-PSDB; X01216.
 XX
 XX Preparing an antibody Fab fragment using yeast - in high yield
 PT

Oy 1 STYYPDTVQG 10
| | | | | | | |
Db 79 styyptvkg 88

Search completed: March 28, 2001, 06:34:34
Job time: 514 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:10 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYPTDTVQG 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	92.9	125	1	US-08-331-398A-65
2	52	92.9	125	2	US-08-331-397B-65
3	52	92.9	125	2	US-08-759-804A-64
4	52	92.9	158	2	US-08-653-402B-6
5	52	92.9	158	2	US-08-653-402B-10
6	48	85.7	119	4	PCT-US94-07659-6
7	48	85.7	121	1	US-08-339-582-2
8	48	85.7	130	1	US-08-398-613A-22
9	48	85.7	130	1	US-08-398-612A-22
10	48	85.7	130	1	US-08-398-611A-22
11	48	85.7	130	2	US-08-491-334A-22
12	48	85.7	130	3	US-09-027-449-19
13	48	85.7	130	3	US-08-804-444A-19
14	48	85.7	130	3	US-09-026-985-19
15	48	85.7	138	2	US-08-379-057-14
16	48	85.7	247	4	PCT-US94-07659-2
17	48	85.7	251	1	US-08-398-612A-30
18	48	85.7	251	1	US-08-398-611A-30
19	48	85.7	251	2	US-08-491-334A-30
20	48	85.7	251	3	US-09-027-449-27
21	48	85.7	251	3	US-08-804-444A-27
22	48	85.7	251	3	US-09-026-985-27
23	48	85.7	252	1	US-08-398-613A-30
24	48	85.7	443	4	PCT-US96-13152-4
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27	46	82.1	122	4	PCT-US93-08435-12
28	46	82.1	122	4	PCT-US93-08435-14

29 46 82.1 122 4 PCT-US93-08435-43 Sequence 43, Appl
30 45 80.4 119 2 US-08-475-000-16 Sequence 16, Appl
31 45 80.4 119 2 US-08-483-199-16 Sequence 16, Appl
32 45 80.4 119 2 US-08-484-508-16 Sequence 16, Appl
33 45 80.4 467 1 US-08-704-744-81 Sequence 81, Appl
34 44 78.6 109 2 US-08-793-490-6 Sequence 6, Appl
35 44 78.6 113 1 US-07-789-344A-10 Sequence 10, Appl
36 44 78.6 116 2 US-08-888-366-10 Sequence 10, Appl
37 44 78.6 116 2 US-08-888-366-12 Sequence 12, Appl
38 44 78.6 225 5 5455030-5 Patent No. 5455030
39 44 78.6 236 5 5455030-7 Patent No. 5455030
40 44 78.6 247 5 5455030-9 Patent No. 5455030
41 44 78.6 248 5 5455030-11 Patent No. 5455030
42 44 78.6 300 2 US-08-661-052-4 Sequence 4, Appl
43 44 78.6 301 2 US-08-661-052-14 Sequence 14, Appl
44 44 78.6 447 5 5455030-1 Patent No. 5455030
45 44 78.6 553 2 US-08-661-052-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-65
: Sequence 65, Application US/08331398A
: Patent No. 5608039
: GENERAL INFORMATION:
: APPLICANT: Fastan, Ira
: APPLICANT: Willingham, Mark
: APPLICANT: Fitzgerald, David
: APPLICANT: Brinkmann, Ulrich
: APPLICANT: Pai, Lee
: TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
: TITLE OF INVENTION: and Their Uses (as amended)
: NUMBER OF SEQUENCES: 68
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: One Market Plaza, Steuart Street Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105-1492
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/331,398A
: FILING DATE: 28-OCT-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/767,331
: FILING DATE: 30-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/596,289
: FILING DATE: 12-OCT-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Hunter, Tom
: REGISTRATION NUMBER: 38,498
: REFERENCE/DOCKET NUMBER: 015280-1261100S
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 65:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Region

LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-398A-65

Query Match 92.9%; Score 52; DB 1; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.026;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

RESULT 2

US-08-331-397B-65
Sequence 65, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-1261200S
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-397B-65

Query Match 92.9%; Score 52; DB 2; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.026;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

QY 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

RESULT 3

US-08-759-804A-64
Sequence 64, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:

APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
Fusion Proteins, and Uses Thereof
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-1261400S
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION:
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-759-804A-64

Query Match 92.9%; Score 52; DB 2; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.026;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

```
RESULT 4
US-08-653-402B-6
; Sequence 6, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-6

Query Match 92.9%; Score 52; DB 2; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85

RESULT 5
US-08-653-402B-10
; Sequence 10, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-10

Query Match 92.9%; Score 52; DB 2; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85

RESULT 6
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESS: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match 85.7%; Score 48; DB 4; Length 119;
Best Local Similarity 88.9%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

QY 2 TYPTDVTG 10
DB 58 TYPTDVTG 66

RESULT 7
US-08-339-582-2
Sequence 2, Application US/08339582
Patent No. 5558952
GENERAL INFORMATION:
APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5558852th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,582
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-89
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-582-2

Query Match 85.7%; Score 48; DB 1; Length 121;
Best Local Similarity 80.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 0;

QY 1 STYYPDVTG 10
DB 60 STYYPDVTG 69

RESULT 8
US-08-398-613A-22
Sequence 22, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammato
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-3
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-398-613A-22

Query Match 85.7%; Score 48; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 0;

QY 1 STYYPDVTG 10
DB 57 STYYPDVTG 66

RESULT 9
US-08-398-612A-22
Sequence 22, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice

APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-612A-22

Query Match 85.7%; Score 48; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|||||:|
Db 57 STYYPDSVKG 66

RESULT 10
US-08-398-611A-22
Sequence 22, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-611A-22

Query Match 85.7%; Score 48; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|||||:|
Db 57 STYYPDSVKG 66

RESULT 11
US-08-491-334A-22
Sequence 22, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
TITLE OF INVENTION: Disorders and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-491-334A-22

Query Match 85.7%; Score 48; DB 2; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYPTDVOG 10
Db 57 STYPTDVKG 66

RESULT 12
US-09-027-449-19
Sequence 19, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-19

Query Match 85.7%; Score 48; DB 3; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYPTDVOG 10

Db 57 STYPTDVKG 66

RESULT 13
US-08-804-444A-19
Sequence 19, Application US/08804444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-19

Query Match 85.7%; Score 48; DB 3; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYPTDVOG 10
Db 57 STYPTDVKG 66

RESULT 14
US-09-026-985-19
Sequence 19, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/026,985
;; FILING DATE: 20-Feb-1998
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: PI085R3-1
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-09-026-985-19

Query Match 85.7%; Score 48; DB 3; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 57 STYYPDSVKG 66

RESULT 15

US-08-379-057-14
;; Sequence 14, Application US/08379057
;; Patent No. 5876950
;; GENERAL INFORMATION:
;; APPLICANT: Siadak, Anthony W.
;; APPLICANT: Hollenbaugh, Diane L.
;; APPLICANT: Gilliland, Lisa K.
;; APPLICANT: Gordon, Marcia L.
;; APPLICANT: Bajorath, Jorgen
;; APPLICANT: Aruffo, Alejandro A.
;; TITLE OF INVENTION: Monoclonal Antibodies Specific For
;; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
;; TITLE OF INVENTION: In Diagnosis and Therapy
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Bristol-Myers Squibb Company
;; STREET: 3005 First Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/379,057
;; FILING DATE: 26-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ON0133-
;; TELEPHONE: (206) 727-3670
;; TELEFAX: (206) 727-3601
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 138 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: N-terminal
US-08-379-057-14

Query Match 85.7%; Score 48; DB 2; Length 138;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 75 STYYPDSVRG 84

Search completed: March 28, 2001, 06:39:10
Job time: 764 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:50 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-58

Perfect score: 53

Sequence: 1 STYYLDTVEG 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	81.1	83	2 S21593	Ig heavy chain V r
2	42	79.2	111	2 S51211	Ig heavy chain V r
3	42	79.2	113	2 S02717	Ig heavy chain V r
4	42	79.2	113	2 S26468	Ig heavy chain V r
5	42	79.2	115	2 PH1538	Ig H chain V regio
6	42	79.2	117	1 HVMSRF	Ig heavy chain pre
7	42	79.2	117	1 HVMS84	Ig heavy chain pre
8	42	79.2	117	1 HVMS34	Ig heavy chain pre
9	42	79.2	117	2 PH1352	Ig H chain V regio
10	42	79.2	119	2 PH1548	Ig H chain V regio
11	42	79.2	119	2 PH1549	Ig H chain V regio
12	41	77.4	92	2 S56009	Ig heavy chain var
13	41	77.4	150	2 I47200	Ig heavy chain var
14	40	75.5	90	2 S24248	Ig heavy chain V r
15	40	75.5	97	2 S26935	Ig heavy chain V r
16	40	75.5	97	2 S46462	Ig heavy chain V r
17	40	75.5	98	2 S26929	Ig heavy chain V r
18	40	75.5	98	2 S26889	Ig heavy chain V r
19	40	75.5	98	2 S54856	Ig heavy chain V r
20	40	75.5	99	2 S24359	Ig heavy chain V r
21	40	75.5	100	2 S24258	Ig heavy chain V r
22	40	75.5	101	2 S24257	Ig heavy chain V r
23	40	75.5	102	2 S24260	Ig heavy chain V r
24	40	75.5	104	2 S24255	Ig heavy chain V r
25	40	75.5	105	2 S24249	Ig heavy chain V r
26	40	75.5	106	2 S24256	Ig heavy chain V r
27	40	75.5	108	2 PH1648	Ig heavy chain V r
28	40	75.5	109	2 PH1649	Ig heavy chain V r
29	40	75.5	109	2 S24254	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S21593

Ig heavy chain V region (10C5) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S21593

R:Kaartinen, M.

submitted to the EMBL Data Library, May 1992

A:Reference number: S21591

A:Accession: S21593

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-83 <KAA>

A:Cross-references: EMBL:X66457; NID:g51598; PIDN:CAA47072.1; PID:g51599

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 81.1%; Score 43; DB 2; Length 83;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Caps 0;

Qy 1 STYYLDTVEG 10

Db 27 STYYSDTVKG 36

RESULT 2

S51211

Ig heavy chain V region (AC7) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997

C:Accession: S51211; S58929

C:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.

FEBS Lett. 354, 169-172, 1994

A>Title: A synthetic peptide with anti-platelet activity derived from a CDR of an ant

A:Reference number: S51210; MUID:95046326

A:Accession: S51211

A:Molecule type: mRNA

A:Residues: 9-111 <JAR>

A:Accession: S58929

A:Molecule type: protein

A:Residues: 1-20 <JAR2>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 79.2%; Score 42; DB 2; Length 111;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 STYYLDTVKG 10
Db 57 STYYPDTVKG 66

RESULT 3

S02717
Ig heavy chain V region (clone pH62) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: S02717
R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Giotz, D.; Capra, J.D.; Zanetti, M.
submitted to the EMBL Data Library, February 1989
A:Reference number: S02717
A:Accession: S02717
A:Molecule type: DNA
A:Residues: 1-113 <SOL>
A:Cross-references: EMBL:Y00744; NID:52472; PID:CAA68713.1; PID:g1334095
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.61;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVKG 10
Db 57 STYYPDTVKG 66

RESULT 4

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PID:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.61;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVKG 10
Db 53 STYYPDTVKG 62

RESULT 5

PH1538
Ig H chain V region (clone 13G12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1538
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1538
A:Molecule type: mRNA

A:Residues: 1-115 <MUK>
A:Note: the stop codons X appear in residues 82, 85 and 106
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 115;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVKG 10
Db 56 STYYPDTVKG 65

RESULT 6

HWSRF
Ig heavy chain precursor V region (RF) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0503
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: JT0501; MUID:89279149
A:Accession: JT0503
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; hybridoma; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVKG 10
Db 76 STYYPDTVKG 85

RESULT 7

HWS84
Ig heavy chain precursor V region (5-84) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0505
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: JT0501; MUID:89279149
A:Accession: JT0505
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

```

Query Match          79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 STYYLDTVG 10
    |||| |||:|
Db 76 STYYPDIVKG 85

RESULT 8
HVMS34
Ig heavy chain precursor V region (345) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J0502
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: J0501; MUID:89279149
A:Accession: J0502
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match          79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
    |||| |||:|
Db 76 STYYPDIVKG 85

RESULT 9
PH1552
Ig H chain V region (clone 16E4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1552
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1552
A:Molecule type: mRNA
A:Residues: 1-117 <MUK>
A:Note: the stop codon X appears in residue 87
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match          79.2%; Score 42; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
    |||| |||:|
Db 57 STYYPDIVKG 66

RESULT 10
PH1548
Ig H chain V region (clone 12F4) - mouse (fragment)

```

```

C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1548
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1548
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          79.2%; Score 42; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
    |||| |||:|
Db 57 STYYPDIVKG 66

RESULT 11
PH1549
Ig H chain V region (clone 13F1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1549
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1549
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          79.2%; Score 42; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
    |||| |||:|
Db 57 STYYPDIVKG 66

RESULT 12
S56009
Ig heavy chain variable region against dystrophin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S56009
R:Morris, G.E.; Nguyen, C.; Man, N.T.
Biochem. J. 309, 355-359, 1995
A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-ter
A:Reference number: S56008; MUID:95344393
A:Accession: S56009
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <MOR>
A:Cross-references: EMBL:Z46661
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-86/Domain: immunoglobulin homology <IMM>

Query Match          77.4%; Score 41; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.76;

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Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYLDTVEG 10
|||||:|:|
Db 48 TYLDSVKG 56

RESULT 13

Ig heavy chain variable VDJ region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47200
R:Sun, J.; Kacskovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A:Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A:Reference number: I47177; MUID:95081609
A:Accession: I47200
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-150 <SUN>
A:Cross-references: EMBL:U15459; NID:g571404; PIDN:AAA67025.1; PID:g571405
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 41; DB 2; Length 150;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYLDTVEG 10
|||||:|:|
Db 79 TYLDSVKG 87

RESULT 14

S24248
Ig heavy chain V region (VH26) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24248
R:Stewart, A.K.; Huang, C.; Stollár, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STE>
A:Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA47454.1; PID:g38396
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 75.5%; Score 40; DB 2; Length 90;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDTVEG 10
|||||:|:|
Db 56 STYADSVKG 65

RESULT 15

S26935
Ig heavy chain V region (DP-42) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26935
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117

A:Accession: S26935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12342; NID:g32905; PIDN:CAA78212.1; PID:g32906
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 97;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDTVEG 10
|||||:|:|
Db 56 STYADSVKG 65

Search completed: March 28, 2001, 06:41:50
Job time: 873 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:49 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYYLDTVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues 87993
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	79.2	117	1 HV53_MOUSE	P18524 mus musculus
2	42	79.2	117	1 HV54_MOUSE	P18525 mus musculus
3	42	79.2	117	1 HV55_MOUSE	P18526 mus musculus
4	40	75.5	116	1 HV05_CARAU	P19181 carassius a
5	38	71.7	97	1 HV56_MOUSE	P18527 mus musculus
6	37	69.8	115	1 HV3E_HUMAN	P01767 homo sapien
7	37	69.8	117	1 HV3C_HUMAN	P01764 homo sapien
8	37	69.8	470	1 GLNA_FREDI	P33035 fremyella d
9	37	69.8	473	1 GLNA_SYNP2	P28605 synchococc
10	36	67.9	473	1 GLNA_ANASP	P00964 anabaena sp
11	36	67.9	523	1 YB34_YEAST	P38299 saccharomyc
12	35	66.0	117	1 HV02_CANFA	P01785 canis famil
13	35	66.0	119	1 HV3L_HUMAN	P01773 homo sapien
14	35	66.0	364	1 YK27_AQUAE	O67821 aquifex aeo
15	35	66.0	508	1 YBCK_ECOLI	P77698 escherichia
16	35	66.0	1062	1 CERU_MOUSE	Q61147 mus musculus
17	34	64.2	98	1 HV57_MOUSE	P18528 mus musculus
18	34	64.2	117	1 HV58_MOUSE	P18529 mus musculus
19	34	64.2	117	1 HV59_MOUSE	P18530 mus musculus
20	34	64.2	353	1 GBQ_LYKST	P38411 lymnaea sta
21	34	64.2	711	1 YRFE_ECOLI	P45800 escherichia
22	34	64.2	488	1 RRPB_CVNHJ	P19751 murine coro
23	33	62.3	121	1 HV3J_HUMAN	P01771 homo sapien
24	33	62.3	318	1 ALYS_BPHB3	P32762 streptococc
25	33	62.3	318	1 ALYS_STRPN	P06653 streptococc
26	33	62.3	329	1 PSBO_PEA	P14226 pisum sativ
27	33	62.3	332	1 PSBO_ARATH	P23321 arabidopsis
28	33	62.3	332	1 PSBO_SPIOL	P12359 spinacia ol
29	33	62.3	333	1 PSBO_SOLTU	P26320 solanum tub
30	33	62.3	471	1 TNAA_ECOLI	P00913 escherichia
31	33	62.3	473	1 GLNA_SYNY3	P77961 synchocyst
32	33	62.3	654	1 BFR2_HUMAN	Q01742 homo sapien
33	33	62.3	821	1 FGR2_HUMAN	P21802 homo sapien

34	33	62.3	821	1 FGR2_MOUSE	P21803 mus musculus
35	33	62.3	823	1 CER3_CHICK	P18461 gallus gall
36	33	62.3	1008	1 DPOL_HSV2	P52367 equine herp
37	32	60.4	250	1 LFA3_HUMAN	P19256 homo sapien
38	32	60.4	331	1 PUR7_ARCFU	O28996 archaeglob
39	32	60.4	332	1 GALT_HAEIN	P31766 haemophilus
40	32	60.4	354	1 GBQ_LOLFO	P38412 loligo forb
41	32	60.4	457	1 YMS9_YEAST	Q03648 saccharomyc
42	32	60.4	553	1 DPOL_BPPRD	P10479 bacterioph
43	32	60.4	631	1 OE66_NPVLS	P89518 leucania se
44	32	60.4	813	1 FGR2_XENLA	Q03364 xenopus lae
45	32	60.4	1005	1 MANA_DICDI	P34098 dictyostell

ALIGNMENTS

RESULT 1
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION RF PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE: 89273149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0503; HVMSRF.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 79.2%
Best Local Similarity 80.0%
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
Db 76 STYYPDTVKG 85

RESULT 2
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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RN  SEQUENCE FROM N.A.
RC  STRAIN=BALB/CJ;
RX  MEDLINE; 89279149.
RA  Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during
RL  the primary immune response.";
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR  PIR: JT0505; HVMS84.
DR  INTERPRO: IPR003006; -.
DR  PFAM: PF00047; ig; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 19
FT  CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT  DOMAIN 20 49 FRAMEWORK 1.
FT  DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT  DOMAIN 55 68 FRAMEWORK 2.
FT  DOMAIN 69 85 FRAMEWORK 3.
FT  DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT  DISULFID 41 115 BY SIMILARITY.
FT  NON_TER 117
SQ  SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
Db 76 STYYPDTVKG 85

RESULT 3
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR: JT0502; HVMS34.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 STYYLDTVEG 10
Db 76 STYYPDTVKG 85

RESULT 4
HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 88144476.
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
and family relationships of two genes and a pseudogene in a teleost
fish.";
RT fish.
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR: B28966; B28966.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.41;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 75 STYYADSVKG 84

RESULT 5
HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JT0504; HVMS91.
DR INTERPRO: IPR003006; -.

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```
DR PFAM: PF00047; ig: 1.
KW Immunoglobulin V region.
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 71.7%; Score 38; DB 1; Length 97;
Best Local Similarity 70.0%; Pred. No. 0.84;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVG 10
DB 56 STYYPDSVKG 65

RESULT 6
HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP MEDLINE; 78137069.
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region.
FT NON_TER 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 115;
Best Local Similarity 60.0%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVG 10
DB 56 TTYVADSVKG 65

RESULT 7
HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP MEDLINE; 81101090.
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC
CC EMBL; L05609; AAA23288.1; -.
CC PIR; JC1403; JC1403.
CC HSSP; P06201; 2LGS.
CC INTERPRO; IPR001637; -.
CC INTERPRO; IPR001691; -.
CC PFAM; PF00120; gln-synt; 1.
CC PROSITE; PS00180; GLNA_1; 1.
CC PROSITE; PS00181; GLNA_ATP; 1.
CC PROSITE; PS00182; GLNA_ADENYLATION; 1.
CC KW Ligase.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC SQ SEQUENCE 470 AA; 52919 MW; ADD7B49A7769B832 CRC64;
```

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DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVG 10
DB 76 STYYGDSVKG 85

RESULT 8
GLNA_FREDI STANDARD; PRT; 470 AA.
AC P33035;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLNA.
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella.
RN [1]
RP MEDLINE; 93129187.
RA Elmerjani K., Liotenberg S., Houmard J., de Marsac N.T.;
RT "Molecular characterization of the gene encoding glutamine synthetase
RT in the cyanobacterium Calothrix sp. PCC 7601.";
RL Biochem. Biophys. Res. Commun. 189:1296-1302(1992).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) -> ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL; L05609; AAA23288.1; -.
DR PIR; JC1403; JC1403.
DR HSSP; P06201; 2LGS.
DR INTERPRO; IPR001637; -.
DR INTERPRO; IPR001691; -.
DR PFAM; PF00120; gln-synt; 1.
DR PROSITE; PS00180; GLNA_1; 1.
DR PROSITE; PS00181; GLNA_ATP; 1.
DR PROSITE; PS00182; GLNA_ADENYLATION; 1.
CC KW Ligase.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC SQ SEQUENCE 470 AA; 52919 MW; ADD7B49A7769B832 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 470;
 Best Local Similarity 75.0%; Pred. No. 8;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLDTVEG 10
 ||:|:|

Db 150 YVDSVEG 157

RESULT 9

ID GLNA_SYN2 STANDARD; PRT; 473 AA.
 AC P28605;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
 GN GLNA.

OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PR-6;
 RX MEDLINE; 93139025.
 RA Wagner S.J., Thomas S.P., Kaufman R.I., Nixon B.T., Stevens S.E. Jr.;
 RT "The glnA gene of the cyanobacterium Agmenellum quadruplicatum PR-6
 is nonessential for ammonium assimilation."
 RL J. Bacteriol. 175:604-612(1993).
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 ORTHOPHOSPHATE.
 CC -!- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 HEXAGON.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

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EMBL; Z13965; CAA78366.1;
 PIR; S23852; S23852.
 PIR; A47050; A47050.
 HSSP; P06201; 2LGS.
 INTERPRO; IPR001691;
 PFAM; PF00120; gln-synt; 1.
 PROSITE; PS00180; GLNA_1; 1.
 PROSITE; PS00181; GLNA_ATP; 1.
 KW Nitrogen fixation; Ligase; Heterocyst.
 FT INIT MET 0 BY SIMILARITY.
 FT CONFLICT 106 106 R -> P (IN CAA24982).
 SQ SEQUENCE 473 AA; 53030 MW; 495C6C7A1EDBC576 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 8;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLDTVEG 10
 ||:|:|

Db 152 YVDSVEG 159

RESULT 10

ID GLNA_ANASP STANDARD; PRT; 473 AA.
 AC P00964;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).

GN GLNA.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tumer N.E., Robinson S.J., Haselkorn R.;
 RT "Different promoters for the Anabaena glutamine synthetase gene
 during growth using molecular or fixed nitrogen."
 RL Nature 306:337-342(1983).
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 ORTHOPHOSPHATE.
 CC -!- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 HEXAGON.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- MISCELLANEOUS: IN ANABAENA, IT IS PRESENT IN AMMONIA-GROWN
 VEGETATIVE CELLS AS WELL AS IN HETEROCYSTIS (FOR NITROGEN
 FIXATION).
 CC -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

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EMBL; X00147; CAA24982.1;
 PIR; A01192; AJA10.
 HSSP; P06201; 2LGS.
 INTERPRO; IPR001637;
 INTERPRO; IPR001691;
 PFAM; PF00120; gln-synt; 1.
 PROSITE; PS00180; GLNA_1; 1.
 PROSITE; PS00181; GLNA_ATP; 1.
 PROSITE; PS00182; GLNA_ADENYLATION; 1.
 KW Nitrogen fixation; Ligase; Heterocyst.
 FT INIT MET 0 BY SIMILARITY.
 FT CONFLICT 106 106 R -> P (IN CAA24982).
 SQ SEQUENCE 473 AA; 53005 MW; 373C7F94943A4E9 CRC64;

Query Match 67.9%; Score 36; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLDTVEG 10
 ||:|:|

Db 150 YLDSVEG 157

RESULT 11

ID YB34_YEAST STANDARD; PRT; 523 AA.
 AC P38299;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL 60.6 KDA PROTEIN IN SMP1-MB1 INTERGENIC REGION.
 GN YBR184W OR YBR1306.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE; 95176710.
 RA Demolis N., Jacquet M., Mallet L.;
 RT "A 12.5 kb fragment of the yeast chromosome II contains two adjacent
 genes encoding ribosomal proteins and six putative new genes, one of
 which encodes a putative transcriptional factor."
 RL Yeast 10:1511-1525(1994).

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CC -----
 DR EMBL; U02073; AAB60278.1; -;
 DR EMBL; Z36053; CAA85145.1; -;
 DR PIR; S46056; S46056.
 DR SGD; S0000388; YBR184W.
 KW Hypothetical protein.
 SQ SEQUENCE 523 AA; 60642 MW; 9BFFBD192C85472F CRC64;

Query Match 67.9%; Score 36; DB 1; Length 523;
 Best Local Similarity 70.0%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYLDTVVEG 10
 ||| ||: ||
 DB 441 STYLDLSAEG 450

RESULT 12
 HV02_CANFA STANDARD; PRT; 117 AA.
 ID HV02_CANFA STANDARD; PRT; 117 AA.
 AC P01785;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOO.
 OS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE OF 1-112.
 RX MEDLINE; 77242268.
 RA Wasserman R.L., Capra J.D.;
 RT "Primary structure of the variable regions of two canine
 RT immunoglobulin heavy chains.";
 RL Biochemistry 16:3160-3168(1977).
 RN [2]
 RP SEQUENCE OF 113-117.
 RX MEDLINE; 80077682.
 RA McCumber L.J., Capra J.D.;
 RT "The complete amino-acid sequence of a canine mu chain.";
 RL Mol. Immunol. 16:565-570(1979).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A02068; MIDGMO.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 117;
 Best Local Similarity 66.7%; Pred. No. 4.1;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYLDTVVEG 10
 ||| | |:
 DB 57 TYADVAVKG 65

RESULT 13
 HV3L_HUMAN STANDARD; PRT; 119 AA.
 ID HV3L_HUMAN
 AC P01773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION BUR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE; 79151016.
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
 RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874(1979).
 DR PIR; A02056; ALHUBR.
 DR HSSP; P01772; 2IG2.
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. .).
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 119;
 Best Local Similarity 66.7%; Pred. No. 4.2;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYLDTVVEG 10
 ||| | |:
 DB 58 TYADSVRG 66

RESULT 14
 YK27_AQUAE STANDARD; PRT; 364 AA.
 ID YK27_AQUAE STANDARD; PRT; 364 AA.
 AC O67821;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HYPOTHETICAL PROTEIN AQ_2027.
 GN AQ_2027.
 OS Aquifex aeolicus.
 CC Bacteria; Aquificales; Aquificaceae; Aquifex.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RX MEDLINE; 98196666.
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aufay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus".
 RL Nature 392:353-358(1998).
 CC -1- SIMILARITY: TO B.BURGDORFFERI BB0374.

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CC -----
 DR EMBL; AE000768; AAC07788.1; -;
 DR INTERPRO; IPR002819; -;
 DR PFAM; PF01966; HD; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 364 AA; 42016 MW; 4022756E079B7276 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 364;

Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
| | | | | : |
Db 203 SPYLDSTIG 212

RESULT 15

YBCK_ECOLI STANDARD; PRT; 508 AA.
AC P77698;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 57.5 KDA PROTEIN IN EMRE-RUS INTERGENIC REGION.
GN YBCK.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R.; Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AE000160; AAC73645.1; -.
DR EMBL; U82598; AAB40741.1; -.
DR ECOGENE; EG13627; YBCK.
KW Hypothetical protein.
SQ SEQUENCE 508 AA; 57526 MW; F85C07DBF45105CD CRC64;

Query Match 66.0%; Score 35; DB 1; Length 508;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTV 8
| | | | | :
Db 36 SDYYLDTI 43

Search completed: March 28, 2001, 07:29:50
Job time: 1657 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:48 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYVLDVTEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	75.5	121	4 Q9UL71	Q9ul71 homo sapien
2	40	75.5	1642	13 Q91132	Q91132 naja naja (
3	38	71.7	262	13 Q9PWM6	Q9pwm6 brachydanio
4	38	71.7	473	2 050210	O50210 synechococc
5	37	69.8	116	10 Q9LHW3	Q9lhw3 oryza sativ
6	37	69.8	752	5 062534	O62534 drosophila
7	37	69.8	755	5 Q9M0V3	Q9m0v3 drosophila
8	36	67.9	77	4 Q75741	O75741 homo sapien
9	36	67.9	118	4 Q9UL72	Q9ul72 homo sapien
10	36	67.9	258	2 Q9RA41	Q9ra41 trichodesmi
11	36	67.9	268	2 Q9RS44	O9rs44 deinococcus
12	36	67.9	339	2 Q32822	O32822 listeria mo
13	36	67.9	474	2 Q9RH21	Q9rh21 anabaena az
14	36	67.9	934	5 Q91436	P91436 caenorhabdi
15	35	66.0	195	5 Q9VZM0	Q9vzm0 drosophila
16	35	66.0	214	5 O18547	O18547 drosophila
17	35	66.0	290	5 Q9VRT2	Q9vrt2 drosophila
18	35	66.0	328	2 O68786	O68786 versinia pe
19	35	66.0	499	2 Q55174	Q55174 synechocyst

ALIGNMENTS

RESULT 1

Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -;
DR HSSP; P01772; 2FBA.
DR INTERPRO: IPR003006; -;
DR PFAM; PF00047; ig; 1.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 75.5%; Score 40; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYVLDVTEG 10

Db 57 STYVADSVKG 66

RESULT 2

Q91132 ID Q91132 PRELIMINARY; PRT; 1642 AA.
AC Q91132;

DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE COBRA VENOM FACTOR PRECURSOR.
OS Naja naja (Indian cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=35670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RX MEDLINE=95108041; PubMed=7809120;
RA Fritzinger D.C., Bredehorst R., Vogel C.W.;
RT "Molecular cloning and derived primary structure of cobra venom
factor."
RL Proc. Natl. Acad. Sci. U.S.A. 91:12775-12779(1994).
DR EMBL; 009969; AAA68989.1; -;
DR HSSP; P01024; IC3D.
DR INTERPRO; IPR000020; -;
DR INTERPRO; IPR001134; -;
DR INTERPRO; IPR001599; -;
DR INTERPRO; IPR001840; -;
DR INTERPRO; IPR002048; -;
DR INTERPRO; IPR002890; -;
DR PFAM; PF00207; A2M; 1.
DR PFAM; PF01759; NTR; 1.
DR PFAM; PF01821; ANATO; 1.
DR PFAM; PF01835; A2M_N; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR PRODOM; PD003264; -; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 648 ALPHA CHAIN OF COBRA VENOM FACTOR.
FT CHAIN 1264 1642 BETA CHAIN OF COBRA VENOM FACTOR.
SQ SEQUENCE 1642 AA; 184516 MW; 2A71B2BD61D612A3 CRC64;

Query Match 75.5%; Score 40; DB 13; Length 1642;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVE 9
|:|||||
Db 1007 ATYYLDTTE 1015

RESULT 3
QSPWM6 PRELIMINARY; PRT; 262 AA.
ID Q9PWM6
AC Q9PWM6
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE HEMOBBOX PROTEIN.
GN HOXD9A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RT "Zebrafish hox clusters and vertebrate genome evolution."
RL Science 282:1711-1714(1998).
DR EMBL; AF071268; AAD15961.1; -;

DR HSSP; P02834; 1B8I.
DR INTERPRO; IPR000047; -;
DR INTERPRO; IPR001356; -;
DR PFAM; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX
DR PRINTS; PR00031; HTHREPRESSR.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 262 AA; 29731 MW; 93BC979F8677CA27 CRC64;

Query Match 71.7%; Score 38; DB 13; Length 262;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|:|||||
Db 8 SSYYVDITMG 17

RESULT 4
O50210 PRELIMINARY; PRT; 473 AA.
ID O50210
AC O50210
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE GLUTAMINE SYNTHETASE.
GN GLNA.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA Cohen-Kupiec R.;
RL Thesis (1993), Unknown Institution.
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA Phung L.T.;
RL Thesis (1997), Unknown Institution.
RN [3]
RP SEQUENCE OF 1-4 FROM N.A.
RC STRAIN=PCC 7942;
RX MEDLINE=94064573; PubMed=7902350;
RA Cohen-Kupiec R., Gurevitz M., Zilberstein A.;
RT "Expression of glnA in the cyanobacterium Synecococcus sp. strain PCC
7942 is initiated from a single nif-like promoter under various
nitrogen conditions."
RL J. Bacteriol. 175:7727-7731(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA Phung L.T., Cohen-Kupiec R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031129; AAB87965.1; -;
DR HSSP; P06201; ILGR.
DR INTERPRO; IPR001637; -;
DR INTERPRO; IPR001691; -;
DR PFAM; PF00120; gln-synt; 1.
DR PROSITE; PS00180; GLNA_1; 1.
DR PRODOM; PD001057; -; 1.
SQ SEQUENCE 473 AA; 53045 MW; F228C865640D2555 CRC64;

Query Match 71.7%; Score 38; DB 2; Length 473;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|:|||||

Db 150 SYYVDSIEG 159

RESULT 5
Q9LHW3
ID Q9LHW3 PRELIMINARY; PRT; 116 AA.
AC Q9LHW3
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:PO515G01."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001633; BAA94223.1; --
SQ SEQUENCE 116 AA; 12974 MW; 628AFFC798CBB8EC CRC64;

Query Match 69.8%; Score 37; DB 10; Length 116;
Best Local Similarity 66.78; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 STYYLDTVE 9
|||||
Db 44 STYYFDTL 52

RESULT 6
O62534
ID O62534 PRELIMINARY; PRT; 752 AA.
AC O62534
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE SERINE/THREONINE PROTEIN KINASE.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Prorygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MacDougall C.N.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y07908; CAA69216.1; --
DR HSP; P05132; IBKX.
DR FLYBASE: FBgn020386; PK61C.
DR INTERPRO: IPR000719; --
DR INTERPRO: IPR002290; --
DR PFAM: PF00069; pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Serine/threonine-protein kinase.
SQ SEQUENCE 752 AA; 85422 MW; 95E6DDE3AAE7C068 CRC64;

Query Match 69.8%; Score 37; DB 5; Length 752;
Best Local Similarity 77.88; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TYILDVTEG 10
|||||
Db 655 TYILDDPEG 663

RESULT 7
Q9W0V3
ID Q9W0V3 PRELIMINARY; PRT; 755 AA.
AC Q9W0V3
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CG1201 PROTEIN.
GN CG1201.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brill J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fouts R.C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fierman C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS; ISOFORM 1 (SHOWN HERE),
ISOFORM 2 AND ISOFORM 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL: AE003467; AAF47327.1; --
DR EMBL: AE003467; AAF47330.1; --
DR EMBL: AE003467; AAF47331.1; --
DR HSP; P05132; IFMO.
DR FLYBASE: FBgn0035098; CG1201.
DR INTERPRO: IPR000719; --
DR INTERPRO: IPR002290; --
DR PFAM: PF00069; pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Alternative splicing; Hypothetical protein.
FT VARSPLIC 1 3 MISSING (IN ISOFORM 2).
FT VARSPLIC 1 216 MISSING (IN ISOFORM 3).

SQ SEQUENCE 755 AA; 85613 MW; 6375A99A25089FDD CRC64;

Query Match 69.8%; Score 37; DB 5; Length 755;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYVLDTVEG 10
| | | | | | | |
Db 658 TYVLDDEG 666

RESULT 8

O75741 ID O75741 PRELIMINARY; PRT; 77 AA.
AC O75741;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE;
RA Fischer M., Kueppers R.;
RT "Human IgA and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ009540; CAA08745.1; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8734 MW; 9858BD6D428BD049 CRC64;

Query Match 67.9%; Score 36; DB 4; Length 77;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYVLDTVEG 10
| | | | | | | |
Db 26 TYVADSVKG 34

RESULT 9

O90L72 ID O90L72 PRELIMINARY; PRT; 118 AA.
AC O90L72;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035042; AAD56278.1; -
DR HSSP: P01772; 2FB4.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.

FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 67.9%; Score 36; DB 4; Length 118;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYVLDTVEG 10
| | | | | | | |
Db 56 SSYYADSVKG 65

RESULT 10

O9RA41 ID O9RA41 PRELIMINARY; PRT; 258 AA.
AC O9RA41;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLUTAMINE SYNTHASE (FRAGMENT).
GN GLNA.
OS Trichodesmium sp. IMS101.
OC Bacteria; Cyanobacteria; Oscillatoriales; Trichodesmium.
OX NCBI_TaxID=57878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMS101;
RA Dominic B., Zehr J.P.;
RT "Transcriptional analysis of the global nitrogen control gene ntcA and
RT nitrogen assimilation gene glnA in relation to nif genes of
RT Trichodesmium sp. IMS101."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF169960; AAD53079.1; -
DR HSSP: P06201; 1LGR.
DR INTERPRO: IPR001691; -
DR PFAM: PF00120; gln-synt; 1.
DR PROSITE: PS00181; GLNA_ATP; 1.
FT NON_TER 1
FT NON_TER 258
SQ SEQUENCE 258 AA; 28741 MW; A9A98E7AA78E9CC2 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 258;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YVLDTVEG 10
| | | | | | | |
Db 24 YVVDSEIG 31

RESULT 11

O9RS44 ID O9RS44 PRELIMINARY; PRT; 268 AA.
AC O9RS44;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MANGANESE ABC TRANSPORTER, PERMEASE PROTEIN, PUTATIVE.
GN DR2283.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,

RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome Sequence of the Radioresistant Bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE002060; AAF11829.1; -;
 DR TIGR: DR2283; -;
 DR INTERPRO: IPR001626; -;
 DR PFAM: PF00950; ABC-3; 1.
 SQ SEQUENCE 268 AA; 27919 MW; 2D16BE531E8D9033 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 268;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYLDTVEG 10
 :||||| I
 DB 239 ASYLDTAPG 248

RESULT 12
 O32822 PRELIMINARY; PRT; 339 AA.
 AC O32822;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HYPOPHETICAL 39.7 KDA PROTEIN (FRAGMENT).
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD;
 RA Borovik I., Mislovati M., Cohen G., Aharonowitz Y.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF009622; AAB63803.1; -;
 DR INTERPRO: IPR001440; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 339 AA; 39702 MW; 601CE3B46B06D006 CRC64;

Query Match 67.9%; Score 36; DB 2; Length 339;
 Best Local Similarity 70.0%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYLDTVEG 10
 :||||| I
 DB 148 SSYLDGVEG 157

RESULT 13
 Q9RHZ1 PRELIMINARY; PRT; 474 AA.
 AC Q9RHZ1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2).
 GN GLNA.
 OS Anabaena azollae.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=1164;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Francisco F.J.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA Crespo J.L., Guerrero M.G., Florencio F.J.;
 RT "Mutational analysis of Asp-51 of Anabaena azollae glutamine
 RT synthetase. D51E mutation confers resistance to the active site
 RT inhibitors L-methionine-DL-sulfoximine and phosphinothricin.";
 RL Eur. J. Biochem. 266:1202-1209(1999).
 DR EMBL: AJ249658; CAB64594.1; -;
 DR HSSP: P06201; ILGR.
 DR INTERPRO: IPR001637; -;
 DR INTERPRO: IPR001691; -;
 DR PFAM: PF00120; gln-synt; 1.
 DR PROSITE: PS00180; GLNA_1; 1.
 DR PROSITE: PS00181; GLNA_ATP; 1.
 DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 KW Ligase.
 SQ SEQUENCE 474 AA; 52993 MW; 54FDF2975DF5EFBC CRC64;

Query Match 67.9%; Score 36; DB 2; Length 474;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYLDTVEG 10
 :||||| I
 DB 151 YELDSVEG 158

RESULT 14
 P91438 PRELIMINARY; PRT; 934 AA.
 ID P91438;
 AC P91438;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE CODED FOR BY C. ELEGANS CDNA YK29C11.5.
 GN T07F8.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden K., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Pauley A.;
 RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U08954; AAB38098.1; -;
 SQ SEQUENCE 934 AA; 106811 MW; 1ACAB327A514DC73 CRC64;

Query Match 67.9%; Score 36; DB 5; Length 934;
 Best Local Similarity 70.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 ||||| | | |
 Db 234 STYYVDQVLG 243

RESULT 15
 Q9VZM0
 ID Q9VZM0 PRELIMINARY; PRT; 195 AA.
 AC Q9VZM0;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE AWH PROTEIN.
 GN AWH.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003479; AAF47800.1; -
 DR FLYBASE: FBgn0013751; Awh.
 DR INTERPRO; IPR001356; -
 DR INTERPRO; IPR001781; -
 DR PFAM; PF00046; homeobox; 1.
 DR PFAM; PF00412; LIM; 2.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 1.
 DR PROSITE; PS50023; LIM_DOMAIN_2; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 SQ SEQUENCE 195 AA; 21806 MW; 105A341C68530FF7 CRC64;

Query Match 56.0%; Score 35; DB 5; Length 195;
 Best Local Similarity 75.0%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLDTVEG 10
 :||:||||
 Db 84 HYLETVEG 91

Search completed: March 28, 2001, 07:27:52
 Job time: 1665 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:34 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-58

Perfect score: 53

Sequence: 1 STYLDTRVEG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*
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3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT.*
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21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	19 W76019	LM609 grafted anti
2	50	94.3	10	19 W76009	LM609 grafted anti
3	50	94.3	117	19 W76001	Vitaxin antibody h
4	50	94.3	117	19 W76003	LM609 antibody hea
5	50	94.3	117	20 Y06381	Murine monoclonal
6	50	94.3	130	20 Y06379	Murine monoclonal
7	43	81.1	10	19 W76018	LM609 grafted anti
8	43	81.1	21	20 W93565	Immunoglobulin IgG
9	43	81.1	30	20 W93570	Immunoglobulin IgG
10	43	81.1	30	21 Y78332	Anti-DNA monoclonal
11	43	81.1	31	20 W93572	Immunoglobulin IgG
12	43	81.1	33	20 W93571	Immunoglobulin IgG

13	43	81.1	49	20 W99573	Immunoglobulin IgG
14	42	79.2	17	18 W27342	CDR2 from murine a
15	42	79.2	117	16 W79155	Human IgE receptor
16	42	79.2	117	18 W27357	Heavy chain variab
17	42	79.2	117	18 W27526	Heavy chain variab
18	42	79.2	117	18 W27354	Heavy chain variab
19	42	79.2	118	16 W79161	Human IgE receptor
20	42	79.2	120	17 W00240	EGF receptor chime
21	42	79.2	127	15 R47510	LSH241 heavy chai
22	42	79.2	139	18 W21652	Humanised reshaped
23	42	79.2	139	18 W21656	Chimeric MAb 15 PC
24	42	79.2	140	18 W21654	Mouse MAb 15 heavy
25	42	79.2	158	18 W19577	Mouse anti-idiotyp
26	42	79.2	158	18 W19579	Mouse anti-idiotyp
27	42	79.2	239	20 W73874	Human anti-IFC epsi
28	42	79.2	242	20 W73876	Human anti-IFC epsi
29	42	79.2	260	16 W77617	Anti-CS MAb N19/8
30	41	77.4	13	20 W86109	Peptide from human
31	41	77.4	13	20 W86083	Peptide from human
32	41	77.4	117	19 W48865	Murine monoclonal
33	41	77.4	117	19 W48866	Chimeric humanized
34	41	77.4	117	20 W86135	Protein sequence o
35	41	77.4	117	20 W86137	Protein sequence o
36	41	77.4	117	20 W86139	Protein sequence o
37	41	77.4	117	20 W86141	Protein sequence o
38	41	77.4	136	15 R56962	MAb A33 heavy chai
39	41	77.4	237	20 W95440	A33/212 single cha
40	41	77.4	237	21 Y54836	Linked fusion prot
41	41	77.4	241	20 W95441	A33/218 single cha
42	41	77.4	241	21 Y54837	Linked fusion prot
43	41	77.4	245	20 W97891	A33/218 single cha
44	41	77.4	264	19 W73049	Humanised A33 scab
45	41	77.4	532	19 W73051	Z33dCH2.z chimeric

ALIGNMENTS

RESULT 1

W76019
ID W76019 standard; Protein; 10 AA.

XX W76019;

XX W76019;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR2 protein fragment #5.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

OS Mus sp.

PN W09833919-A2.

XX W09833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49856.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX Claim 61; Page 41; 129pp; English.
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX SQ Sequence 10 AA;
SQ
Query Match 100.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 STYYLDTVEG 10
|||||
Db 1 styyltdtveg 10

RESULT 2
W76009
ID W76009 standard; Protein; 10 AA.
AC W76009;
XX
XX '02-NOV-1998 (first entry)
DT
XX LM609 grafted antibody V-H region CDR2 protein fragment #2.
DE
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; V49846.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX Disclosure; Page 40; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX SQ Sequence 10 AA;
SQ
Query Match 94.3%; Score 50; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0026;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 STYYLDTVEG 10
|||||
Db 1 styyltdtveg 10

RESULT 3
W76001
ID W76001 standard; Protein; 117 AA.
XX
AC W76001;
XX
XX 02-NOV-1998 (first entry)
DT
XX Vitaxin antibody heavy chain variable region protein fragment.
DE
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; V49820.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 1; Fig 1a; 129pp; English.
XX
XX This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 |||||:|
 Db 57 styyldtvqg 66

RESULT 4

W76003
 ID W76003 standard; Protein; 117 AA.

XX AC W76003;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody heavy chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.

CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3

CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus

CC block integrin-mediated signal transduction. This is useful in the

CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,

CC specifically angiogenesis and restenosis (but also e.g. (non-)immune

CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,

CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

CC etc.). The antibodies contain non-murine framework regions so are

CC suitable for use in humans. Enhanced types of LM609 have affinity more

CC than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 |||||:|
 Db 57 styyldtvqg 66

RESULT 5

Y06381
 ID Y06381 standard; Protein; 117 AA.

XX AC Y06381;

XX DT 06-SEP-1999 (first entry)

XX DE Murine monoclonal antibody LM609.VH region.

XX KW Humanised antibody; antibody humanisation; antibody engineering;

XX LM609; monoclonal antibody; complementarity determining region;

XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX KW cancer; therapy; diagnosis.

XX OS Mus. musculus.

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized

CC antibodies, a light chain CDR from a mouse antibody such as LM609 is

CC grafted onto a human light chain, and a heavy chain CDR from a mouse

CC antibody is grafted onto a human antibody heavy chain to produce

CC libraries from which a humanised murine antibody having the desired

CC specificity is selected. By preserving the original CDR sequences

CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the

CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 |||||:|
 Db 57 styyldtvqg 66

RESULT 6

Y06379
 ID Y06379 standard; Protein; 130 AA.

XX AC Y06379;

DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

DE Humanised antibody; antibody humanisation; antibody engineering;

XX LM609; monoclonal antibody; complementarity determining region;

KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

KW cancer; therapy; diagnosis.

XX Mus musculus.

OS

XX

XX Key Location/Qualifiers

FT Peptide 1..2

FT /note= "vector-encoded residues"

FT Region 28..32

FT /note= "CDR1"

FT Region 47..63

FT /note= "CDR2"

FT Region 96..103

FT /note= "CDR3"

XX W09929888-A1.

PN 17-JUN-1999.

PD

XX 04-DEC-1998; 98WO-US25828.

PF

XX 05-DEC-1997; 97US-0986016.

PR

XX (SCRI) SCRIPPS RES INST.

PA

XX Barbas CF, Rader C;

PI

XX WPI; 1999-394979/33.

DR

XX Production of humanized mouse monoclonal antibodies

PT

XX Disclosure; Page 49-50; 55pp; English.

PS

XX This sequence represents the light chain V kappa region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized

CC antibodies, a light chain CDR from a mouse antibody such as LM609 is

CC grafted onto a human light chain, and a heavy chain CDR from a mouse

CC antibody is grafted onto a human antibody heavy chain to produce

CC libraries from which a humanised murine antibody having the desired

CC specificity is selected. By preserving the original CDR sequences

CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the

CC humanisation strategy ensures epitope conservation.

XX

SQ Sequence 130 AA;

Query Match 94.3%; Score 50; DB 20; Length 130;

Best Local Similarity 90.0%; Pred. No. 0.046;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLYDTVEG 10

Db |||||:|

54 stylydtvgg 63

RESULT 7

W76018

ID W76018 standard; Protein; 10 AA.

XX

XX W76018;

AC

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR2 protein fragment #4.

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

XX

XX Mus sp.

OS

XX W09833919-A2.

PN

XX 06-AUG-1998.

PD

XX 30-JAN-1998; 98WO-US01826.

PF

XX 30-JAN-1997; 97US-0791391.

PR

XX (IXSY-) IXSYS INC.

PA

XX Glaser SM, Huse WD;

PI

XX WPI; 1998-437472/37.

DR

XX N-PSDB; V49855.

DR

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PT

XX Claim 61; Page 41; 129pp; English.

PS

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

CC

SQ Sequence 10 AA;

Query Match 81.1%; Score 43; DB 19; Length 10;

Best Local Similarity 80.0%; Pred. No. 0.049;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYLYDTVEG 10

Db |||||:|

1 stylydtvgg 10

RESULT 8

W99565

ID W99565 standard; peptide; 21 AA.

XX

XX W99565;

AC

XX

XX 22-JUN-1999 (first entry)

DT

XX Immunoglobulin IgG2a CDR2-derived peptide #1.

DE

XX Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;

KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.

KW

XX

XX Synthetic.

OS

XX Homo sapiens.

XX PN FR2766826-A1.
 XX PD 05-FEB-1999.
 XX PF 04-AUG-1997; 97FR-0009972.
 XX PR 04-AUG-1997; 97FR-0009972.
 XX PA (INSP) INST PASTEUR.
 XX PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
 XX DR WPI; 1999-156194/14.
 XX PT New polypeptide including sequence from single antibody chain and
 PT able to penetrate a cell - used as vector for delivering attached
 PT components, e.g. nucleic acid or antigen, to cells, useful in gene
 PT therapy and vaccination
 XX PS Example 2; Page 20; 36pp; French.
 XX CC This sequence corresponds to a peptide derived from the complementary
 CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
 CC used in the production of a polypeptide that (i) comprises a unique or
 CC repeated peptide motif; (ii) includes a sequence consisting of one or
 CC more different antibody fragments and (iii) can penetrate into cells.
 CC The polypeptides are vectors for delivering a substance to cells
 CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
 CC (gene therapy, or where the substance is an antigen, for vaccination,
 CC in which case the polypeptide acts effectively as an adjuvant).
 XX SQ Sequence 21 AA;
 Query Match 81.1%; Score 43; DB 20; Length 21;
 Best Local Similarity 80.0%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STYVLDTVVEG 10
 Db IIII III:I
 10 stysdvtvkg 19
 RESULT 9
 W99570
 ID W99570 standard; peptide; 30 AA.
 XX AC W99570;
 XX DT 22-JUN-1999 (first entry)
 XX DE Immunoglobulin IgG2a CDR2-derived peptide #6.
 XX KW Primer: PCR; amplification; immunoglobulin; IgG2a: repeat motif;
 KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN FR2766826-A1.
 XX PD 05-FEB-1999.
 XX PF 04-AUG-1997; 97FR-0009972.
 XX PR 04-AUG-1997; 97FR-0009972.
 XX PA (INSP) INST PASTEUR.
 XX PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
 XX DR WPI; 1999-156194/14.

XX PT New polypeptide including sequence from single antibody chain and
 PT able to penetrate a cell - used as vector for delivering attached
 PT components, e.g. nucleic acid or antigen, to cells, useful in gene
 PT therapy and vaccination
 XX PS Example 2; Page 20; 36pp; French.
 XX CC This sequence corresponds to a peptide derived from the complementary
 CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
 CC used in the production of a polypeptide that (i) comprises a unique or
 CC repeated peptide motif; (ii) includes a sequence consisting of one or
 CC more different antibody fragments and (iii) can penetrate into cells.
 CC The polypeptides are vectors for delivering a substance to cells
 CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
 CC (gene therapy, or where the substance is an antigen, for vaccination,
 CC in which case the polypeptide acts effectively as an adjuvant).
 XX SQ Sequence 30 AA;
 Query Match 81.1%; Score 43; DB 20; Length 30;
 Best Local Similarity 80.0%; Pred. No. 0.17;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STYVLDTVVEG 10
 Db IIII III:I
 10 stysdvtvkg 19
 RESULT 10
 Y78332
 ID Y78332 standard; peptide; 30 AA.
 XX AC Y78332;
 XX DT 04-MAY-2000 (first entry)
 XX DE Anti-DNA monoclonal antibody heavy chain variable region peptide.
 XX KW Cell membrane permeant; medical imaging; diagnosis; radiotherapy;
 KW pharmaceutical therapy; drug delivery.
 XX OS Unidentified.
 XX PN WO9967284-A2.
 XX PD 29-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US13660.
 XX PR 20-JUN-1998; 98US-0090087.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Pivnica-Worms D;
 XX DR WPI; 2000-160576/14.
 XX PT New membrane permanent peptide complexes for medical imaging,
 XX diagnostics and therapy
 XX PS Claim 3; Page 17; 65pp; English.
 XX CC The present invention describes compound comprising a cell membrane
 CC permeant peptide, a diagnostic or an active substance and a functional
 CC linker moiety linking them, where the functional linker moiety confers
 CC target cell specificity to the compound or a salt of the compound. The
 CC compounds and compositions are useful in the fields of medical imaging,
 CC diagnostics and pharmaceutical therapy. The composition are for medical
 CC imaging, evaluating intracellular processes, radiotherapy of
 CC intracellular targets and drug delivery. The cell membrane permeant
 CC peptides conjugate coordination and covalent complexes have target cell

CC specificity, therefore, the Tat peptide and other cell membrane permeant
 CC peptides can be used to selectively deliver non- or poorly permeant
 CC drugs, diagnostic substances such as oligonucleotides, peptides, peptide
 CC nucleic acids, fluorochromes, dyes, enzyme substrates and metals useful
 CC in medical therapy, imaging and/or diagnostics selectively to cells
 CC in vivo only when functional linkers are introduced into permeant peptide
 CC constructs. The present sequence represents a specifically claimed
 CC cell membrane permeant peptide from the present invention.

XX Sequence 30 AA;

Query Match 81.1%; Score 43; DB 21; Length 30;
 Best Local Similarity 80.0%; Pred. No. 0.17;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 Db 10 styystdtkg 19

RESULT 11
 W99572
 ID W99572 standard; peptide; 31 AA.

AC W99572;
 XX
 DT 22-JUN-1999 (first entry)

DE Immunoglobulin IgG2a CDR2-derived peptide #8.

KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
 KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.

OS Synthetic.
 OS Homo sapiens.

XX FR2766826-A1.

XX 05-FEB-1999.

PF 04-AUG-1997; 97FR-0009972.

XX 04-AUG-1997; 97FR-0009972.

XX (INSP) INST PASTEUR.

XX Avrameas A, Avrameas S, Buttin G, Ternynck T;

XX WPI; 1999-156194/14.

XX New polypeptide including sequence from single antibody chain and
 PT able to penetrate a cell - used as vector for delivering attached
 PT components, e.g. nucleic acid or antigen, to cells, useful in gene
 PT therapy and vaccination

PS Example 2; Page 21; 36pp; French.

XX This sequence corresponds to a peptide derived from the complementary
 CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
 CC used in the production of a polypeptide that (i) comprises a unique or
 CC repeated peptide motif; (ii) includes a sequence consisting of one or
 CC more different antibody fragments and (iii) can penetrate into cells.
 CC The polypeptides are vectors for delivering a substance to cells
 CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
 CC (gene therapy, or where the substance is an antigen, for vaccination,
 CC in which case the polypeptide acts effectively as an adjuvant).

XX Sequence 31 AA;

Query Match 81.1%; Score 43; DB 20; Length 31;
 Best Local Similarity 80.0%; Pred. No. 0.18;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 Db 11 styystdtkg 20

RESULT 12
 W99571
 ID W99571 standard; peptide; 33 AA.

XX W99571;

XX 22-JUN-1999 (first entry)

DE Immunoglobulin IgG2a CDR2-derived peptide #7.

XX Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
 KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.

OS Synthetic.
 OS Homo sapiens.

XX FR2766826-A1.

XX 05-FEB-1999.

PF 04-AUG-1997; 97FR-0009972.

XX 04-AUG-1997; 97FR-0009972.

XX (INSP) INST PASTEUR.

XX Avrameas A, Avrameas S, Buttin G, Ternynck T;

XX WPI; 1999-156194/14.

XX New polypeptide including sequence from single antibody chain and
 PT able to penetrate a cell - used as vector for delivering attached
 PT components, e.g. nucleic acid or antigen, to cells, useful in gene
 PT therapy and vaccination

PS Example 2; Page 20; 36pp; French.

XX This sequence corresponds to a peptide derived from the complementary
 CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
 CC used in the production of a polypeptide that (i) comprises a unique or
 CC repeated peptide motif; (ii) includes a sequence consisting of one or
 CC more different antibody fragments and (iii) can penetrate into cells.
 CC The polypeptides are vectors for delivering a substance to cells
 CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
 CC (gene therapy, or where the substance is an antigen, for vaccination,
 CC in which case the polypeptide acts effectively as an adjuvant).

XX Sequence 33 AA;

Query Match 81.1%; Score 43; DB 20; Length 33;
 Best Local Similarity 80.0%; Pred. No. 0.19;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 Db 10 styystdtkg 19

RESULT 13
 W99573
 ID W99573 standard; peptide; 49 AA.

XX W99573;

XX 22-JUN-1999 (first entry)

XX Immunoglobulin IgG2a CDR2-3 derived peptide CDR2-3-PL19.
DE XX
XX Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX FR2766826-A1.
PN
XX
XX 05-FEB-1999.
PD
XX 04-AUG-1997; 97FR-0009972.
PF
XX 04-AUG-1997; 97FR-0009972.
PR
XX
XX (INSP) INST PASTEUR.
PA
XX Avrameas A, Avrameas S, Buttin G, Ternynck T;
PI
XX WPI; 1999-156194/14.
DR
XX
XX New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
PT
XX Example 5; Page 23; 36pp; French.
PS
XX
XX This sequence corresponds to a peptide derived from the complementary
CC determining region 2/3 (CDR2/3) of an immunoglobulin IgG2a protein and
CC is used in the production of a polypeptide that (i) comprises a unique
CC or repeated peptide motif; (ii) includes a sequence consisting of one
CC or more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
XX
XX Sequence 49 AA;
SQ

Query Match 81.1%; Score 43; DB 20; Length 49;
Best Local Similarity 80.0%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
DB 29 styytdtvkg 38

RESULT 14
W27342
ID W27342 standard; peptide; 17 AA.
XX
AC W27342;
XX
XX 12-DEC-1997 (first entry)
DT
XX CDR2 from murine anti-human IgE receptor antibody heavy chain.
DE
XX Complementarity determining region; CDR2; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAB; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy.
XX
XX Mus spp.
OS
XX JP09191886-A.
PN
XX 29-JUL-1997.
PD
XX

PF 19-JAN-1996; 96JP-0024816.
XX
PR 19-JAN-1996; 96JP-0024816.
XX
XX (ASAK) ASAHI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHIIN KK.
PA (TSURU) TSURA T.
XX
XX WPI; 1997-429186/40.
DR
XX Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PT
XX Claim 1; Page 12; 26pp; Japanese.
PS
XX The present complementarity determining region 2 (CDR2), which is
CC from a murine, anti-human high affinity immunoglobulin E (IgE)
CC receptor, monoclonal antibody (MAB) heavy chain variable region,
CC can be used in the preparation of humanised or semi-chimeric
CC anti-human high affinity IgE receptor MAB. The MAB can be used to
CC treat or prevent diseases, specifically allergies, associated with
CC the receptor. The humanised, semi-chimeric or chimeric MAB have
CC very low antigenicity in humans.
XX
XX Sequence 17 AA;
SQ

Query Match 79.2%; Score 42; DB 18; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
DB 8 styyptdvkg 17

RESULT 15
R79155
ID R79155 standard; peptide; 117 AA.
XX
AC R79155;
XX
XX 04-MAR-1996 (first entry)
DT
XX Human IgE receptor-binding antibody-related peptide heavy chain.
DE
XX Immunoglobulin E; antibody; receptor; monoclonal; detection;
KW complementarity determining region.
KW
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1H
FT /note= "all CDR regions are claimed"
FT 50..66
FT /label= CDR2H
FT /note= "all CDR regions are claimed"
FT 99..106
FT /label= CDR3H
FT /note= "all CDR regions are claimed"
FT
XX JP07165799-A.
PN
XX 27-JUN-1995.
PD
XX 22-OCT-1993; 93JP-0264792.
XX
XX 22-OCT-1993; 93JP-0264792.
PR
XX (ASAK) ASAHI BREWERIES LTD.
PA

PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAHUKIN KK.
PA (TSUR/) TSURA T.

XX
DR WPI: 1995-261292/34.
DR N-PSDB; Q96282.

XX
PT Novel monoclonal antibody against human high-affinity IgE receptor -
PT and DNA fragment encoding the MAb, for the specific identification
PT of human Fc-epsilon RI

XX
PS Claim 3; Page 13; 20pp; Japanese.

XX
CC Polypeptides which specifically recognise human IgE receptor (Fc-
CC epsilon-RI) have been isolated and sequenced. The new peptides are
CC related to a monoclonal antibody against Fc-epsilon-RI and are
CC either heavy or light chain molecules. The heavy chain molecules
CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
CC Q96280, Q96282, Q96284, Q96286 and Q96288. FR1 is a polypeptide
CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
CC the light chains have the general formula FR5-CDRL1-FR6-CDR2L-FR7-
CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
CC peptides are derived from mouse hybridoma cells and are useful in
CC the detection of the human Fc-epsilon-RI or for the elucidation of
CC an antigen recognising region of a monoclonal antibody against
CC human Fc-epsilon-RI.

XX
SQ Sequence 117 AA;

Query Match 79.2%; Score 42; DB 16; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 styyptvkg 66

Search completed: March 28, 2001, 06:34:34
Job time: 514 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:10 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYLDTRVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgnl_7/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	79.2	125	1 US-08-331-398A-65	Sequence 65, Appl
2	42	79.2	125	2 US-08-331-397B-65	Sequence 65, Appl
3	42	79.2	125	2 US-08-759-804A-64	Sequence 64, Appl
4	42	79.2	158	2 US-08-653-402B-6	Sequence 6, Appl
5	42	79.2	158	2 US-08-653-402B-10	Sequence 10, Appl
6	41	77.4	136	1 US-08-253-877C-57	Sequence 57, Appl
7	41	77.4	136	2 US-08-452-164A-57	Sequence 57, Appl
8	41	77.4	237	2 US-08-224-591-16	Sequence 16, Appl
9	41	77.4	237	2 US-08-926-789-16	Sequence 16, Appl
10	41	77.4	241	2 US-08-224-591-18	Sequence 18, Appl
11	41	77.4	241	2 US-08-926-789-18	Sequence 18, Appl
12	40	75.5	17	1 US-08-264-093-22	Sequence 22, Appl
13	40	75.5	95	3 US-09-043-514-2	Sequence 2, Appl
14	40	75.5	113	3 US-08-974-899-6	Sequence 6, Appl
15	40	75.5	116	3 US-08-545-809A-135	Sequence 135, App
16	40	75.5	116	3 US-08-983-607-36	Sequence 36, Appl
17	40	75.5	117	3 US-08-428-197-36	Sequence 36, Appl
18	40	75.5	117	3 US-08-545-809A-109	Sequence 109, App
19	40	75.5	117	3 US-08-983-607-46	Sequence 46, Appl
20	40	75.5	117	4 PCT-US93-10555-36	Sequence 36, Appl
21	40	75.5	118	2 US-08-652-816A-11	Sequence 11, Appl
22	40	75.5	118	2 US-08-652-816A-12	Sequence 12, Appl
23	40	75.5	118	2 US-08-379-057-30	Sequence 30, Appl
24	40	75.5	118	3 US-08-545-809A-125	Sequence 125, App
25	40	75.5	119	3 US-08-983-607-22	Sequence 22, Appl
26	40	75.5	120	1 US-08-264-093-14	Sequence 14, Appl
27	40	75.5	120	2 US-08-428-197-20	Sequence 20, Appl
28	40	75.5	120	2 US-08-428-197-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-65
; Sequence 65, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region

Sequence 24, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 40, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 40, Appl
Sequence 21, Appl

LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-398A-65

Query Match 79.2%; Score 42; DB 1; Length 125;
Best Local Similarity 80.0%; Pred. No. 0.99;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 1 STYXLDTVG 10
Db 57 STYYPDTVK 66

RESULT 2

US-08-331-397B-65
Sequence 65, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-397B-65

Query Match 79.2%; Score 42; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 0.99;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYXLDTVG 10
Db 57 STYYPDTVK 66

RESULT 3

US-08-759-804A-64
Sequence 64, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-759-804A-64

Query Match 79.2%; Score 42; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 0.99;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYXLDTVG 10
Db 57 STYYPDTVK 66

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RESULT 4
US-08-653-402B-6
; Sequence 6, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-6

Query Match 79.2%; Score 42; DB 2; Length 158;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVKG 10
Db 76 STYYDPTVKG 85

RESULT 5
US-08-653-402B-10
; Sequence 10, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653.402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-10

Query Match 79.2%; Score 42; DB 2; Length 158;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVKG 10
Db 76 STYYDPTVKG 85

RESULT 6
US-08-253-877C-57
; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253.877C
; FILING DATE: 03-JUN-1994
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-57

Query Match 77.4%; Score 41; DB 1; Length 136;
Best Local Similarity 77.8%; Pred. NO. 1.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 TYLDTVEG 10
DB 77 TYLDSVKG 85

RESULT 7
US-08-452-164A-57
Sequence 57, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methylthio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452.164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-57

Query Match 77.4%; Score 41; DB 2; Length 136;
Best Local Similarity 77.8%; Pred. NO. 1.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 TYLDTVEG 10
DB 77 TYLDSVKG 85
RESULT 8
US-08-224-591-16
Sequence 16, Application US/08224591
Patent No. 5856456
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,591
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-224-591-16

Query Match 77.4%; Score 41; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. NO. 3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 TYLDTVEG 10
DB 179 TYLDSVKG 187

RESULT 9
US-08-926-789-16
Sequence 16, Application US/08926789
Patent No. 5950275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; NAME: Goldstein, Jorge A.
; REGISTRATION/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-926-789-16

Query Match 77.4%; Score 41; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYIYLDTVVEG 10
Db 179 TYIYLDVSKG 187

RESULT 10
US-08-224-591-18
; Sequence 18, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
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;
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; NAME: Goldstein, Jorge A.
; REGISTRATION/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-224-591-18

Query Match 77.4%; Score 41; DB 2; Length 241;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYIYLDTVVEG 10
Db 183 TYIYLDVSKG 191

RESULT 11
US-08-926-789-18
; Sequence 18, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; NAME: Goldstein, Jorge A.
; REGISTRATION/DOCKET NUMBER: 29,021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-224-591-18
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;
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-926-789-18

Query Match 77.4%; Score 41; DB 2; Length 241;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYVLDTVEG 10
|||||1:1:1
DB 183 TYVLDVSKG 191

RESULT 12
US-08-264-093-22
; Sequence 22, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-22

Query Match 75.5%; Score 40; DB 1; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.26;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||1:1:1
DB 8 STYYADSVKG 17

RESULT 13
US-09-043-514-2
; Sequence 2, Application US/09043514A
; Patent No. 6153745

;
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, David
; APPLICANT: BROWN, Daniel
; APPLICANT: ZACCOLO, Manuela C.
; APPLICANT: GHERARDI, Ermanno
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MUTAGENESIS OF NUCLEIC
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 41301/251704
; CURRENT APPLICATION NUMBER: US/09/043,514A
; CURRENT FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: GB 9519425.4
; EARLIER FILING DATE: 1995-09-22
; EARLIER APPLICATION NUMBER: GB 9602011.0
; EARLIER FILING DATE: 1996-02-01
; EARLIER APPLICATION NUMBER: PCT/GB96/02333
; EARLIER FILING DATE: 1996-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-043-514-2

Query Match 75.5%; Score 40; DB 3; Length 95;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||1:1:1
DB 51 STYYADSVKG 60

RESULT 14
US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881

Job time: 764 sec

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-6

Query Match 75.5%; Score 40; DB 3; Length 113;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVVEG 10
|||||!|:|
Db 57 STYYADSVKG 66

RESULT 15
US-08-545-809A-135
; Sequence 135, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-135

Query Match 75.5%; Score 40; DB 3; Length 116;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVVEG 10
|||||!|:|
Db 75 STYYADSVKG 84

Search completed: March 28, 2001, 06:39:10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:50 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-60

Perfect score: 58

Sequence: 1 ARNHGSEFAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	196	2 H64968	acetyl CoA acetyl
2	39	67.2	222	2 G81124	DnaA-related prote
3	39	67.2	243	2 B81896	hypothetical prote
4	37	63.8	150	2 D69081	deoxyuridine 5-tri
5	37	63.8	257	2 B81155	conserved hypothet
6	37	63.8	257	2 C81949	hypothetical prote
7	37	63.8	731	1 JC2464	probable copper-tr
8	36	62.1	108	2 S26316	Ig heavy chain v r
9	36	62.1	110	2 S26317	Ig heavy chain v r
10	36	62.1	470	2 H71667	glutamate--L-RNA li
11	35	62.1	473	2 D70405	glutamate--L-RNA li
12	35	60.3	233	2 H82163	arginyl-L-RNA-prote
13	35	60.3	272	2 S27819	vitelline B1 precu
14	35	60.3	272	2 S27820	vitelline B2 precu
15	35	60.3	282	2 T46541	hypothetical prote
16	35	60.3	448	1 A60003	nucleocapsid prote
17	35	60.3	480	2 C69438	hypothetical prote
18	35	60.3	483	2 TS1272	hypothetical prote
19	35	60.3	538	2 T28874	hypothetical prote
20	35	60.3	628	1 A56707	protein-tyrosine k
21	35	60.3	722	2 S64492	hypothetical prote
22	35	60.3	736	2 T06757	hypothetical prote
23	35	60.3	1797	2 T21889	hypothetical prote
24	35	60.3	1805	2 T21888	hypothetical prote
25	34	58.6	129	2 H70727	conserved hypothet
26	34	58.6	154	2 E72126	hypothetical prote
27	34	58.6	170	2 D75554	hypothetical prote
28	34	58.6	219	1 QOECAS	hypothetical 23.4K
29	34	58.6	231	1 ISECP4	L-ribulose-phospha

ALIGNMENTS

RESULT 1

H64968

acetyl CoA acetyltransferase - Escherichia coli

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Jun-1999

C:Accession: H64968; I69646; I69656

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: H64968

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-196 <BLAT>

A:Cross-references: GB:AF000294; GB:U00096; NID:g1788338; PIDN:AAC75094.1; PID:g17883

A:Experimental source: strain K-12, substrain MG1655

R:Yao, Z.; Valvano, M.A.

J. Bacteriol. 176, 4133-4143, 1994

A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r

erotypes Y and 4a.

A:Reference number: I55053; MUID:94292434

A:Accession: I69646

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>

A:Cross-references: EMBL:U03041; NID:G501028; PIDN:AAC31635.1; PID:g510256

R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W

J. Bacteriol. 176, 4144-4156, 1994

A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its

A:Reference number: I55054; MUID:94292435

A:Accession: I69656

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>

A:Cross-references: EMBL:U09876; NID:G508236; PID:g508245

C:Genetics:

A:Gene: yefH

A:Map position: 45 min

C:Superfamily: galactoside acetyltransferase

Query Match 67.2%; Score 39; DB 2; Length 196;

Best Local Similarity 75.0%; Pred. No. 5.2;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 HNHGSFAY 10

|||||

Db 105 HNHGSFKH 112

RESULT 2

G81124
DnaA-related protein NMB1076 [imported] - Neisseria meningitidis (group B strain MD58)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: G81124
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: G81124
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TET>
A:Cross-references: GB:AE002458; GB:AE002098; NID:g7226311; PIDN:AAF41471.1; PID:g722631
A:Experimental source: serogroup B, strain MMD58
C:Genetics:
A:Gene: NMB1076

Query Match 67.2%; Score 39; DB 2; Length 222;
Best Local Similarity 66.7%; Pred No. 5, 9;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNGSFAY 10
|| || || ||
Db 32 RHKGQFIY 40

RESULT 3
B81896
hypothetical protein NMA1279 [imported] - Neisseria meningitidis (group A strain Z2491)
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C:Accession: B81896
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; MUID:2022556
A:Accession: B81896
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84531.1; PID:g737995
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1279

Query Match 67.2%; Score 39; DB 2; Length 243;
Best Local Similarity 66.7%; Pred. No. 6, 4;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNGSFAY 10
|| || || || || || || ||
Db 53 RHKGQFIY 61

RESULT 4
D69081
deoxyuridine 5-triphosphate nucleotidohydrolase related protein MTH1605 [imported] - Meth C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Mar-2000
C:Accession: D69081
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.W.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A:Reference number: A69000; MUID:98037514

A:Accession: D69081
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-150 <MTH>
A:Cross-references: GB:AE000920; GB:AE000666; NID:g2622729; PIDN:AA86078.1; PID:g262 A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1605
C:Superfamily: dCTP deaminase

Query Match 63.8%; Score 37; DB 2; Length 150;
Best Local Similarity 62.5%; Pred. No. 9, 3;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HHNGSFAY 10
|| || || || || || || ||
Db 115 HHNGEVEY 122

RESULT 5
B81155
conserved hypothetical protein NMB0803 [imported] - Neisseria meningitidis (group B s C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: B81155
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: B81155
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <TET>
A:Cross-references: GB:AE002435; GB:AE002098; NID:g7226049; PIDN:AAF41216.1; PID:g722 A:Experimental source: serogroup B, strain MMD58
C:Genetics:
A:Gene: NMB0803

Query Match 63.8%; Score 37; DB 2; Length 257;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HHNGSFAY 10
|| || || || || || || ||
Db 245 HHNSAYAY 253

RESULT 6
CB1949
hypothetical protein NMA1013 [imported] - Neisseria meningitidis (group A strain Z249 C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C:Accession: CB1949
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491 A:Reference number: AB1775; MUID:2022556
A:Accession: CB1949
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84282.1; PID:g737 A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1013

Query Match 63.8%; Score 37; DB 2; Length 257;
 Best Local Similarity 62.5%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPAY 10
 |||::|||
 Db 246 HNHSAAY 253

RESULT 7
 JC2464
 Probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.
 C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
 C:Accession: JC2464
 R:Trenor III., C.; Lin, W.; Andrews, N.C.
 Blochem. Biophys. Res. Commun. 205, 1644-1650, 1994
 A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
 A:Reference number: JC2464; MUID:95110304
 A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <PRE>
 A:Cross-references: GB:U16658; NID:9643612; PIDN:AAA62113.1; PID:9643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
 C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembra
 F:7-92/Region: Hls-rich
 F:135-477/Domain: ATPase transduction domain homology <ATT>
 F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:287/Active site: Glu #status predicted
 F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 63.8%; Score 37; DB 1; Length 731;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 |::|||
 Db 88 AHHHGSF 95

RESULT 8
 S26316
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26316
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26316
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <STA>
 A:Cross-references: EMBL:X59190; NID:952066; PIDN:CAA1900.1; PID:gl334035
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 36; DB 2; Length 108;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 10
 |||::|||
 Db 84 ARGNYGNAV 93

RESULT 9

S26317
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protei
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:Cross-references: EMBL:X59186
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 36; DB 2; Length 110;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 10
 |||::|||
 Db 86 ARGNYGNAV 95

RESULT 10
 H71667
 glutamate--tRNA ligase (EC 6.1.1.17) (gltx2) RP623 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 20-Jun-2000
 C:Accession: H71667
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499
 A:Accession: H71667
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-470 <AND>
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:93861033; PIDN:CAA15066.1; PID:9386
 A:Experimental source: strain Madrid E
 C:Genetics:

Query Match 62.1%; Score 36; DB 2; Length 470;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 |||::|||
 Db 31 ARHNHGSF 38

RESULT 11
 D70405
 glutamate--tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
 C:Accession: D70405
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666
 A:Accession: D70405
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-473 <AOF>
A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00065
A:Experimental source: strain VFS
C:Genetics:

A:Gene: gltX
C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F:4-276/Domain: glutamine--tRNA ligase homology <EGL>

Query Match 62.1%; Score 36; DB 2; Length 473;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
|||||
DB 31 ARHNNGGF 38

RESULT 12

H82163
arginyl-tRNA-protein transferase-related protein VC1736 [imported] - Vibrio cholerae (gr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: H82163
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833

A:Accession: H82163

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <HEI>

A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94886.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1736

A:Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGS 7
|||||
DB 117 ARHRHGS 123

RESULT 13

S27819
vitelline B1 precursor - liver fluke
N:Alternate names: eggshell protein B1
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: A48436; A48437; B48437; A59161; S27819
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
Mol. Biochem. Parasitol. 54, 129-141, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression o
A:Reference number: A48436; MUID:93063029
A:Accession: A48436

A:Molecule type: mRNA; protein

A:Residues: 1-272 <RIC>

A:Cross-references: EMBL:M93024; NID:gl59065; PIDN:AAA29143.1; PID:gl59066

A>Note: sequence extracted from NCBI backbone (NCBIN:117208, NCBIP:117210)

R:Waite, J.H.; Rice-Ficht, A.C.

Mol. Biochem. Parasitol. 54, 143-151, 1992

A:Title: Eggshell precursor proteins of Fasciola hepatica, II. Microheterogeneity in vit
A:Reference number: A48437; MUID:93063030

A:Accession: A48437

A>Status: preliminary

A:Molecule type: protein
A:Residues: 20-47 <WAII>
A:Cross-references: PID:g259030; PIDN:AAB23982.1
A>Note: sequence extracted from NCBI backbone (NCBIP:117211)
A:Accession: B48437
A>Status: preliminary
A:Molecule type: protein
A:Residues: 172-193 <WA2>
A:Cross-references: PID:g259031; PIDN:AAB23983.1
A>Note: sequence extracted from NCBI backbone (NCBIP:117213)
R:Waite, J.H.
Anal. Biochem. 192, 429-433, 1991

A:Title: Detection of peptidyl-3,4-dihydroxyphenylalanine by amino acid analysis and
A:Reference number: A59161; MUID:91241559

A:Accession: A59161

A:Molecule type: protein

A:Residues: 62-70 <WA3>

A:Experimental source: egg shell

C:Keywords: egg shell

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-272/Product: vitelline B1 #status predicted <MAT>

F:63/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
|||||
DB 19 ARHPHGKF 26

RESULT 14

S27820
vitelline B2 precursor - liver fluke
N:Alternate names: eggshell protein B2
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993. #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: S27820
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
submitted to the EMBL Data Library, May 1992
A:Description: Eggshell precursor proteins of Fasciola hepatica: I. structure and exp
A:Reference number: S27819

A:Accession: S27820

A:Molecule type: mRNA

A:Residues: 1-272 <RIC>

A:Cross-references: EMBL:M93025; NID:gl59067; PIDN:AAA29144.1; PID:gl59068

C:Keywords: egg shell

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-272/Product: vitelline B2 #status predicted <MAT>

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
|||||
DB 19 ARHPHGKF 26

RESULT 15

T46541
hypothetical protein gra-orf30 [imported] - Streptomyces violaceoruber
C:Species: Streptomyces violaceoruber
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 11-May-2000
C:Accession: T46541
R:Ichinose, K.; Bedford, D.J.; Tornus, D.; Bechthold, A.; Bibb, M.J.; Revill, W.P.; F
Chem. Biol. 5, 647-659, 1998
A:Title: The granaticin biosynthetic gene cluster of Streptomyces violaceoruber Tu22:
A:Reference number: Z23045; MUID:99051446
A:Accession: T46541

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-282 <ICH>
A:Cross-references: EMBL:AJ011500; PIDN:CAA09657.1
A:Experimental source: strain Tu22
C:Genetics:
A:Note: gra-orf30

Query Match 60.3%; Score 35; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 HGSPAY 10
|||||
Db 162 HGSPAY 167

Search completed: March 28, 2001, 06:41:52
Job time: 875 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:50 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-60

Perfect score: 58

Sequence: 1 ARHNGSPAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	196	1 WBBJ_ECOLI	P37750 escherichia
2	36	62.1	218	1 Y4VH_RHISN	Q53216 rhizobium s
3	36	62.1	470	1 SYE2_RICPR	Q92ct8 rickettsia
4	36	62.1	470	1 SYE_AQUAE	O67271 aquifex aeo
5	35	60.3	197	1 EGG5_FASHE	P07915 fasciola he
6	35	60.3	448	1 NCAP_CVHOC	P33469 human coron
7	35	60.3	567	1 CC45_XENLA	Q39h26 xenopus lae
8	35	60.3	629	1 KSYK_RAT	Q64725 rattus norv
9	35	60.3	722	1 PBPI_YEAST	P53297 saccharomyc
10	34	58.6	129	1 YP56_MYCTU	Q50742 mycobacteri
11	34	58.6	213	1 PNCA_ECOLI	P21369 escherichia
12	34	58.6	231	1 ARAD_ECOLI	P08203 escherichia
13	34	58.6	231	1 ARAD_SALTY	P06190 salmonella
14	34	58.6	231	1 SGBE_ECOLI	P37680 escherichia
15	34	58.6	231	1 SGBE_HABIN	P44989 haemophilus
16	34	58.6	284	1 YNB9_YEAST	P53975 saccharomyc
17	34	58.6	284	1 YND3_YEAST	P33964 saccharomyc
18	34	58.6	297	1 YC24_ANTSP	Q02857 antithamnio
19	34	58.6	339	1 LYCA_BPCP1	P15057 bacterioph
20	34	58.6	339	1 LYCA_BPCP9	P19386 bacterioph
21	34	58.6	349	1 XYJ9_YEAST	P41903 saccharomyc
22	34	58.6	538	1 NADP_PSEAE	Q51363 pseudomonas
23	34	58.6	1446	1 IE18_PRVKA	P33479 pseudorabie
24	34	58.6	1461	1 IE18_PRVIF	P1675 pseudorabie
25	33.5	57.8	172	1 LGUL_PSEPU	P16635 pseudomonas
26	33	56.9	302	1 YEQ6_YEAST	P40049 saccharomyc
27	33	56.9	480	1 SYE_HAEIN	P43818 haemophilus
28	33	56.9	966	1 M172_HUMAN	Q14596 homo sapien
29	33	56.9	1403	1 YDF3_SCHPO	Q10475 schizosacch
30	32	55.2	190	1 SLYD_HAEIN	P44830 haemophilus
31	32	55.2	235	1 NHAB_RHOSO	Q53117 rhodococcus
32	32	55.2	316	1 YX12_CAEEL	Q11123 caenorhabdi
33	32	55.2	322	1 FATB_VIBAN	P11460 vibrio angu

RESULT 1

ID	WBBJ_ECOLI	STANDARD;	PRT;	196 AA.
AC	P37750; P76375;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	PUTATIVE LIPOPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ (EC 2.3.1.-).			
DE	WBBJ.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / W3110;			
RX	MEDLINE; 94292434.			
RA	Yao Z., Valvano M.A.;			
RT	"Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb) of Escherichia coli K-12 W3110: identification of genes that confer group 6 specificity to Shigella flexneri serotypes Y and 4a.";			
RL	J. Bacteriol. 176:4133-4143(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / WGI;			
RX	MEDLINE; 94292435.			
RA	Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,			
RA	Redmond J.W., Lindquist L., Reeves P.R.;			
RT	"Structure of the O antigen of Escherichia coli K-12 and the sequence of its rfb gene cluster.";			
RL	J. Bacteriol. 176:4144-4156(1994).			
RN	[3]			
RP	REVIEWS TO 168-176 AND 187-189.			
RC	STRAIN=K12 / WGI;			
RA	Stevenson G.;			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / WGI655;			
RX	MEDLINE; 97426617.			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE; 97251358.			
RA	Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,			
RA	Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,			
RA	Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,			
RA	Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,			
RA	Salto N., Sampei G., Seki Y., Sivasubram S., Tagami H.,			

P08431 saccharomyc
O08376 mycobacteri
P29723 treponena p
O13969 schizosacch
P51689 homo sapien
P43405 homo sapien
Q46684 e periplasm
P20030 trypanosoma
O70423 mus musculu
P48308 mouse adeno
Q09822 schizosacch
Q13370 homo sapien

ALIGNMENTS

RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 CC -!- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
 ON THE O ANTIGEN
 CC -!- PATHWAY: LIPOPOLYSACCHARIDE BIOSYNTHESIS.
 CC -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC -----
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 CC EMBL; U03041; AAC31635.1; -;
 DR EMBL; U09876; AAB88406.1; -;
 DR EMBL; AE000294; AAC75094.1; -;
 DR EMBL; D90841; CAB21803.1; -;
 DR EMBL; D90842; CAB21811.1; -;
 DR EMBL; E011984; WBBJ. -;
 DR INTERPRO: IPR001451; -;
 DR PFAM; PF00132; hexapep; 1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE NEG.
 KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
 FT CONFLICT 168 176 SPENTVIA -> LPRKYCHC (IN REF. 1).
 FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
 SQ SEQUENCE 196 AA; 21675 MW; D1C2FA7D3B29A1B1 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 196;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
 DB 105 HNHGSFKH 112
 |||||

RESULT 2
 Y4VH_RHISN
 ID Y4VH_RHISN STANDARD; PRT; 218 AA.
 AC Q53216;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 24.6 KDA PROTEIN Y4VH.
 GN Y4VH.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym pNGR234a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97305956.
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes.";
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96389014.
 RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
 RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
 NGR234 using dye terminators and a thermostable 'sequenase': a
 beginning.";
 RL Genome Res. 6:590-600(1996).
 CC -!- SIMILARITY: NONE OBVIOUS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z68203; CAA92423.1; -;
 DR EMBL; AE000101; AAB91896.1; -;
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 218;
 Best Local Similarity 66.7%; Pred. No. 8.6;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 DB 68 ARDNHGSYS 76
 |||||

RESULT 3
 SYE2_RICPR
 ID SYE2_RICPR STANDARD; PRT; 470 AA.
 AC Q9ZCT8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
 DE (GLURS 2).
 GN GLUT2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E.
 RX MEDLINE; 99039499.
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 mitochondria.";
 RL Nature 396:133-140(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
 PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ235272; CAA15066.1; -;
 DR HSSP; P27000; 1GLN.
 DR INTERPRO: IPR000924; -;
 DR INTERPRO: IPR001412; -;
 DR PFAM; PF00749; trna-synt_lc; 1.
 DR PRINTS; PR00987; TRNASYNTHGLU.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
 KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 10 20 "HIGH" REGION.
 FT SIMILAR 239 243 "HWSK" REGION.
 FT BINDING 242 242 ATP (BY SIMILARITY).
 SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 62.1%; Score 36; DB 1; Length 470;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
 |||||
 DB 31 ARHNGKF 38

RESULT 4

ID SVE_AQUAE STANDARD; PRT; 473 AA.
 AC 06721;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
 DE (GLURS)
 GN GLTX OR AQ_1221.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE; 98196666.
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE000729; AAC07230.1;
 DR INTERPRO: IPR000924;
 DR PFAM: PF00749; TRNA-synt_lc; 1.
 DR PRINTS: PR00987; TRNASYNTHGLU.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl-trna synthetase: Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 10 20 "HIGH" REGION.
 FT SIMILAR 242 246 "RMSKS" REGION.
 FT BINDING 245 245 ATP (BY SIMILARITY).
 SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 62.1%; Score 36; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
 |||||
 DB 31 ARHNGKF 38

RESULT 5

EGGS_FASHE STANDARD; PRT; 197 AA.
 ID EGGS_FASHE
 AC P07915;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PUTATIVE EGGSHELL PROTEIN PRECURSOR.
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87175670.
 RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
 RT "Cloning and characterization of a female genital complex cDNA from
 RT the liver fluke Fasciola hepatica";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
 CC -----
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 CC -----
 CC EMBL: M15871; AAA29138.1;
 DR Eggshell; Signal.
 KW SIGNAL 1 17
 FT CHAIN 18 197 PUTATIVE EGGSHELL PROTEIN.
 SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 197;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
 |||||
 DB 17 ARPHGKF 24

RESULT 6

NCAP_CVHOC STANDARD; PRT; 448 AA.
 ID NCAP_CVHOC
 AC P33469;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE NUCLEOCAPSID PROTEIN.
 GN N.
 OS Human coronavirus (strain OC43).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89243809.
 RA Kanahora T., Soe L.H., Lai M.M.C.;
 RT "Sequence analysis of nucleocapsid gene and leader RNA of human
 RT coronavirus OC43";
 RL Virus Res. 12:1-9(1989).
 DR PIR; A60003; A60003.
 DR INTERPRO: IPR001218;
 DR PFAM; PF00937; Corona_nucleoca; 1.
 KW Nucleocapsid.
 SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 448;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
 |||||
 DB 103 RHNHGSF 109

RESULT 7

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CC45_XENLA
ID CC45_XENLA STANDARD; PRT; 567 AA.
AC Q9VHZ6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CDC45-RELATED PROTEIN.
GN CDC45.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98429493.
RA Minura S., Takisawa H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RT chromatin under the control of S-phase cdk."
RL EMBO J. 17:5699-5707(1998).
CC -1- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
CC
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CC
CC EMBL: AF062494; AAC67520.1;
CC DNA replication; Cell cycle; Nuclear protein.
KW DNA replication; Cell cycle; Nuclear protein.
SQ SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 567;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGS 7
DB 251 SRNHGN 257
:||||:

RESULT 8
KSYK_RAT
ID KSYK_RAT STANDARD; PRT; 629 AA.
AC Q64725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.12) (SPLEEN TYROSINE KINASE).
GN SYK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95279402.
RA Rowley R.B., Bolen J.B., Fargnoli J.;
RT "Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
RT splicing."
RL J. Biol. Chem. 270:12659-12664(1995).
CC -1- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
CC LYMPHOCYTE ACTIVATION.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYK AND SYKB (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

DOMAIN. BELONGS TO THE SYK/ZAP-70 SUBFAMILY.
CC
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CC
CC EMBL: U21684; AAA75167.1;
CC EMBL: U21683; AAA75166.1;
CC HSSP: P43405; ICSY.
CC INTERPRO: IPR000719;
CC INTERPRO: IPR000980;
CC INTERPRO: IPR001245;
CC PFAM: PF00017; SH2; 2.
CC PFAM: PF00069; pkinase; 1.
CC PRINTS: PR00401; SH2DOMAIN.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS50001; SH2; 2.
CC
CC SH2 transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC SH2 domain; Alternative splicing.
KW SH2 domain; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
FT DOMAIN 14 106 SH2.
FT DOMAIN 167 258 SH2.
FT DOMAIN 365 625 PROTEIN_KINASE.
FT NP_BIND 371 379 ATP (BY SIMILARITY).
FT BINDING 396 396 ATP (BY SIMILARITY).
FT ACT_SITE 488 488 BY SIMILARITY.
FT MOD_RES 519 519 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPIC 277 299 MISSING (IN ISOFORM SYKA).
SQ SEQUENCE 629 AA; 71528 MW; 81169A643EC6A8FE_CRC64;

Query Match 60.3%; Score 35; DB 1; Length 629;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
DB 195 ARDNGSFA 203
:||||:

RESULT 9
PBPI_YEAST
ID PBPI_YEAST STANDARD; PRT; 722 AA.
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAB1-BINDING PROTEIN 1.
GN PBPI OR MRS16 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delli H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DSBY747;
RA Mecklenbrauer I.;
RT "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns."
RL Thesis (1996), Vienna Biocentre, Austria.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE: 99038243.
RX Mangus D.A., Amrani N., Jacobson A.;

```

RT "Pbplp, a factor interacting with Saccharomyces cerevisiae poly(A)-
 binding protein, regulates polyadenylation."
 RL Mol. Cell. Biol. 18:7383-7396(1998).
 CC -!- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
 CC ABSENCE OF PBPLP, THE 3'TERMINI OF PRE-MRNAS ARE PROPERLY CLEAVED
 CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
 CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
 CC -!- SUBUNIT: INTERACTS WITH PAB1.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
 CC
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 CC
 DR EMBL; 272963; CAA97204.1; -.
 DR EMBL; U46931; AAB94294.1; -.
 DR SGD; S0003410; PBPL.
 KW Nuclear protein.
 SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

 Query Match 60.3%; Score 35; DB 1; Length 722;
 Best Local Similarity 85.7%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNHGSF 8
 DB 474 RHNHGSF 480

 RESULT 10
 YP56_MYCTU STANDARD; PRT; 129 AA.
 ID YP56_MYCTU
 AC Q50742;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 13.9 KDA PROTEIN RV2556C.
 GN RV2556C OR MTCY9C4.12.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Mycobacteriaceae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriineae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE; 98295987.
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekalia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998)
 CC -!- SIMILARITY: BELONGS TO THE UPF0047 FAMILY.
 CC
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 CC
 DR EMBL; 277250; CAB01048.1; -.
 DR TUBERCULLIST; RV2556C; -.

DR INTERPRO; IPR001602; -.
 DR PFAM; PF01894; UPF0047; 1.
 DR PROSITE; PS01314; UPF0047; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 129 AA; 13925 MW; AABE57AEB76B6923 CRC64;

 Query Match 58.6%; Score 34; DB 1; Length 129;
 Best Local Similarity 55.6%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 QY 2 RHNHGSFAY 10
 DB 69 RHNHGSYGH 77

 RESULT 11
 PNCA_ECOLI STANDARD; PRT; 213 AA.
 ID PNCA_ECOLI
 AC P21369; P76229; P76910;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRAZINAMIDASE/NICOTINAMIDASE [INCLUDES: PYRAZINAMIDASE (EC 3.5.1.1.-)
 DE (PZASE); NICOTINAMIDASE (EC 3.5.1.19) (NICOTINE DEAMIDASE)].
 GN PNCA OR NAM.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 89357501.
 RA Jerlstroem P.G., Bezjak D.A., Jennings M.P., Beacham I.R.;
 RT "Structure and expression in Escherichia coli K-12 of the
 RT L-asparaginase I-encoding ansA gene and its flanking regions."
 RL Gene 78:37-46(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96338362.
 RA Frothingham R., Meeker-O'Connell W.A., Talbot E.A., George J.W.,
 RA Kreuzer K.N.;
 RT "Identification, cloning, and expression of the Escherichia coli
 RT pyrazinamidase and nicotinamidase gene, pncA."
 RL Antimicrob. Agents Chemother. 40:1426-1431(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
 RA Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K.,
 RA Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,
 RA Katataka M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,
 RA Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,
 RA Yanamoto Y., Yano M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: NICOTINAMIDE + H(2)O = NICOTINATE + NH(3).
 CC -!- PATHWAY: PYRIDINE NUCLEOTIDE CYCLE.
 CC -!- SIMILARITY: TO YEAST YGL037C.
 CC
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DR EMBL; M26934; AAA23447.1; -;
 DR EMBL; AE000271; AAC74838.1; ALT_INIT.
 DR EMBL; D90820; BAA15559.1; -;
 DR EMBL; D90821; BAA15566.1; -;
 DR PIR; JU0048; QOECAS.
 DR ECOGENE; EG11135; PNCA.
 DR INTERPRO; IPR000868; -;
 DR PFAM; PF00857; Isochorismatase; 1.
 KW Hydrolase.
 SQ SEQUENCE 213 AA; 23362 MW; B9F8D946FA18433F CRC64;

Query Match 58.6%; Score 34; DB 1; Length 213;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSFA 9

Db 57 NHGSFA 62

RESULT 12

ARAD_ECOLI STANDARD; PRT; 231 AA.
 AC P08203;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE L-RIBULOSE-5-PHOSPHATE 4-EPIMERASE (EC 5.1.3.4).
 GN ARAD.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B;
 RX MEDLINE; 87163495.
 RA Lee N., Gielow W., Martin R., Hamilton E., Fowler A.;
 RT "The organization of the arabid operon of Escherichia coli.";
 RL Gene 47:231-244(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 91083835.
 RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
 RT "Nucleotide sequence and deletion analysis of the polB gene of
 RT Escherichia coli.";
 RL DNA Cell Biol. 9:631-635(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 91067495.
 RA Mineno J., Fukui H., Ishino Y., Kato I., Shinagawa H.;
 RT "Nucleotide sequence of the arad gene of Escherichia coli K12
 RT encoding the L-ribulose 5-phosphate 4-epimerase.";
 RL Nucleic Acids Res. 18:6722-6722(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 92334977.
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
 RA Isono K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 RT the 0-2.4 min region.";
 RL Nucleic Acids Res. 20:3305-3308(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;

RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [6]
 RP SEQUENCE OF 222-231 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 91017565.
 RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
 RT "DNA polymerase II is encoded by the DNA damage-inducible dinA gene
 RT of Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
 RN [7]
 RP SEQUENCE OF 158-231 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE; 91238699.
 RA Iwasaki H., Ishino Y., Toh H., Nakata A., Shinagawa H.;
 RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA
 RT polymerases.";
 RL Mol. Gen. Genet. 226:24-33(1991).
 CC -!- CATALYTIC ACTIVITY: L-RIBULOSE 5-PHOSPHATE - D-XYLOSE 5-PHOSPHATE.
 CC -!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
 CC -!- PATHWAY: THIRD STEP OF L-ARABINOSE CATABOLISM.
 CC -!- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
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 CC -----
 CC EMBL; M15263; AAA23464.1; -;
 DR EMBL; M35371; -; NOT_ANNOTATED_CDS.
 DR EMBL; M62646; AAA24405.1; -;
 DR EMBL; D10483; BAA01332.1; -;
 DR EMBL; AE000116; AAC73172.1; -;
 DR EMBL; M37727; AAA23683.1; -;
 DR EMBL; M38283; AAA63763.1; -;
 DR EMBL; X56048; CAA39519.1; -;
 DR PIR; D29022; ISECP4.
 DR PIR; S13593; ISECK4.
 DR PIR; A36236; A36236.
 DR PIR; S40577; S40577.
 DR ECO2DBASE; G028.1; 6TH EDITION.
 DR ECOGENE; EG10055; ARAD.
 DR INTERPRO; IPR001303; -;
 DR PFAM; PF00596; Aldolase_II; 1.
 KW Arabinose catabolism; Isomerase; Zinc.
 FT METAL 76 76 ZINC (BY SIMILARITY).
 FT METAL 95 95 ZINC (BY SIMILARITY).
 FT METAL 97 97 ZINC (BY SIMILARITY).
 FT METAL 171 171 ZINC (BY SIMILARITY).
 FT VARIANT 50 50 V -> I.
 FT VARIANT 70 70 T -> A.
 FT VARIANT 216 216 D -> N.
 SQ SEQUENCE 231 AA; 25519 MW; 1753F75958332163 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
 Best Local Similarity 62.5%; Pred. No. 21;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 NHGSFA 10

Db 169 HSHGPPAW 176

RESULT 13

```

4
ARAD_SALTY STANDARD; PRT; 231 AA.
ID ARAD_SALTY STANDARD; PRT; 231 AA.
AC P06190;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE L-RIBULOSE-5-PHOSPHATE 4-EPIMERASE (EC 5.1.3.4).
GN ARAD.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
[1]
SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE; 85232046.
RA Lin H.-C., Lei S.-P., Studnicka G., Wilcox G.;
RT "The arabad operon of Salmonella typhimurium LT2. III. Nucleotide
RT sequence of arabd and its flanking regions, and primary structure of
RT its product, L-ribulose-5-phosphate 4-epimerase."
RL Gene 34:129-134(1985).
RN
[2]
IDENTIFICATION OF PROBABLE FRAMESHIFT.
RP Bairoch A.;
RA Unpublished observations (AUG-1995).
RL
CC -1- CATALYTIC ACTIVITY: L-RIBULOSE 5-PHOSPHATE = D-XULOSE 5-PHOSPHATE.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- PATHWAY: THIRD STEP OF L-ARABINOSE CATABOLISM.
CC -1- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 204
CC ONWARD AND IS LONGER (248 AA) DUE TO A FRAMESHIFT.
CC
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CC
CC EMBL; M11047; AAA27025.1; ALT_FRAME.
DR PIR; A24986; ISEB4T.
DR TYGENE; SG10015; ARAD.
DR INTERPRO; IPR001303; -.
DR PFAM; PF00596; Aldolase_II; 1.
KW Arabinose catabolism; Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25540 MW; DA473505738A1570 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
Db 169 HSHGPFAY 176

RESULT 14
SGBE_ECOLI STANDARD; PRT; 231 AA.
ID SGBE_ECOLI STANDARD; PRT; 231 AA.
AC P37680;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROBABLE SUGAR ISOMERASE SGBE (EC 5.1.-.-).
GN SGBE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.

```

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RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE; 94316500.
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes."
RL Nucleic Acids Res. 22:2576-2586(1994).
RN
[2]
DISCUSSION OF SEQUENCE.
RP Reizer J., Charbit A., Reizer A., Saler M.H. Jr.;
RA "Novel phosphotransferases system genes revealed by bacterial genome
RT analysis: operons encoding homologues of sugar-specific permealase
RT domains of the phosphotransferase system and pentose catabolic
RT enzymes."
RL Genome Sci. Technol. 1:53-75(1996).
CC -1- FUNCTION: PROBABLE PENTULOSE-5-PHOSPHATE-4-EPIMERASE.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
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CC
CC EMBL; U00039; AAB18560.1; -.
DR EMBL; AE000435; AAC76607.1; -.
DR ECGENE; EG12287; SGBE.
DR INTERPRO; IPR001303; -.
DR PFAM; PF00596; Aldolase_II; 1.
KW Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25561 MW; F4FF4D7EC2A80B3A CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
Db 169 HSHGPFAY 176

RESULT 15
SGBE_HAEIN STANDARD; PRT; 231 AA.
ID SGBE_HAEIN STANDARD; PRT; 231 AA.
AC P44989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROBABLE SUGAR ISOMERASE SGBE (EC 5.1.-.-).
GN SGBE OR H11025.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN
[1]
SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE; 95350630.
RA Fleischmann R.D., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Kerlavage A.R., Bult C.J., Fitch W., Fields C.A., Cocayne J.D.,
RA McKenney K., Sutton G., Fitzhugh W., Glodek A., Keiley J.M.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Keiley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

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RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RL influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: PROBABLE PENTULOSE-5-PHOSPHATE-4-EPIMERASE.
CC -!- COPACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
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CC -----
DR EMBL; U32783; AAC22685.1; -.
DR TIGR; H11025; -.
DR INTERPRO; IPR001303; -.
DR PFAM; PF00596; Aldolase_II; 1.
KW Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25980 MW; 9DE3485E54B10DC7 CRC64;

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Query Match          58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. NO. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 3 HNHGSFAY 10
   |::|::
Db 169 HSHGPFAY 176

```

Search completed: March 28, 2001, 07:29:52
Job time: 1659 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:52 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: us-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNGSYAY 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	77.6	108	2 S26316	Ig heavy chain V r
2	45	77.6	110	2 S26317	Ig heavy chain V r
3	42	72.4	446	2 T19625	hypothetical prote
4	40	69.0	316	2 T15395	hypothetical prote
5	38	65.5	236	2 T27233	hypothetical prote
6	38	65.5	428	2 T03934	DNA binding protei
7	38	65.5	482	2 T01932	RNA binding protei
8	37	63.8	289	2 T34688	probable lipoprote
9	37	63.8	420	2 T51088	L-SF precursor - J
10	37	63.8	1144	2 A36968	PI-like adhesin pr
11	36	62.1	9	2 S36850	Ig heavy chain V r
12	36	62.1	113	2 S26468	Ig heavy chain V r
13	36	62.1	143	2 HSUR52	histone H2B.2, spe
14	36	62.1	301	2 JW0079	heterogeneous nucl
15	36	62.1	349	1 S52763	hypothetical prote
16	36	62.1	349	2 T33263	hypothetical prote
17	36	62.1	626	2 T18733	hypothetical prote
18	35	60.3	119	2 E30562	Ig heavy chain V r
19	35	60.3	119	2 C30562	Ig heavy chain V r
20	35	60.3	119	2 D30562	Ig heavy chain V r
21	35	60.3	150	2 D69081	deoxyuridine 5-tri
22	35	60.3	155	2 T03042	hypothetical prote
23	35	60.3	241	2 T16802	hypothetical prote
24	35	60.3	246	1 C64705	gerC2 protein - He
25	35	60.3	246	2 C71815	ubiquitinone/menaq
26	35	60.3	257	2 B81155	conserved hypothet
27	35	60.3	257	2 C81949	hypothetical prote
28	35	60.3	281	2 S71251	C-5 sterol desatur
29	35	60.3	293	2 F64969	glucose-1-phosphat

ALIGNMENTS

RESULT 1
S26316

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26316

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421

A:Accession: S26316

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <STA>

A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.35;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNGSYAY 10
|||
Db 84 ARGNGYAY 93

RESULT 2
S26317

Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26317

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421

A:Accession: S26317

A:Molecule type: mRNA

A:Residues: 1-110 <STA>

A:Cross-references: EMBL:X59186

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 110;
Best Local Similarity 80.0%; Pred. No. 0.36;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| |||
Db 86 ARHNYGSYAY 95

RESULT 3

T19625 hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 72.4%; Score 42; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSYA 9

||||| |

Db 51 RHNYGSHA 58

RESULT 4

T15395 hypothetical protein C03F11.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15395

R:Bentley, D.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C03F11.

A:Reference number: Z18342

A:Accession: T15395

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-316 <BEN>

A:Cross-references: EMBL:U39744; NID:g1049465; PID:g1049467; PIDN:AAA80440.1; CESP:C03F11

C:Genetics:

A:Gene: CESP:C03F11.2

A:Introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 69.0%; Score 40; DB 2; Length 316;
Best Local Similarity 70.0%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

||||| |

Db 69 ARHFGSYEY 78

RESULT 5

T27233 hypothetical protein Y57G11C.21 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27233

R:McMurray, A.

submitted to the EMBL Data Library, September 1997

Query Match 65.5%; Score 38; DB 2; Length 482;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

A:Reference number: Z20330

A:Accession: T27233

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-236 <WIL>

A:Cross-references: EMBL:Z99281; PIDN:CAB16522.1; GSPDB:GN00022; CESP:Y57G11C.21

A:Experimental source: clone Y57G11C

C:Genetics:

A:Gene: CESP:Y57G11C.21

A:Map position: 4

Query Match 65.5%; Score 38; DB 2; Length 236;

Best Local Similarity 60.0%; Pred. No. 13;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

||||| |

Db 118 AYHNFNYAY 127

RESULT 6

T03934

DNA binding protein ACBF - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: T03934

R:Sequin, A.; Laible, G.; Leyva, A.; Dixon, R.A.; Lamb, C.J.

Plant Mol. Biol. 35, 281-291, 1997

A:Title: Characterization of a gene encoding a DNA-binding protein that interacts in

A:Reference number: Z15144; MUID:98009965

A:Accession: T03934

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-428 <SEG>

A:Cross-references: EMBL:U90212; NID:g1899187; PIDN:AAC49850.1; PID:g1899188

A:Experimental source: tissue-type stem

A:Note: interacts in vitro with vascular-specific cis-elements of the phenylalanine a

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro

Query Match 65.5%; Score 38; DB 2; Length 428;

Best Local Similarity 66.7%; Pred. No. 24;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10

||||| |

Db 387 RQNYGGYGY 395

RESULT 7

T01932

RNA binding protein homolog - common tobacco (fragment)

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-May-2000

C:Accession: T01932

R:Deslandes, L.; Manevski, A.; Lescure, B.; Marco, Y.; Tremousaygue, D.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z14459

A:Accession: T01932

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-482 <DES>

A:Cross-references: EMBL:AF029351; NID:g2708531; PID:g2708532

C:Genetics:

A:Gene: QRBP-1

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro

Query Match 65.5%; Score 38; DB 2; Length 482;

Best Local Similarity 66.7%; Pred. No. 27;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSYAY 10
| | | | |
Db 442 RQNYGGYGY 450

RESULT 8

T34688
probable lipoprotein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

C:Accession: T34688

R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z21553

A:Accession: T34688

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-289 <HAR>

A:Cross-references: EMBL:AL023517; PIDN:CAA18984.1; GSPDB:GN000070; SCOEDB:SC1B5.10C

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC1B5.10C

Query Match

Best Local Similarity 63.8%; Score 37; DB 2; Length 289;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
| | | | |
Db 144 ANHSYSHYAY 153

RESULT 9

I51088

L-Sr precursor - Japanese medaka

C:Species: Oryzias latipes (Japanese medaka)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999

C:Accession: I51088

R:Murata, K.; Sasaki, T.; Yasumasu, S.; Iuchi, I.; Enami, J.; Yasumasu, I.; Yamagami, K.

Dev. Biol. 167, 9-17, 1995

A:Title: Cloning of cDNAs for the precursor protein of a low-molecular-weight subunit of

A:Reference number: I51088; MUID:95154588

A:Accession: I51088

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-420 <MUR>

A:Cross-references: GB:D38630; NID:gi060937; PIDN:BAA07610.1; PID:gl060938

C:Genetics:

A:Gene: l-sf

C:Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology

F:84-338/Domain: ZP domain homology <ZPH>

Query Match

Best Local Similarity 63.8%; Score 37; DB 2; Length 420;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
| | | | |
Db 21 AQHNYGKPSY 30

RESULT 10

A36968

P1-like adhesin precursor - Mycoplasma pirum

C:Species: Mycoplasma pirum

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999

C:Accession: A36968

R:Tham, T.N.; Ferris, S.; Bahraoui, E.; Canarelli, S.; Montagnier, L.; Blanchard, A.

J. Bacteriol. 176, 781-788, 1994

A:Title: Molecular characterization of the P1-like adhesin gene from Mycoplasma pirum.

A:Reference number: A36968; MUID:94131957

A:Accession: A36968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1144 <THA>
A:Cross-references: GB:L19685; NID:g404770; PIDN:AAC36866.1; PID:g404771
C:Genetics:
A:Genetic code: SGC3

Query Match

Best Local Similarity 63.8%; Score 37; DB 2; Length 1144;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSYAY 10
| | | | |
Db 885 RQNYGSYFY 893

RESULT 11

S36850

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

C:Accession: S36850

R:Jacob, J.; Kelsoe, G.

submitted to the EMBL Data Library, July 1992

A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)

A:Reference number: S25024

A:Accession: S36850

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-9 <JAC>

A:Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799.1; PID:e51594; PID:gl333387

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 62.1%; Score 36; DB 2; Length 9;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSY 8
| | | | |
Db 1 ARYDYGSY 8

RESULT 12

S26458

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26458

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26458

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 62.1%; Score 36; DB 2; Length 113;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSY 8
| | | | |
Db 93 ARHPYGNV 100

RESULT 13

HSURB2
 histone H2B.2, sperm - sea urchin (Lytechinus pictus)
 C:Species: Lytechinus pictus (painted urchin)
 C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 22-Jun-1999
 C:Accession: A24329; B25381
 R:Lai, Z.C.; Childs, G.
 Nucleic Acids Res. 14, 6845-6856, 1986
 A:Title: Isolation and characterization of the gene encoding the testis specific histone H2B.
 A:Reference number: A93637; MUID:87016329
 A:Accession: A24329
 A:Molecule type: DNA
 A:Residues: 1-143 <LAI>
 A:Cross-references: GB:X04384; NID:g9618; PIDN:CAA27971.1; PID:g9619
 A:Experimental source: testis
 R:Lieber, T.; Weissner, K.; Childs, G.
 Mol. Cell. Biol. 6, 2602-2612, 1986
 A:Title: Analysis of histone gene expression in adult tissues of the sea urchins Strongylocentrotus purpuratus.
 A:Reference number: A93078; MUID:87064560
 A:Accession: B25381
 A:Molecule type: mRNA
 A:Residues: 59-75, 'A', 77-137, 'N', 139-143 <LIE>
 A:Cross-references: GB:W13635; NID:g161315; PIDN:AAA30001.1; PID:g161316
 A:Experimental source: testis
 A:Note: this sequence most likely represents an alternative allele of the same gene
 C:Superfamily: histone H2B
 C:Keywords: chromosomal protein; DNA binding; nucleosome core
 F:2-143/Product: histone H2B.2, sperm #status predicted <MAT>

Query Match 62.1%; Score 36; DB 1; Length 143;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10

I :||||| I

Db 52 RESYGSYIY 60

RESULT 14

JW0079
 heterogeneous nuclear ribonucleoprotein homolog JKTPB [imported] - human
 N:Alternate names: JKTPB
 C:Species: Homo sapiens (man)
 C:Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 02-Sep-2000
 C:Accession: JW0079
 R:Tsuchiya, N.; Kamei, D.; Takano, A.; Matsui, T.; Yamada, M.
 J. Biochem. 123, 499-507, 1998
 A:Title: Cloning and characterization of a cDNA encoding a novel heterogeneous nuclear ribonucleoprotein.
 A:Reference number: JW0079; MUID:98207031
 A:Accession: JW0079
 A:Molecule type: mRNA
 A:Residues: 1-301 <TSU>
 A:Cross-references: DDBJ:D89092; NID:g2780747; PIDN:BA24361.1; PID:d1025273; PID:g2780747
 C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein repeat
 F:28-101,113-187/Domain: RNA-binding #status predicted <RNA>
 F:30-96/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 62.1%; Score 36; DB 2; Length 301;
 Best Local Similarity 62.5%; Pred. No. 39;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10

:||||| I

Db 263 YNYGNYGY 270

RESULT 15

S52763
 hypothetical protein YJR019c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein J1456
 C:Species: Saccharomyces cerevisiae

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: S52763; S55209; S57034; S65928
 R:Hani, J.; Stumpf, G.; Domdey, H.
 submitted to the EMBL Data Library, March 1995
 A:Description: PFT1 encodes an essential protein in Saccharomyces cerevisiae, which s
 A:Reference number: S52762
 A:Accession: S52763
 A:Molecule type: DNA
 A:Residues: 1-349 <HAN>
 A:Cross-references: EMBL:X85972; NID:g758283; PID:g758285
 R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S55183
 A:Accession: S55209
 A:Molecule type: DNA
 A:Residues: 1-349 <DEH>
 A:Cross-references: EMBL:X87611; NID:g854567; PID:g854594
 R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56771
 A:Accession: S57034
 A:Molecule type: DNA
 A:Residues: 1-349 <ZAG>
 A:Cross-references: EMBL:Z49519; NID:g1015654; PID:g1015655; GSPDB:GN00010; MIPS:YJR0
 R:Hani, J.; Stumpf, G.; Domdey, H.
 FEBS Lett. 365, 198-202, 1995
 A:Title: PFT1 encodes an essential protein in Saccharomyces cerevisiae, which shows s
 A:Reference number: S65927; MUID:95300974
 A:Accession: S65928
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-349 <HAW>
 A:Cross-references: EMBL:X85972; NID:g758283; PIDN:CAA59960.1; PID:g758285
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
 C:Genetics:
 A:Gene: SGD:TES1; MIPS:YJR019c
 A:Cross-references: SGD:S0003780; MIPS:YJR019c
 A:Map position: 10R
 C:Superfamily: acyl-CoA thioesterase II

Query Match 62.1%; Score 36; DB 1; Length 349;
 Best Local Similarity 60.0%; Pred. No. 45;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

||:||||:|I|

Db 247 ARNYVAFAY 256

Search completed: March 28, 2001, 06:41:55
 Job time: 878 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:52 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	909	1	HEX_ADEM1
2	40	69.0	316	1	YX12_CAEEL
3	36	62.1	142	1	H2B2_LXTPI
4	36	62.1	202	1	AMEL_MONDO
5	36	62.1	349	1	YJY9_YEAST
6	35	60.3	233	1	RBA1_ECOLI
7	34	58.6	150	1	Y736_CHLTR
8	34	58.6	189	1	AMEL_PIG
9	34	58.6	213	1	AMEX_BOVIN
10	34	58.6	218	1	Y4VH_RHTSN
11	34	58.6	225	1	DH4_HORVU
12	34	58.6	448	1	ASTE_PSAE
13	34	58.6	456	1	KICH_SCHPO
14	34	58.6	576	1	PX5_PICPA
15	34	58.6	1150	1	C9EA_BACTA
16	34	58.6	1156	1	C9AA_BACTG
17	34	58.6	1157	1	C9CA_BACTO
18	34	58.6	1169	1	C9DA_BACTP
19	33	56.9	180	1	CH19_DROSO
20	33	56.9	405	1	VGLM_EBV
21	33	56.9	419	1	YMD2_CAEEL
22	33	56.9	425	1	PURA_FUSNU
23	33	56.9	520	1	PAX7_HUMAN
24	33	56.9	629	1	KSYP_MOUSE
25	33	56.9	635	1	KSYP_HUMAN
26	33	56.9	649	1	GPDM_SCHPO
27	33	56.9	786	1	EXOP_RHIME
28	33	56.9	809	1	UBPL1_YEAST
29	33	56.9	1569	1	GLI3_XENLA
30	33	56.9	1596	1	GLI3_HUMAN
31	33	56.9	1596	1	GLI3_MOUSE
32	32	55.2	79	1	CYB_DIPCA
33	32	55.2	79	1	CYB_DIPHE

34	32	55.2	79	1	CYB_DIPPA	P16357 dipodomys p
35	32	55.2	129	1	YP56_MYCTU	Q50742 mycobacteri
36	32	55.2	134	1	CYB_DRYNI	Q03713 dryomys nit
37	32	55.2	198	1	HB2G_HUMAN	P01911 homo sapien
38	32	55.2	202	1	DHSC_BACSU	P08064 bacillus su
39	32	55.2	263	1	CYBB_BACTJ	O32322 bacillus th
40	32	55.2	266	1	HB2A_HUMAN	P01913 homo sapien
41	32	55.2	266	1	HB2B_HUMAN	P01912 homo sapien
42	32	55.2	266	1	HB2C_HUMAN	P01914 homo sapien
43	32	55.2	266	1	HB2D_CANFA	P18470 canis famli
44	32	55.2	266	1	HB2D_HUMAN	P13759 homo sapien
45	32	55.2	266	1	HB2E_HUMAN	P04229 homo sapien

ALIGNMENTS

RESULT 1

HEX_ADEM1	STANDARD;	PRT;	909 AA.
AC	P48308; O11839;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	HEXON PROTEIN (LATE PROTEIN 2).		
GN	PII.		
OS	Mouse adenovirus type 1 (MAV-1).		
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FL;		
RX	MEDLINE: 94157453.		
RA	Weber J.M., Cai F., Murali R., Burnett R.M.;		
RT	"Sequence and structural analysis of murine adenovirus type 1 hexon.";		
RL	J. Gen. Virol. 75:141-147(1994).		
RN	[2]		
RP	REVISIONS TO 443.		
RA	Weber J.M.;		
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE		
CC	-!- VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.		
CC	-!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).		
CC	-----		
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CC	-----		
DR	EMBL; M81889; AAB48187.1; -		
DR	HSSP; P03277; IDHX.		
DR	INTERPRO; IPR000736; -		
DR	PFAM; PF01065; Adeno_hexon.1.		
KW	Coat protein; Hexon protein; Late protein.		
SQ	SEQUENCE 909 AA; 102368 MW; 7E1C17DF7F0E95A0 CRC64;		

Query Match 70.7%; Score 41; DB 1; Length 909;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NYGSYAY 10
|||||
Db 210 NYGSYAY 216

RESULT 2

YX12_CAEEL	STANDARD;	PRT;	316 AA.
ID	YX12_CAEEL		
AC	Q11123;		
DT	01-NOV-1997 (Rel. 35, Created)		

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 35.1 KDA PROTEIN C03F11.2 IN CHROMOSOME X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Bentley D.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C-ELEGANS F53B1.5.
CC -----
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CC -----
CC EMBL: U39744; AAA80440.1; -
DR WORKPEP; C03F11.2; CE03914.
KW Hypothetical protein.
SQ SEQUENCE 316 AA; 35107 MW; 6A725FCAC21CF676 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 316;
Best Local Similarity 70.0%; Pred. No. 6.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
| | | : | | | |
DB 69 ARHFGSYEY 78

RESULT 3
H2B2_LYTP1 ID H2B2_LYTP1 STANDARD; PRT; 142 AA.
AC P08146;
DT 01-JAN-1998 (Rel. 06, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HISTONE H2B-2, SPERM.
OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA MEDLINE; 87016329.
RA Lai Z.-C., Childs G.J.;
RT "Isolation and characterization of the gene encoding the testis
RT specific histone protein H2B-2 from the sea urchin Lytechinus
RT pictus."
RL Nucleic Acids Res. 14:5845-5856(1986).
RN [2]
RP SEQUENCE OF 58-142 FROM N.A.
RC TISSUE-TESTIS;
RA MEDLINE; 87064560.
RA Lieber T., Weisser K., Childs G.;
RT "Analysis of histone gene expression in adult tissues of the sea
RT urchins Strongylocentrotus purpuratus and Lytechinus pictus:
RT tissue-specific expression of sperm histone genes."
RL Mol. Cell. Biol. 6:2602-2612(1986).
CC -!- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
CC -----
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CC -----
CC EMBL: X04384; CAA27971.1; -
DR EMBL; M13635; AAA30001.1; -
DR PIR; A24329; HSURB2.
DR INTERPRO; IPR000166; -
DR INTERPRO; IPR000558; -
DR PFAM; PF00125; histone; 1.
DR PROSITE; PR00621; HISTONEH2B.
KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding;
KW Multigene family.
FT INIT-MET 0 0
FT VARIANT 75 75 G -> A.
FT VARIANT 137 137 K -> N.
SQ SEQUENCE 142 AA; 15805 MW; 8BF47E2C5EB878D5 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 142;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
| : | | | |
DB 51 RESYGSYIY 59

RESULT 4
AMEL_MONDO ID AMEL_MONDO STANDARD; PRT; 202 AA.
AC Q28462;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE AMELOGENIN.
GN AMEL.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-42.
RX MEDLINE; 97113826.
RA Hu C.C., Zhang C., Qian Q., Ryu O.H., Moradian-Oldak J., Fincham A.G.,
RA Simmer J.P.;
RT "Cloning, DNA sequence, and alternative splicing of opossum
RT amelogenin mRNAs".
RL J. Dent. Res. 75:1728-1734(1996).
CC -!- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTH. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- SIMILARITY: BELONGS TO THE AMALOGENIN FAMILY.
CC -----
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CC -----
CC EMBL: U43407; AAB41109.1; -
DR INTERPRO; IPR002965; -
DR PRINTS; PR01217; PRICHEXTENSN.

KW Extracellular matrix; Phosphorylation; Enamel; Repeat;
 KW Alternative splicing.
 FT MOD_RES 16 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 32 HE -> QQ (IN AA SEQUENCE).
 SQ SEQUENCE 202 AA; 22996 MW; 277FD2935211A6C6 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 202;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
 Db 31 RHEYPYGY 39

RESULT 5
 YJY9_YEAST STANDARD; PRT; 349 AA.
 ID YJY9_YEAST
 AC P41903;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 40.3 KDA PROTEIN IN ESS1-MER2 INTERGENIC REGION.
 GN YJY019C OR J1456.

OS Saccharomycetes cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DH484;
 RA Hani J., Stumpf G., Domdey H.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RA de Haan M., Smits P.H.M., Grivell L.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]

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DR EMBL; X85972; CAA59960.1; -;
 DR EMBL; X87611; CAA60943.1; -;
 DR EMBL; Z49519; CAA89543.1; -;
 DR SGD; S0003780; YJR019C.
 KW Hypothetical protein.
 SQ SEQUENCE 349 AA; 40259 MW; F1B5A51C9A46783E CRC64;

Query Match 62.1%; Score 36; DB 1; Length 349;
 Best Local Similarity 60.0%; Pred. No. 32;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 Db 247 ARYNYVAFY 256

RESULT 6
 RBAL_ECOLI STANDARD; PRT; 293 AA.
 ID RBAL_ECOLI
 AC P37744; P78081;

DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24) (DTDP-GLUCOSE
 DE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHORYLASE).

GN RFBA OR RMLA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / WGI;
 RX MEDLINE; 94292435.

RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
 RA Redmond J.W., Lindquist L., Reeves P.R.;
 RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
 RT of its rfb gene cluster.";
 RL J. Bacteriol. 176:4144-4156(1994).
 RN [2]

RP REVISION TO 288.
 RC STRAIN=K12 / WGI;
 RA Stevenson G.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;
 RX MEDLINE; 97426617.

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=K12;

RX MEDLINE; 97251358.
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubraman S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 RN [5]

RP SEQUENCE OF 247-293 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE; 94292434.

RA Yao Z., Valvano M.A.;
 RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
 RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
 RT that confer group 6 specificity to Shigella flexneri serotypes Y and
 RT 4a.";

RL J. Bacteriol. 176:4133-4143(1994).
 CC -!- CATALYTIC ACTIVITY: DTPP + ALPHA-D-GLUCOSE 1-PHOSPHATE =
 CC PYROPHOSPHATE + DTDP-GLUCOSE.
 CC -!- PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN
 CC BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.

CC -!- SIMILARITY: BELONGS TO THE GLUCOSE-1-PHOSPHATE
 CC THYMIDYLTRANSFERASE FAMILY.

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 CC -----

DR EMBL; U09876; AAB8400.1; -;
 DR EMBL; AE000294; AAC75100.1; -;
 DR EMBL; D90841; CAB21785.1; -;
 DR EMBL; D90842; CAB21817.1; -;
 DR EMBL; U03041; AAC31629.1; -;
 DR EMBL; EG11978; RFBA.
 DR INTERPRO; IPR001825; -;

DR PFAM; PF00483; NTP_transferase; 1.
 KW Lipopolysaccharide biosynthesis; Transferase; Kinase;
 FT Nucleotidyltransferase.
 SQ CONFLICT 247 247 Q -> P (IN REF. 5).
 SEQUENCE 293 AA; 32693 MW; BA895362D1C5CA55 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 293;
 Best Local Similarity 55.6%; Pred. NO. 40;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10

Db 278 KNYGQYLY 286

RESULT 7

Y736_CHLTR STANDARD; PRT; 150 AA..

AC O84741;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 30-MAY-2000 (Rel. 39, Last annotation update)

DN HYPOTHETICAL PROTEIN CT736.

GN CT736.

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-D/UW-3/CX;

RX MEDLINE; 99000809.

RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,

RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,

RA Davis R.W.

RT "Genome sequence of an obligate intracellular pathogen of humans:

RT Chlamydia trachomatis."

RL Science 282:754-759(1998).

CC -!- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.

CC

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CC -----

CC EMBL; AE001344; AAC68331.1;

DR KW Hypothetical protein.

SQ SEQUENCE 150 AA; 16508 MW; E480FE4899354C67 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 150;
 Best Local Similarity 60.0%; Pred. NO. 32;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNVGSYAY 10

Db 103 AKRYYFYAY 112

RESULT 8

AMEL_PIG

ID AMEL_PIG STANDARD; PRT; 189 AA.

AC P45561;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE AMELOGENIN PRECURSOR (AMELOGENIN 173A/173B) [CONTAINS: LEUCINE-RICH

DE AMELOGENIN PEPTIDE (LRAP)].

GN AMEL.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 97113827.

RA Hu C.C., Bartlett J.D., Zhang C.H., Qian Q., Ryu O.H., Simmer J.P.;

RT "Cloning, cDNA sequence, and alternative splicing of porcine

RT amelogenin mRNAs."

RL J. Dent. Res. 75:1735-1741(1996).

RN [2]

RP SEQUENCE OF 17-61 AND 78-181.

RC TISSUE-TOOTH;

RX MEDLINE; 94071951.

RA Fincham A.G., Moradian-Oldak J.;

RT "Amelogenin post-translational modifications: carboxy-terminal

RT processing and the phosphorylation of bovine and porcine 'TRAP' and

RT 'LRAP' amelogenins."

RL Biochem. Biophys. Res. Commun. 197:248-255(1993).

CC -!- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTH. SEEMS

CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY

CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN

CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING

CC ENAMEL.

CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE

CC SPLICING. ONE OF THESE FORMS, LRAP, LACKS THE CENTRAL SECTION OF

CC AMELOGENIN.

CC -!- SIMILARITY: BELONGS TO THE AMALOGENIN FAMILY.

CC -----

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CC -----

CC EMBL; U43405; AAB41110.1;

DR EMBL; U43406; AAB41111.1;

DR PIR; PC2006; PC2006.

DR PIR; PC2008; PC2008.

KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;

KW Alternative splicing.

FT SIGNAL 1 16

FT CHAIN 17 189

FT MOD_RES 32 32

FT VARSPPLIC 34 45

FT VARSPPLIC 6 6

FT VARSPPLIC 14 16

FT VARSPPLIC 189 AA; 21387 MW; 6392212E0A31D00C CRC64;

SQ SEQUENCE 189 AA; 21387 MW; 6392212E0A31D00C CRC64;

Query Match 58.6%; Score 34; DB 1; Length 189;

Best Local Similarity 66.7%; Pred. NO. 39;

Matches 6; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 RHNYGSYAY 10

Db 47 RHPTSYGY 55

RESULT 9

AMEX_BOVIN

ID AMEX_BOVIN STANDARD; PRT; 213 AA.

AC P02817;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE AMELOGENIN, CLASS I PRECURSOR.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE: 91113686.
RA Gibson C., Golub E., Herold R., Risser M., Ding W., Shimokawa H.,
RA Young M., Termine J., Rosenbloom J.;
RT "Structure and expression of the bovine amelogenin gene.";
RL Biochemistry 30:1075-1079(1991).
RN (2)
RP PRELIMINARY SEQUENCE OF 17-201.
RX MEDLINE: 84231410.
RA Takagi T., Suzuki M., Baba T., Minegishi K., Sasaki S.;
RT "Complete amino acid sequence of amelogenin in developing bovine
RT enamel";
RL Biochem. Biophys. Res. Commun. 121:592-597(1984).
RN (3)
RP ALTERNATIVE SPLICING (LRAP).
RX TISSUE-TOOTH;
RX MEDLINE: 91144612.
RA Gibson C.W., Golub E., Ding W., Shimokawa H., Young M., Termine J.,
RA Rosenbloom J.;
RT "Identification of the leucine-rich amelogenin peptide (LRAP) as the
RT translation product of an alternatively spliced transcript.";
RL Biochem. Biophys. Res. Commun. 174:1306-1312(1991).
RN (4)
RP SEQUENCE OF 17-49 AND 188-213.
RX MEDLINE: 94071951.
RA Fincham A.G., Moradian-Oldak J.;
RT "Amelogenin post-translational modifications: carboxy-terminal
RT processing and the phosphorylation of bovine and porcine 'TRAP' and
RT 'LRAP' amelogenins";
RL Biochem. Biophys. Res. Commun. 197:248-255(1993).
RN (5)
RP STRUCTURE BY NMR.
RX MEDLINE: 90091473.
RA Renuopalakrishnan V., Prabhakaran M., Huang S.G., Balasubramaniam A.,
RA Strawich E., Glimcher M.J.;
RT "Secondary structure and limited three-dimensional structure of
RT bovine amelogenin.";
RL Connect. Tissue Res. 22:131-138(1989).
CC -!- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTH. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. ONE OF THESE FORMS, LRAP, LACKS THE CENTRAL SECTION OF
CC AMELOGENIN.
CC -!- MISCELLANEOUS: AMELOGENIN IS THE PREDOMINANT PROTEIN IN DEVELOPING
CC DENTAL ENAMEL.
CC -!- MISCELLANEOUS: CLASS I AMELOGENINS LOCATED ON X CHROMOSOME.
CC -!- SIMILARITY: BELONGS TO THE AMELOGENIN FAMILY.

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DR EMBL: M63499; AAA30372.1; -
DR EMBL: M63631; AAA30625.1; -
DR PIR: A03300; JMBQ.
DR PIR: JN0123; JN0123.
DR PIR: PC2007; PC2007.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 213 AMELOGENIN, CLASS I.
FT VARSPLIC 50 187 MISSING (IN LRAP).
FT MOD_RES 32 32 PHOSPHORYLATION.
FT SEQUENCE 213 AA; 24119 MW; 163BD538806366DF CRC64;

Query Match 58.6%; Score 34; DB 1; Length 213;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSYAY 10
||| |||
Db 47 RHPVPSYGY 55

RESULT 10

Y4VH_RHISN
ID Y4VH_RHISN STANDARD; PRT; 218 AA.
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 24.6 KDA PROTEIN Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 97305956.
RA Freiberg C.A., Fellay R., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE: 96389014.
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase'; a
RT beginning";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: NONE OBVIOUS.

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DR EMBL: Z68203; CAA92423.1; -
DR EMBL: AE000101; AAB91896.1; -
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSYA 9
||| |||
Db 68 ARDNHGSYS 76

RESULT 11

DH4_HORVU
ID DH4_HORVU STANDARD; PRT; 225 AA.
AC P12949;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE DEHYDRIN DHN4 (B18).
GN DHN4.
OS Hordeum vulgare (Barley).

CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=CV, HIMALAYA; TISSUE=SEEDLING;
 RX MEDLINE; 93357436.
 RA Close T.J., Kortt A.A., Chandler P.M.;
 RT "A cDNA-based comparison of dehydration-induced proteins (dehydrins)
 RL in barley and corn."
 CC Plant Mol. Biol. 13:95-108(1989).
 CC -!- INDUCTION: BY ABSCISIC ACID AND WATER-STRESS.
 CC -!- SIMILARITY: STRONG TO BARLEY DHN1 AND DHN2, MAIZE DHN1, AND
 CC ESPECIALLY TO BARLEY DHN3. TWO EXTREMELY CONSERVED BLOCKS WERE
 CC IDENTIFIED, WITH A LESS CONSERVED REPEATING UNIT POSITIONED
 CC BETWEEN THEM. DEHYDRIN DHN4 HAS FIVE SUCH SEMI-CONSERVED TANDEM
 CC REPEATING UNITS.
 CC -!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; X15287; CAA33361.1; -
 CC PIR; S05546; S05546;
 CC INTERPRO; IPR000167; -
 CC PFAM; PF00257; dehydrin; 2.
 CC PROSITE; PS00315; DEHYDRIN_1; 1.
 CC PROSITE; PS00823; DEHYDRIN_2; 2.
 CC Dehydrin; Repeat.
 FT DOMAIN 60 68 POLY-SER.
 FT DOMAIN 105 199 5 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 105 118 1.
 FT REPEAT 119 136 2.
 FT REPEAT 137 159 3.
 FT REPEAT 160 178 4.
 FT REPEAT 179 199 5.
 SQ SEQUENCE 225 AA; 22574 MW; F0636B368CE5FFIC CRC64;
 Query Match 58.6%; Score 34; DB 1; Length 225;
 Best Local Similarity 55.6%; Pred. No. 46;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNYGSYAY 10
 DB 97 QHNAGTYGY 105
 RESULT 12
 ASTB_PSEAE STANDARD; PRT; 448 AA.
 ID ASTB_PSEAE
 AC Q50175;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE SUCCINYLARGININE DIHYDROLASE (EC 3.-.-.-).
 GN ASTB OR ARUB.
 OS Pseudomonas aeruginosa.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE; 98053840.
 RA Icon Y.;
 RT "Cloning and characterization of the *aru* genes encoding enzymes of
 RT the catabolic arginine succinyltransferase pathway in *Pseudomonas*
 RT *aeruginosa*."
 RL J. Bacteriol. 179:7280-7290(1997).

CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF N(2)-SUCCINYLARGININE INTO
 CC N(2)-SUCCINYLORNITHINE, AMMONIA AND CO(2).
 CC -!- PATHWAY: SECOND STEP IN ARGININE CATABOLISM BY THE ARGININE
 CC SUCCINYLTRANSFERASE PATHWAY.
 CC -----
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 CC -----
 CC EMBL; AF011922; AAC46013.1; -
 CC Arginine metabolism; Hydrolase.
 KW Arginine metabolism; Hydrolase.
 SQ SEQUENCE 448 AA; 48875 MW; 39F9F379CCCC16196 CRC64;
 Query Match 58.6%; Score 34; DB 1; Length 448;
 Best Local Similarity 62.5%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 HNYGSYAY 10
 DB 16 HNYGGLSY 23
 RESULT 13
 KICH_SCHPO STANDARD; PRT; 456 AA.
 ID KICH_SCHPO
 AC Q10276;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PUTATIVE CHOLINE KINASE (EC 2.7.1.32).
 GN SPAC13G7.12C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 CC Schizosaccharomycetaceae; Schizosaccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (Feb-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + CHOLINE = ADP + O-PHOSPHOCHOLINE.
 CC -!- PATHWAY: CDP-CHOLINE AND CDP-ETHANOLAMINE PATHWAYS IN THE
 CC SYNTHESIS OF PHOSPHOLIPIDS (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE CHOLINE/ETHANOLAMINE KINASES FAMILY.
 CC -----
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 CC -----
 CC EMBL; Z69729; CAA93600.1; -
 CC INTERPRO; IPR002573; -
 CC PFAM; PF01633; Choline_kinase; 1.
 KW Hypothetical protein; Transferase; Kinase.
 FT ACT_SITE 242 242 BY SIMILARITY.
 SQ SEQUENCE 456 AA; 52536 MW; 08284FF1FC5FA089 CRC64;
 Query Match 58.6%; Score 34; DB 1; Length 456;
 Best Local Similarity 75.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ARHNYGSY 8
 DB 11 ARHNYGSY 8


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Db 116 ARHNIGPY 123

RESULT 14
PEX5_PICPA
ID PEX5_PICPA STANDARD; PRT; 576 AA.
AC P33292; Q01967;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEROXISOMAL TARGETING SIGNAL RECEPTOR (PEROXISOMAL PROTEIN PAS8)
DE (PEROXIN-5) (PTS1 RECEPTOR).
GN PEX5 OR PAS8.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 11430;
RX MEDLINE; 93260010.
RA McCollum D., Monosov E., Subramani S.;
RT "The pas8 mutant of Pichia pastoris exhibits the peroxisomal protein
RT import deficiencies of Zellweger syndrome cells -- the PAS8 protein
RT binds to the COOH-terminal tripeptide peroxisomal targeting signal,
RT and is a member of the TPR protein family.";
RL J. Cell Biol. 121:761-774(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Gould S.J., Kalish J.E., Morrel J.C., Bjorkman J., Urquhart A.J.,
RA Crane D.I.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE; 95369234.
RA Terlecky S.R., Nuttle W.M., McCollum D., Sock E., Subramani S.;
RT "The Pichia pastoris peroxisomal protein PAS8p is the receptor for
RT the C-terminal tripeptide peroxisomal targeting signal.";
RL EMBO J. 14:3627-3634(1995).
CC -1- FUNCTION: BINDS TO THE C-TERMINAL PTS1-TYPE TRIPEPTIDE PEROXISOMAL
CC TARGETING SIGNAL (SKL-TYPE) AND PLAYS AN ESSENTIAL ROLE IN
CC PEROXISOMAL PROTEIN IMPORT.
CC -1- SUBCELLULAR LOCATION: ITS DISTRIBUTION APPEARS TO BE DYNAMIC. IT
CC IS PROBABLY A CYCLING RECEPTOR FOUND MAINLY IN THE CYTOPLASM AND
CC AS WELL ASSOCIATED TO THE PEROXISOMAL MEMBRANE THROUGH A DOCKING
CC FACTOR (PEX13).
CC -1- SIMILARITY: CONTAINS 7 TPR DOMAINS.
CC -1- SIMILARITY: STRONG, TO OTHER PEROXISOMAL TARGETING SIGNAL
CC RECEPTORS.
CC -----
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CC -----
DR EMBL; Z19592; CAA79640.1; -.
DR EMBL; U59222; AAB40613.1; -.
DR PIR; A40688; A40688.
DR INTERPRO; IPR001440; -.
DR PFAM; PF00515; TPR; 4.
KW Peroxisome; Repeat; TPR domain; Transport; Protein transport.
FT DOMAIN 19 232 GLN-RICH.
FT REPEAT 278 311 TPR 1.
FT REPEAT 312 345 TPR 2.
FT REPEAT 346 383 TPR 3.
FT REPEAT 384 421 TPR 4.
FT REPEAT 422 455 TPR 5.
FT REPEAT 456 489 TPR 6.
FT REPEAT 490 523 TPR 7.
FT CONFLICT 243 259 DQFOAQWEKDFAOYAEQ -> RPYVSGSMGERFCPIRRR
FT (IN REF. 1).

SQ SEQUENCE 576 AA; 65083 MW; C249FBE50FDE5247 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 576;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 260 RLNYGEYKY 268

RESULT 15
C9EA_BACTA
ID C9EA_BACTA STANDARD; PRT; 1150 AA.
AC Q9ZNL9;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PESTICIDIAL CRYSTAL PROTEIN CRY9EA (INSECTICIDAL DELTA-ENDOTOXIN
DE CRYIXE(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
DE PROTEIN).
GN CRY9EA OR CRYIXE(A).
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSK-10;
RA Midoh N., Oyama K.;
RT "Bacillus thuringiensis cry gene for insecticidal crystal protein.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDCUT
CC EPITHELIAL CELLS OF INSECTS.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB011496; BAA34908.1; -.
DR HSP; P07130; IDLC.
DR INTERPRO; IPR001178; -.
DR PFAM; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;

Query Match 58.6%; Score 34; DB 1; Length 1150;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNIGSYAY 10
Db 767 ARENYPTYIY 776

Search completed: March 28, 2001, 07:29:54
Job time: 1661 sec

```

Gencore version 4.5

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:56 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-62

Perfect score: 58

Sequence: 1 ARHNYGSYAY 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	446	5	O62086
2	40	69.0	839	10	O91IE5
3	39	67.2	576	9	O64311
4	39	67.2	3115	5	O9VQV1
5	38	65.5	236	5	O18245
6	38	65.5	271	10	O9XEI2
7	38	65.5	271	10	O9XEI2
8	38	65.5	428	10	P93843
9	38	65.5	428	10	O91EB3
10	38	65.5	482	10	O48955
11	37	63.8	289	2	O69838
12	37	63.8	420	13	O91184
13	37	63.8	1144	2	O50371
14	36	62.1	94	8	O9T882
15	36	62.1	301	11	O92I30
16	36	62.1	349	5	O76436
17	36	62.1	420	4	O14979
18	36	62.1	626	5	O62017
19	36	62.1	1049	12	O83611

20	35	60.3	89	7	O19495
21	35	60.3	111	8	O9MEJ5
22	35	60.3	114	7	O9TNU3
23	35	60.3	115	7	O9TNU4
24	35	60.3	116	7	O9TNU5
25	35	60.3	120	7	O98183
26	35	60.3	120	7	O98186
27	35	60.3	150	1	O27642
28	35	60.3	155	12	O55705
29	35	60.3	219	5	O9VVY8
30	35	60.3	226	2	O9RGM4
31	35	60.3	241	5	O22205
32	35	60.3	246	2	O26017
33	35	60.3	246	2	O9ZJD6
34	35	60.3	257	2	O9K023
35	35	60.3	257	2	O9TV35
36	35	60.3	261	7	O9TQ47
37	35	60.3	279	10	O9M883
38	35	60.3	281	10	O39208
39	35	60.3	281	10	O9SWU4
40	35	60.3	281	10	O9SYS2
41	35	60.3	299	2	O9KKW8
42	35	60.3	326	9	O38652
43	35	60.3	377	10	O24324
44	35	60.3	378	8	O21173
45	35	60.3	417	5	O17705

ALIGNMENTS

RESULT 1

ID	O62086	PRELIMINARY;	PRT;	446 AA.
AC	O62086;			
DT	01-AUG-1998 (TREMBlrel. 07, Created)			
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)			
DT	01-JUN-2000 (TREMBlrel. 14, Last annotation update)			
DE	C3IH5.6 PROTEIN.			
GN	C3IH5.6.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kershaw J.;			
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
KX	MEDLINE=94150718; PubMed=7906398;			
RA	Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,			
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,			
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,			
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,			
RA	Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,			
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,			
RA	Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.			
RT	elegans.";			
RL	Nature 368:32-38(1994).			
DR	EMBL; Z93778; CAB07846.1;			
DR	INTERPRO; IPR000379;			
DR	INTERPRO; IPR002925;			
DR	PFAM; PF01738; DLH; 2.			
SQ	SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;			

Query Match 72.4%; Score 42; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 11;

Matches 7: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSYA 9
|||||:|

Db 51 RHNYGSHA 58

RESULT *2

ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,
RT TAC and BAC clones";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -;
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 69.08; Score 40; DB 10; Length 839;
Best Local Similarity 75.08; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSY 8
|||||:

Db 274 SRHNYGSF 281

RESULT 3

ID O64311 PRELIMINARY; PRT; 576 AA.
AC O64311;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REPLICASE.
OS bacteriophage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC serumgroup IV.
OX NCBI_TaxID=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).

RN [3]

RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14705.1; -;
SQ SEQUENCE 576 AA; 65012 MW; 6075160795D366FD CRC64;

Query Match 67.2%; Score 39; DB 9; Length 576;

Best Local Similarity 66.7%; Pred. No. 47;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
||:||||

Db 503 RHEFGSYLY 511

RESULT 4

ID Q9VOV1 PRELIMINARY; PRT; 3115 AA.
AC Q9VOV1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CG3921 PROTEIN.
RN CG3921.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).

DR EMBL: AE003578; AAF51061.1; -;
 DR FLYBASE; FBgn0031571; CG3921.
 DR INTERPRO; IPR001190; -;
 DR PFAM; PF00530; SRCR; 2;
 DR PRINTS; PR00258; SPERACTRCPTR.
 SQ SEQUENCE 3115 AA; 349451 MW; A17EA222A4718112 CRC64;

Query Match 67.2%; Score 39; DB 5; Length 3115;

Best Local Similarity 87.5%; Pred. No. 2.9e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSY 8

|||||

Db 2550 ARHNYWSY 2557

RESULT 5

O18245 PRELIMINARY; PRT; 236 AA.
 AC O18245;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
 DE Y57G11C.21 PROTEIN.
 GN Y57G11C.21.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 [1]
 RP SEQUENCE FROM N.A.
 RA McMurray A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: Z99281; CAB16522.1; -;
 SQ SEQUENCE 236 AA; 26579 MW; 8E92144E065E7D30 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 236;

Best Local Similarity 60.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10

|||||

Db 118 AVHNSYAY 127

RESULT 6

Q92T29 PRELIMINARY; PRT; 271 AA.
 AC Q92T29;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE STEROL-C5(6)-DESATURASE.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. XANTHI SH6; TISSUE=CALLI DERIVED FROM LEAF PROTOPLASTS;
 RA Husselstein T., Schaller H., Gachotte D., Benveniste P.;
 RT "sterol-C5(6)-desaturase: molecular characterization and functional
 expression of wild-type and mutant alleles.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF081794; AAD04034.1; -;
 DR MENDEL; 36287; Nicta; 1710; 36287.
 DR INTERPRO; IPR001541; -;
 DR PFAM; PF01598; Sterol_desat; 1.
 SQ SEQUENCE 271 AA; 31842 MW; 361520EAAAB56D86F CRC64;

Query Match 65.5%; Score 38; DB 10; Length 271;

Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8

|||||

Db 243 RHNYGHY 249

RESULT 7

Q9XE12 PRELIMINARY; PRT; 271 AA.
 AC Q9XE12;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE STEROL-C5(6)-DESATURASE HOMOLOG.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. XANTHI SH6; TISSUE=LEAF;
 RX MEDLINE=99273992; PubMed=10344195;
 RA Husselstein T., Schaller H., Gachotte D., Benveniste P.;
 RT "Delta7-sterol-C5-desaturase: molecular characterization and
 functional expression of wild-type and mutant alleles.";
 RL Plant Mol. Biol. 39:891-906(1999).
 DR EMBL: AF099969; AAD20458.1; -;
 DR INTERPRO; IPR001541; -;
 DR PFAM; PF01598; Sterol_desat; 1.
 SQ SEQUENCE 271 AA; 32036 MW; 1E705A0B69C320D4 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 271;

Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8

|||||

Db 243 RHNYGHY 249

RESULT 8

P93843 PRELIMINARY; PRT; 428 AA.
 ID P93843
 AC P93843;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE DNA BINDING PROTEIN ACBF.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:35 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: I ARHNYGSVAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19 W76021	LM609 grafted anti
2	54	93.1	10	19 W76010	LM609 grafted anti
3	54	93.1	117	19 W76001	Vitaxin antibody h
4	54	93.1	117	19 W76003	LM609 antibody hea
5	54	93.1	117	20 Y06381	Murine monoclonal
6	54	93.1	117	20 Y06387	Humanised LM609 an
7	54	93.1	118	20 Y06384	Humanised LM609 an
8	54	93.1	118	20 Y06385	Humanised LM609 an
9	54	93.1	118	20 Y06386	Humanised LM609 an
10	54	93.1	118	20 Y06383	Humanised LM609 an
11	54	93.1	130	20 Y06379	Murine monoclonal
12	49	84.5	10	19 W76020	LM609 grafted anti

13	48	82.8	10	19 W76022	LM609 grafted anti
14	48	82.8	10	19 W76023	LM609 grafted anti
15	47	81.0	10	19 W76024	LM609 grafted anti
16	47	81.0	10	19 W76025	LM609 grafted anti
17	47	81.0	10	19 W76026	LM609 grafted anti
18	47	81.0	10	19 W76027	LM609 grafted anti
19	47	81.0	10	19 W76028	LM609 grafted anti
20	47	81.0	10	19 W76029	LM609 grafted anti
21	47	81.0	10	19 W76030	LM609 grafted anti
22	46	79.3	110	20 W84099	Vitronectin alpha-
23	46	79.3	117	20 W84093	Murine vitronectin
24	46	79.3	117	20 W84097	Humanised anti-alp
25	45	77.6	8	20 Y06371	Murine monoclonal
26	43	74.1	10	19 W76039	LM609 grafted anti
27	43	74.1	10	19 W76040	LM609 grafted anti
28	42	72.4	10	19 W76037	LM609 grafted anti
29	42	72.4	119	19 Y86109	S. pneumoniae derl
30	40	69.0	117	16 R79157	Human IGE receptor
31	40	69.0	117	16 R79155	Human IGE receptor
32	40	69.0	117	18 W27357	Heavy chain variab
33	40	69.0	117	18 W27536	Heavy chain variab
34	40	69.0	117	18 W27354	Heavy chain variab
35	40	69.0	119	18 W01578	Lead binding MAB 8
36	40	69.0	239	20 W73874	Human antiFc epsil
37	40	69.0	242	20 W73876	Human antiFc epsil
38	39	67.2	172	19 W46819	Endo-beta-1,4-gluc
39	38	65.5	10	19 W76038	LM609 grafted anti
40	37	63.8	36	17 W03984	VDJ joint protein,
41	37	63.8	36	18 W41127	VH251 DXP.1 J6 mu
42	37	63.8	36	20 Y40395	Amino acid sequenc
43	37	63.8	1144	16 R76059	Mycoplasma pirum a
44	36	62.1	349	20 Y08620	Yeast COA thioeste
45	35	60.3	246	19 W98752	H. pylori GHPO 105

ALIGNMENTS

RESULT 1

W76021 ID W76021 standard; Protein: 10 AA.

XX AC W76021;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #3.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49858.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
|||||||
Db 1 arhnygsyay 10

RESULT 2
ID W76010 standard; Protein; 10 AA.
XX
AC W76010;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49847.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Disclosure; Page 40; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 93.1%; Score 54; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0032;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
|||||||
Db 1 arhnygsfay 10

RESULT 3
ID W76001 standard; Protein; 117 AA.
XX
AC W76001;
XX
DT 02-NOV-1998 (first entry)
XX
DE Vitaxin antibody heavy chain variable region protein fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49820.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 1; Fig 1a; 129pp; English.
XX
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC: so are suitable for use in humans. Enhanced types of LM609 have affinity
 XX more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 93.1%; Score 54; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
 |||||||:
 Db 97 arhnygsfay 106

RESULT 4
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX AC W76003;
 XX 02-NOV-1998 (first entry)
 XX LM609 antibody heavy chain variable region protein fragment.
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX Mus sp.
 XX WO9833919-A2.
 XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX N-PSDB; V49822.

Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis

Claim 43; Fig 2a; 129pp; English.

This sequence represents the LM609 antibody variable heavy chain region.
 LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 block integrin-mediated signal transduction. This is useful in the
 treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 specifically angiogenesis and restenosis (but also e.g. (non-)immune
 inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 etc.). The antibodies contain non-murine framework regions so are
 suitable for use in humans. Enhanced types of LM609 have affinity more
 than 90 times greater than that of parent the parent antibody.

Qy Sequence 117 AA;

Query Match 93.1%; Score 54; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
 |||||||:
 Db 97 arhnygsfay 106

RESULT 5
 Y06381
 ID Y06381 standard; Protein; 117 AA.
 XX AC Y06381;
 XX 06-SEP-1999 (first entry)
 XX Murine monoclonal antibody LM609 VH region.
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX Mus musculus.
 XX WO9929888-A1.
 XX 17-JUN-1999.
 XX 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 52-53; 55pp; English.

This sequence represents the heavy chain variable region of murine
 monoclonal antibody LM609. LM609 is directed to integrin
 alpha-v beta-3. It selectively promotes apoptosis of vascular
 cells that have been stimulated to undergo angiogenesis, making it
 a tool for cancer diagnosis and therapy. The invention provides
 humanised antibodies, especially humanised LM609. In such humanized
 antibodies, a light chain CDR from a mouse antibody such as LM609 is
 grafted onto a human light chain, and a heavy chain CDR from a mouse
 antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

Qy Sequence 117 AA;

Query Match 93.1%; Score 54; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
 |||||||:
 Db 97 arhnygsfay 106

RESULT 6
 Y06387
 ID Y06387 standard; Protein; 117 AA.
 XX AC Y06387;
 XX

DT 06-SEP-1999 (first entry)
 XX Humanised LM609 antibody VH domain.
 DE
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX 17-JUN-1999.
 XX
 PD
 XX 04-DEC-1998; 98WO-US25828.
 XX
 PF
 XX 05-DEC-1997; 97US-0986016.
 XX
 PR
 XX (SCRI) SCRIPPS RES INST.
 XX
 PA Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX
 PI Production of humanized mouse monoclonal antibodies
 XX
 PT Disclosure; Page 52; 55pp; English.
 XX
 PS
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 117 AA;

Query Match 93.1%; Score 54; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSVAY 10
 |||||:
 Db 97 arnygsfay 106

RESULT 7
 Y06384
 ID Y06384 standard; Protein; 118 AA.
 XX
 AC Y06384;
 XX
 DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX 17-JUN-1999.
 XX
 PD
 XX 04-DEC-1998; 98WO-US25828.
 XX
 PF
 XX 05-DEC-1997; 97US-0986016.
 XX
 PR (SCRI) SCRIPPS RES INST.
 XX
 PA Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX
 PI Production of humanized mouse monoclonal antibodies
 XX
 PT Disclosure; Page 51; 55pp; English.
 XX
 PS
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 118 AA;

Query Match 93.1%; Score 54; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.042;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSVAY 10
 |||||:
 Db 98 arnygsfay 107

RESULT 8
 Y06385
 ID Y06385 standard; Protein; 118 AA.
 XX
 AC Y06385;
 XX
 DT 06-SEP-1999 (first entry)

DE Humanised LM609 antibody VH domain.

XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX
OS Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Peptide 1..2
FT Region /note= "vector-encoded residues"
FT Region 31..37
FT Region /note= "CDR1"
FT Region 52..67
FT Region /note= "CDR2"
FT Region 100..107
FT Region /note= "CDR3"

XX
PN WO9929888-A1.
XX
XX 17-JUN-1999.
PD
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
PI
XX
XX WPI; 1999-394979/33.
DR
XX
XX Production of humanized mouse monoclonal antibodies
PT
XX
XX Disclosure; Page 51; 55pp; English.

XX
XX This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 118 AA;

Query Match 93.1%; Score 54; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.042; Mismatches 0; Gaps 0;
Matches 9; Conservative 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSVAY 10
|||||:|
Db 98 arhnygsfay 107

RESULT 9
Y06386
ID Y06386 standard; Protein; 118 AA.
XX
AC Y06386;
XX
XX 06-SEP-1999 (first entry)
XX
XX Humanised LM609 antibody VH domain.
DE

XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX
OS Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Peptide 1..2
FT Region /note= "vector-encoded residues"
FT Region 31..37
FT Region /note= "CDR1"
FT Region 52..67
FT Region /note= "CDR2"
FT Region 100..107
FT Region /note= "CDR3"

XX
PN WO9929888-A1.
XX
XX 17-JUN-1999.
PD
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
PI
XX
XX WPI; 1999-394979/33.
DR
XX
XX Production of humanized mouse monoclonal antibodies
PT
XX
XX Disclosure; Page 51-52; 55pp; English.

XX
XX This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 118 AA;

Query Match 93.1%; Score 54; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.042; Mismatches 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSVAY 10
|||||:|
Db 98 arhnygsfay 107

RESULT 10
Y06383
ID Y06383 standard; Protein; 118 AA.
XX
AC Y06383;
XX
XX 06-SEP-1999 (first entry)
XX
XX Humanised LM609 antibody VH domain.
DE
XX

KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37 "CDR1"
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 118 AA;

Query Match 93.1%; Score 54; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.042;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 DB 98 arhnygsfay 107
 |||||:||||

RESULT 11

ID Y06379
 Y06379 standard; Protein; 130 AA.

XX Y06379;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

XX Humanised antibody; antibody humanisation; antibody engineering;

KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 28..32
 FT /note= "CDR1"
 FT Region 47..63
 FT /note= "CDR2"
 FT Region 96..103
 FT /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V kappa region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 130 AA;

Query Match 93.1%; Score 54; DB 20; Length 130;
 Best Local Similarity 90.0%; Pred. No. 0.046;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 DB 94 arhnygsfay 103
 |||||:||||

RESULT 12

ID W76020
 W76020 standard; Protein; 10 AA.

XX W76020;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #2.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region.
 OS Mus sp.
 XX
 XX
 PN WO9833919-A2.
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX
 XX Glaser SM, Huse WD;
 PI
 XX
 XX WPI: 1998-437472/37.
 DR
 DR N-PSDB; V49857.
 XX
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 PS
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 84.5%; Score 49; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.021; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 0;
 QY 1 ARHNYGSYAY 10
 Db | | | | | : | |
 1 arnhngsfay 10
 RESULT 13
 W76022
 ID W76022 standard; Protein; 10 AA.
 XX
 AC W76022;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX
 XX LM609 grafted antibody V-H region CDR3 protein fragment #4.
 DE
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 PN

XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX
 XX Glaser SM, Huse WD;
 PI
 XX
 XX WPI: 1998-437472/37.
 DR
 DR N-PSDB; V49859.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 PS
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 82.8%; Score 48; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.031; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1;
 QY 1 ARHNYGSYAY 10
 Db | | | | | : | |
 1 arnhngsfay 10
 RESULT 14
 W76023
 ID W76023 standard; Protein; 10 AA.
 XX
 AC W76023;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX
 XX LM609 grafted antibody V-H region CDR3 protein fragment #5.
 DE
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 PN
 XX
 PD 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR

PA (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 XX
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49860.
 XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX

SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.031;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 1 arhnygsfyf 10

RESULT 15

W76024
 ID W76024 standard; Protein; 10 AA.

XX AC W76024;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WP: 1998-437472/37.

XX DR N-PSDB; V49861.

XX

PT

Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX

W76007-W76040 are protein fragments of the grafted monoclonal antibody
 LM609 heavy and light chain variable region. LM609 and the antibody
 vitaxin bind selectively to integrin alphavbeta3 and can be used to
 inhibit binding of alphavbeta3 to a ligand and thus block
 integrin-mediated signal transduction. This is useful in the treatment,
 prevention and diagnosis of alphavbeta3-mediated disease, specifically
 angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 arthritis, macular degeneration, osteoporosis etc.). The antibodies
 contain non-murine framework regions so are suitable for use in humans.
 Enhanced types of LM609 have affinity more than 90 times greater than
 that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 81.0%; Score 47; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.045;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYA 9

|||||:|

Db 1 arhnygsfa 9

Search completed: March 28, 2001, 06:34:35
 Job time: 515 sec

GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: March 28, 2001, 06:39:11 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-62

Perfect score: 58

Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	69.0	119	3	US-08-767-128-6
2	37	63.8	36	1	US-08-053-131-84
3	37	63.8	36	1	US-08-645-641-84
4	37	63.8	36	1	US-07-853-408B-84
5	37	63.8	36	2	US-08-096-762-84
6	37	63.8	36	2	US-08-308-865-84
7	37	63.8	36	4	PCT-US92-10983-84
8	36	62.1	349	1	US-08-872-784-4
9	36	62.1	349	2	US-09-100-851-4
10	34	58.6	120	2	US-08-851-822A-1
11	34	58.6	120	2	US-09-184-384-1
12	34	58.6	1157	2	US-08-532-547-5
13	34	58.6	1157	2	US-08-379-656B-5
14	34	58.6	1157	3	US-08-455-838-5
15	34	58.6	1157	3	US-09-019-809-5
16	34	58.6	1169	1	US-08-542-921-2
17	34	58.6	1169	2	US-08-880-685-2
18	34	58.6	1169	2	US-08-880-684-2
19	33	56.9	94	3	US-09-147-550-14
20	33	56.9	94	3	US-09-147-550-45
21	33	56.9	94	3	US-09-147-550-48
22	33	56.9	94	3	US-09-147-550-77
23	33	56.9	94	3	US-09-147-550-84
24	33	56.9	94	3	US-09-147-550-90
25	33	56.9	94	3	US-09-147-550-101
26	33	56.9	103	2	US-08-596-319-31
27	33	56.9	122	1	US-08-360-125-11
28	33	56.9	122	2	US-08-450-578-11

29	33	56.9	122	2	US-09-017-628-11	Sequence 11, Appl
30	33	56.9	122	2	US-09-014-880-11	Sequence 11, Appl
31	33	56.9	159	3	US-08-716-190-10	Sequence 10, Appl
32	33	56.9	384	1	US-08-707-793A-5	Sequence 5, Appl
33	33	56.9	384	1	US-08-707-792A-5	Sequence 5, Appl
34	33	56.9	630	2	US-08-394-177-5	Sequence 5, Appl
35	33	56.9	630	2	US-08-596-319-2	Sequence 2, Appl
36	33	56.9	630	3	US-08-394-912A-5	Sequence 5, Appl
37	33	56.9	809	1	US-07-789-915A-4	Sequence 4, Appl
38	33	56.9	809	1	US-08-005-002C-4	Sequence 4, Appl
39	33	56.9	809	1	US-08-487-203A-4	Sequence 4, Appl
40	32	55.2	15	1	US-08-618-464-7	Sequence 7, Appl
41	32	55.2	15	3	US-09-107-615-7	Sequence 7, Appl
42	32	55.2	25	2	US-08-480-190-44	Sequence 44, Appl
43	32	55.2	25	2	US-08-488-379-44	Sequence 44, Appl
44	32	55.2	25	4	PCT-US93-07545-44	Sequence 44, Appl
45	32	55.2	27	1	US-07-720-189-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 69.0%; Score 40; DB 3; Length 119;
Best Local Similarity 77.8%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYA 9
 |||:||||
DB 97 ARHHGYA 105

RESULT 2
US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053.131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-84

Query Match 63.8%; Score 37; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 ||| |||:|
DB 3 ARHYGSGSY 12

RESULT 3
US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-645-641-84

Query Match 63.8%; Score 37; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 ||| |||:|
DB 3 ARHYGSGSY 12

RESULT 4
US-07-853-408B-84
; Sequence 84, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-853-408B-84

Query Match 53.8%; Score 37; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 5
US-08-096-762-84
Sequence 84, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-84.

Query Match 63.8%; Score 37; DB 2; Length 36;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||| :|
Db 3 ARHYGSGSY 12

RESULT 6
US-08-308-865-84
Sequence 84, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-84

Query Match 63.8%; Score 37; DB 2; Length 36;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 3 ARHYGSGSY 12

RESULT 7

PCT-US92-10983-84
Sequence 84, Application PC/TUS9210983
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10983
FILING DATE: 19921217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-10983-84

Query Match 63.8%; Score 37; DB 4; Length 36;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 3 ARHYGSGSY 12

RESULT 8

US-08-872-784-4
Sequence 4, Application US/08872784
Patent No. 5776753
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0293 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 854594
US-08-872-784-4

Query Match 62.1%; Score 36; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 247 ARYNYVAFAY 256

RESULT 9

US-09-100-851-4
Sequence 4, Application US/09100851
Patent No. 5911984
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/100,851
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/872,784
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0293 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 349 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 854594
US-09-100-851-4

Query Match 62.1%; Score 36; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
DB 247 ARNYVAFY 256

RESULT 10
US-08-851-822A-1
; Sequence 1, Application US/08851822A
; Patent No. 5834241
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW VESICLE TRAFFICKING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,822A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0290 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 120 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: LUNGFZT03
;; CLONE: 2358277
US-08-851-822A-1

Query Match 58.6%; Score 34; DB 2; Length 120;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSYAY 10
DB 14 NYGNYGY 20

RESULT 11
US-09-184-384-1
; Sequence 1, Application US/09184384
; Patent No. 5986057
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW VESICLE TRAFFICKING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,384
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/851,822
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0290 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGFZT03
; CLONE: 2358277
US-09-184-384-1

Query Match 58.6%; Score 34; DB 2; Length 120;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSYAY 10

Db 14 NYGNYG 20

RESULT 12

US-08-532-547-5
; Sequence 5, Application US/08532547
; Patent No. 5861543
; GENERAL INFORMATION:
; APPLICANT: LAMBERT, BART
; APPLICANT: JANSSENS, STEFAN
; APPLICANT: VAN AUDENHOVE, KATRIN
; APPLICANT: PEEROEN, MARNIX
; APPLICANT: VAN RIE, JEROEN
; APPLICANT: VAN AARSEN, ROEL
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,547
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-109P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-532-547-5

Query Match 58.6%; Score 34; DB 2; Length 1157;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ARHNYGSYAY 10
Db 774 ARENYPTVIY 783

RESULT 13

US-08-379-656B-5
; Sequence 5, Application US/08379656B
; Patent No. 5885371
; GENERAL INFORMATION:
; APPLICANT: Lambert Bart
; APPLICANT: Janssens, Stefan
; APPLICANT: Van Audenhove, Katrien
; APPLICANT: Peferoen, Marnix
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,656B
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/01820
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93400949.9
; FILING DATE: 09-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92402358.8
; FILING DATE: 27-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-104P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-379-656B-5

Query Match 58.6%; Score 34; DB 2; Length 1157;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ARHNYGSYAY 10
Db 774 ARENYPTVIY 783

RESULT 14

US-08-455-838-5
; Sequence 5, Application US/08455838
; Patent No. 6028246
; GENERAL INFORMATION:
; APPLICANT: Lambert Bart
; APPLICANT: Janssens, Stefan
; APPLICANT: Van Audenhove, Katrien
; APPLICANT: Peferoen, Marnix
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/455,838
;; FILING DATE: 31-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/EP93/01820
;; FILING DATE: 12-JULY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93400949.9
;; FILING DATE: 09-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 92402358.8
;; FILING DATE: 27-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svensson, Leonard R.
;; REGISTRATION NUMBER: 30,330
;; REFERENCE/DOCKET NUMBER: 2121-106P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 205-8000
;; TELEFAX: (703) 205-8050
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1157 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-455-838-5

Query Match 58.6%; Score 34; DB 3; Length 1157;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||:| |
Db 774 ARENYPTYIY 783

RESULT 15

US-09-019-809-5
;; Sequence 5, Application US/09019809
;; Patent No. 6143550
;; GENERAL INFORMATION:
;; APPLICANT: LAMBERT, BART
;; APPLICANT: JANSSENS, STEFAN
;; APPLICANT: VAN AUDENHOVE, KATRIEN
;; APPLICANT: PEEROEN, MARNIX
;; APPLICANT: VAN RIE, JEROEN
;; APPLICANT: VAN AARSEN, ROEL
;; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
;; TITLE OF INVENTION: INSECTICIDAL PROTEINS.
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
;; STREET: P.O. Box 747
;; CITY: Falls Church
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22040-0747
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/019,809
;; FILING DATE: 02-FEB-1998
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SVENSSON, LEONARD R.
;; REGISTRATION NUMBER: 30,330
;; REFERENCE/DOCKET NUMBER: 2121-135P
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (703) 205-8000
;; TELEFAX: (703) 205-8050
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1157 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-019-809-5

Query Match 58.6%; Score 34; DB 3; Length 1157;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
||| ||:| |
Db 774 ARENYPTYIY 783

Search completed: March 28, 2001, 06:39:12
Job time: 766 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:41:55 ; Search time 141.45 Seconds
(without alignments)
4.800 Million cell updates/sec

Title: US-09-016-061-64

Perfect score: 59

Sequence: 1 ARHNYGSFDY 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39.5	66.9	137	2 H32513	Ig heavy chain pre
2	39	66.1	316	2 T15395	hypothetical prote
3	39	66.1	544	2 S75388	probable phenylala
4	38	64.4	82	2 I51106	Major Histocompati
5	38	64.4	89	2 S38688	MHC class II histo
6	38	64.4	89	2 S38683	MHC class II histo
7	38	64.4	89	2 S38684	MHC class II histo
8	38	64.4	117	2 S17586	Ig heavy chain V r
9	38	64.4	225	2 I47095	MHC class II OVAR-
10	38	64.4	605	2 E7134	probable GTP-bindi
11	37.5	63.6	369	2 T04997	hypothetical prote
12	37	62.7	315	2 T46993	hypothetical prote
13	37	62.7	377	2 D64888	outer membrane por
14	36.5	61.9	139	2 S01158	Ig heavy chain pre
15	36	61.0	86	2 D33989	Ig heavy chain V-4
16	36	61.0	369	2 S70847	outer membrane por
17	36	61.0	394	2 S34263	outer membrane por
18	36	61.0	446	2 T19625	hypothetical prote
19	36	61.0	602	2 B71561	probable GTPase -
20	36	61.0	602	2 B72088	GTP-binding protei
21	36	61.0	602	2 B6174	GTP-binding protei
22	36	61.0	783	1 S02755	outer membrane ush
23	36	61.0	922	2 T03854	hypothetical prote
24	36	61.0	1116	2 I54378	gene XI04 protein
25	35	59.3	32	2 PH1735	Ig heavy chain V r
26	35	59.3	81	2 F82731	hypothetical prote
27	35	59.3	108	2 S26316	Ig heavy chain V r
28	35	59.3	110	2 S26317	Ig heavy chain V r
29	35	59.3	304	2 B83032	probable permease

30 35 59.3 371 2 T24853 hypothetical prote
31 35 59.3 420 2 I51088 L-SP precursor - J
32 35 59.3 458 2 T34574 hypothetical prote
33 35 59.3 536 2 T24218 hypothetical prote
34 35 59.3 587 2 E69171 conserved hypothet
35 35 59.3 1166 2 S70413 DNA-directed RNA p
36 34.5 58.5 80 2 S25050 Ig heavy chain V r
37 34.5 58.5 102 2 S25025 Ig heavy chain - m
38 34.5 58.5 106 2 S25036 Ig heavy chain V r
39 34.5 58.5 111 2 S25052 Ig heavy chain V r
40 34.5 58.5 111 2 S25055 Ig heavy chain V r
41 34.5 58.5 111 2 S25054 Ig heavy chain V r
42 34.5 58.5 111 2 S25031 Ig heavy chain V r
43 34.5 58.5 111 2 S25051 Ig heavy chain V r
44 34.5 58.5 111 2 S25030 Ig heavy chain V r
45 34.5 58.5 111 2 S25024 Ig heavy chain V r

ALIGNMENTS

RESULT 1

H32513
Ig heavy chain precursor V region (BXW16) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: H32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Duchosal, M.A
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
A:Reference number: A94689; MUID:88331394
A:Accession: H32513
A:Molecule type: DNA
A:Residues: 1-137 <KOF>
A:Cross-references: GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:g196950
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.9%; Score 39.5; DB 2; Length 137;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARHNYG-SFDY 10
||| ||| ||| |||
Db 116 ARKNGSSFDY 126

RESULT 2

T15395
hypothetical protein C03F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15395
R:Bentley, D.
A:Description: The sequence of C. elegans cosmid C03F11.
A:Reference number: Z18342
A:Accession: T15395
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-316 <BEN>
A:Cross-references: EMBL:U39744; NID:g1049465; PIDN:AAA8040.1; CESP:CO
C:Genetics:
A:Gene: CESP:C03F11.2
A:Introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 66.1%; Score 39; DB 2; Length 316;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNYGSFDY 10
||| :||:|
Db 69 ARHFGSVYEY 78

RESULT 3

S75388
probable phenylalanine--tRNA ligase (EC 6.1.1.20) beta chain - Sulfolobus solfataricus
N;Alternate names: phenylalanyl-tRNA synthetase beta chain; protein c04021
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
C;Accession: S75388
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432
A;Accession: S75388
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-544 <SPN>
A;Cross-references: EMBL:Y08257; NID:g1707772; PIDN:CAA69550.1; PID:g1707793
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: yeast cytosolic phenylalanine--tRNA ligase alpha chain
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 66.1%; Score 39; DB 2; Length 544;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NYGSFDY 10
|||||

Db 350 NYGSYDY 356
|||||

RESULT 4

I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C;Species: Phasianus colchicus (ring-necked pheasant)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C;Accession: I51106
R;Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A;Reference number: I51103; MUID:94245280
A;Accession: I51106
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-82 <WIT>

A;Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 82;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RNYGSFD 9
|||||

Db 75 RNYGVFE 82
|||||

RESULT 5

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
C;Species: Galago senegalensis (northern lesser bushbaby)
C;Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: S38688
R;Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A;Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A;Reference number: S38676

A;Accession: S38688
A;Molecule type: DNA
A;Residues: 1-89 <FIG>
A;Cross-references: EMBL:Z27158
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RNYGSFD 9
|||||

Db 75 RNYGVFE 82
|||||

RESULT 6

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C;Species: Galago senegalensis (northern lesser bushbaby)
C;Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: S38683
R;Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A;Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A;Reference number: S38676
A;Accession: S38683
A;Molecule type: DNA
A;Residues: 1-89 <FIG>
A;Cross-references: EMBL:Z27153
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RNYGSFD 9
|||||

Db 75 RNYGVFE 82
|||||

RESULT 7

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C;Species: Galago senegalensis (northern lesser bushbaby)
C;Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: S38684
R;Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A;Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A;Reference number: S38676
A;Accession: S38684
A;Molecule type: DNA
A;Residues: 1-89 <FIG>
A;Cross-references: EMBL:Z27154
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RNYGSFD 9
|||||

Db 75 RNYGVFE 82
|||||

RESULT 8

S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: SI7586
R:Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A:Title: Biochemical implications from the variable gene sequences of an anti-cytochrome forms.
A:Reference number: SI7586; MUID:92015240
A:Accession: SI7586
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <MYL>
A:Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 38; DB 2; Length 117;
Best Local Similarity 60.0%; Pred. No. 6.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
| :||:|
Db 97 AGDYGNEDY 106
| :||:|

RESULT 9
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility complex class II genes.
A:Reference number: I47095; MUID:94057592
A:Accession: I47095
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 38; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| :||:|
Db 68 RHNYGVFE 75
| :||:|

RESULT 10
E71314
probable GTP-binding membrane protein (lepA) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 26-Aug-1999
C:Accession: E71314
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDermott, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: E71314
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-605 <COL>
A:Cross-references: GB:AE001227; GB:AE000520; NID:g3322797; PIDN:AAC65498.1; PID:g332280
A:Experimental source: strain Nichols

C:Genetics:
A:Gene: TP0510
C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu ho
C:Keywords: GTP binding; P-loop
F:11-140/Domain: translation elongation factor Tu homology <ETU>
F:17-24/Region: nucleotide-binding motif A (P-loop)
F:137-140/Region: GTP-binding NKXD motif
F:168-170/Region: GTP-binding SAK/L motif
F:23,24,59,137,138,140,168/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 64.4%; Score 38; DB 2; Length 605;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFDY 10
| :||:|
Db 470 HGVASEFDY 477
| :||:|

RESULT 11
T04947
hypothetical protein F7J7.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04947
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15391
A:Accession: T04947
A:Molecule type: DNA
A:Residues: 1-369 <BEV>
A:Cross-references: EMBL:AL021960
A:Experimental source: cultivar Columbia; BAC clone F7J7
C:Genetics:
A:Map position: 4
A:Introns: 14/1; 41/2; 98/3; 153/2; 203/3; 244/3; 276/3
A:Note: F7J7.100

Query Match 63.6%; Score 37.5; DB 2; Length 369;
Best Local Similarity 61.5%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 3 HNYGS----FDY 10
| :||:|
Db 269 HNYGSVKLQVFDY 281
| :||:|

RESULT 12
T46993
hypothetical protein [Imported] - Yersinia pestis
C:Species: Yersinia pestis
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C:Accession: T46993
R:Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carn
submitted to the EMBL Data Library, October 1998
A:Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A:Reference number: Z24348
A:Accession: T46993
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-315 <BUC>
A:Cross-references: EMBL:AL031866; PIDN:CAA21336.1
A:Experimental source: strain 6/69
C:Superfamily: outer membrane protein phoE

Query Match 62.7%; Score 37; DB 2; Length 315;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10

Db 105 DYGSFDY 111
:|||||

RESULT 13

D64888
outer membrane porin bl377 precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C:Accession: D64888
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: D64888
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-377 <BLAT>
A:Cross-references: GB:AE000234; GB:U00096; NID:gl787633; PIDN:AAC74459.1; PID:gl787641;
A:Experimental source: strain K-12, substrain M61655
A:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-377/Product: probable outer membrane porin bl377 #status predicted <OPP>

Query Match 62.7%; Score 37; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
:|||||

Db 106 DYGSFDY 112

RESULT 14

S01158
Ig heavy chain precursor (clone c40) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jan-2000
C:Accession: S01158
R:Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus
A:Reference number: S01158; MUID:89052653
A:Accession: S01158
A:Molecule type: mRNA
A:Residues: 1-139 <SCH>
A:Cross-references: EMBL:X14919
A:Note: the sequence of residues 1-18 is not shown
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F:19-139/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:19-134/Domain: V-D-J region #status predicted <VRE>
F:32-114/Domain: immunoglobulin homology <IMM>
F:135-139/Domain: C region (mu chain) (fragment) #status predicted <CRE>

Query Match 61.9%; Score 36.5; DB 2; Length 139;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ARHN-YGSFDY 10
:|||||

Db 113 ARHPIYGSFDY 123

RESULT 15

D33989
Ig heavy chain V-4-D-J region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-May-1997

C:Accession: D33989
R:Hsu, E.; Schwager, J.; Alt, F.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8010-8014, 1989
A:Title: Evolution of immunoglobulin genes: V-H families in the amphibian Xenopus.
A:Reference number: A33989; MUID:90046727
A:Accession: D33989
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-86 <HSU>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 61.0%; Score 36; DB 2; Length 86;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
:|||||

Db 66 ARYGVGAEDY 75

Search completed: March 28, 2001, 06:41:56
Job time: 879 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:52 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSPAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	67.2	222	2 Q9JZF5	Q9jzf5 neisseria m
2	39	67.2	243	2 Q9JUT9	Q9jut9 neisseria m
3	38	65.5	839	10 Q9LIE5	Q9lie5 arabisdopsis
4	37	63.8	150	1 Q27842	Q27842 methanobact
5	37	63.8	257	2 Q9K023	Q9k023 neisseria m
6	37	63.8	257	2 Q9JVG3	Q9jvg3 neisseria m
7	37	63.8	326	2 Q9RJG3	Q9rjg3 streptomyce
8	37	63.8	731	2 Q59369	Q59369 escherichia
9	36	62.1	1049	12 Q83611	Q83611 ectromelia
10	35	60.3	105	12 Q90911	Q9q911 fowl adenov
11	35	60.3	233	2 Q9KRA6	Q9kra6 vibrio chol
12	35	60.3	272	5 Q24950	Q24950 fasciola he
13	35	60.3	272	5 Q24951	Q24951 fasciola he
14	35	60.3	282	2 Q9ZA29	Q9za29 streptomyce
15	35	60.3	282	2 Q9K578	Q9k578 legionella
16	35	60.3	480	1 Q28764	Q28764 archaeoglob
17	35	60.3	483	10 Q9LES4	Q9les4 arabisdopsis
18	35	60.3	534	10 Q9LGI6	Q9lgi6 oryza sativ
19	35	60.3	615	11 Q63614	Q63614 rattus norv

20	35	60.3	651	10	Q22781	Q22781 arabisdopsis
21	35	60.3	736	10	Q9SVX7	Q9svx7 arabisdopsis
22	35	60.3	788	4	Q9P2E5	Q9p2e5 homo sapien
23	35	60.3	977	10	Q9S9V3	Q9s9v3 arabisdopsis
24	35	60.3	1875	5	Q93691	Q93691 caenorhabdi
25	34	58.6	137	12	Q9PY61	Q9py61 pepper leaf
26	34	58.6	154	2	Q9Z9C6	Q9z9c6 chlamydia p
27	34	58.6	170	2	Q9RY07	Q9ry07 delnococtus
28	34	58.6	231	2	Q9KK73	Q9kk73 brevibacter
29	34	58.6	236	10	Q40088	Q40088 ipomoea bat
30	34	58.6	274	2	Q9XAY5	Q9xay5 pelobacter
31	34	58.6	339	9	Q38009	Q38009 bacterioph
32	34	58.6	378	8	Q9TMH5	Q9tmh5 tulbaghia f
33	34	58.6	379	2	Q25568	Q25568 helicobacte
34	34	58.6	381	2	Q9ZKT9	Q9zkt9 helicobacte
35	34	58.6	385	9	Q64373	Q64373 lactobacill
36	34	58.6	415	10	Q22872	Q22872 arabisdopsis
37	34	58.6	426	2	Q9KUL5	Q9kul5 vibrio chol
38	34	58.6	446	5	Q62086	Q62086 caenorhabdi
39	34	58.6	463	5	Q44923	Q44923 caenorhabdi
40	34	58.6	483	12	Q9JGT4	Q9jgt4 northern ce
41	34	58.6	489	2	P72495	P72495 streptomyce
42	34	58.6	489	2	P72497	P72497 streptomyce
43	34	58.6	649	5	Q9VA48	Q9va48 drosophila
44	34	58.6	685	5	Q9V6C3	Q9v6c3 drosophila
45	34	58.6	2831	2	O85166	O85166 bruceella ab

ALIGNMENTS

RESULT 1

Q9JZF5 ID Q9JZF5 PRELIMINARY: PRT: 222 AA.
AC Q9JZF5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE DNAA-RELATED PROTEIN.
GN NMB1076.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002458; AAF41471.1; -.
DR TIGR; NMB1076; -.
SQ SEQUENCE 222 AA; 25427 MW; ECB0D2AA88FC9086 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 222;

Best Local Similarity 66.7%; Pred. No. 9.1;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHHGSPAY 10

|| || ||

DB 32 RHHGQFIY 40

RESULT 2


```

Q9JUJ9
ID Q9JUJ9 PRELIMINARY; PRT; 243 AA.
AC Q9JUJ9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN NMA1279.
GN NMA1279.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moulé S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
DR EMBL; AL162755; CAB84531.1; -.
KW Hypothetical protein.
SQ SEQUENCE 243 AA; 27882 MW; E83E4E1B9498A8DF CRC64;

Query Match 67.2%; Score 39; DB 2; Length 243;
Best Local Similarity 66.7%; Pred. No. 9.9;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNGSFAY 10
DB 53 RHKGQFIY 61

RESULT 3
Q9LIE5
ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 839;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ARNHGGSF 8
DB 274 SRNYGSF 281

RESULT 4
O27642
ID O27642 PRELIMINARY; PRT; 150 AA.
AC O27642;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE DEOXYCYTIDINE-TRIPHOSPHATE DEAMINASE RELATED PROTEIN.
GN MTH1605.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
OX NCBI_TaxID=2166;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000920; AAB86078.1; -.
DR INTERPRO; IPR001428; -.
DR INTERPRO; IPR003232; -.
DR PFAM; PF00692; dUTPase; 1.
DR PRODOM; PD004900; -.
DR SEQUENCE 150 AA; 16996 MW; AFA09D55FB371648 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 150;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
DB 115 HNHGEY 122

RESULT 5
Q9K023
ID Q9K023 PRELIMINARY; PRT; 257 AA.
AC Q9K023;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN NMB0803.
GN NMB0803.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

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RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RL MC58.";
RL Science 287:1809-1815(2000).
DR EMBL: AE002434; AAF41216.1; -.
DR TIGR: NMB0803; -.
SQ SEQUENCE 257 AA; 28718 MW; 0BD50624D6B90C77 CRC64;

Query Match 63.8%; Score 37; DB 2; Length 257;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
Db 246 HNHSAVAY 253
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- - - - -

RESULT 6
Q9JVG3 PRELIMINARY; PRT; 257 AA.
ID Q9JVG3;
AC Q9JVG3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN NMA1013.
GN NMA1013.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=42491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
RL Nature 404:502-506(2000).
DR EMBL: AL162754; CAB84282.1; -.
KW Hypothetical protein.
SQ SEQUENCE 257 AA; 28734 MW; 021A28C018F35281 CRC64;

Query Match 63.8%; Score 37; DB 2; Length 257;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
Db 246 HNHSAVAY 253
||| :|||
- - - - -

RESULT 7
Q9RJG3 PRELIMINARY; PRT; 326 AA.
ID Q9RJG3;
AC Q9RJG3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PUTATIVE ARAC FAMILY TRANSCRIPTIONAL REGULATOR.
GN SCF76.11.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RP Murphy L., Harris D.;

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RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL121600; CAB56731.1; -.
DR INTERPRO: IPR000005; -.
DR PFAM: PF00165; HTH_Arac; 1.
SQ SEQUENCE 326 AA; 34425 MW; 2FEF5346ACAC80D6 CRC64;

Query Match 63.8%; Score 37; DB 2; Length 326;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGGSF 8
Db 85 RHGGSF 91
||| ||||
- - - - -

RESULT 8
Q59369 PRELIMINARY; PRT; 731 AA.
ID Q59369;
AC Q59369;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE HISTIDINE RICH P TYPE ATPASE.
GN HRA-1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=95110304; PubMed=7811248;
RA Tenor C.C., Lin W., Andrews N.C.;
RT "Novel bacterial p-type ATPases with histidine-rich heavy-metal-
associated sequences.";
RL Biochem. Biophys. Res. Commun. 205:1644-1650(1994).
DR EMBL: U16658; AAA62113.1; -.
DR INTERPRO: IPR001757; -.
DR PFAM: PF00122; EI-E2_ATPase; 1.
DR PROSITE: PS00154; ATPASE_EI_E2; UNKNOWN_1.
KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
SQ SEQUENCE 731 AA; 78453 MW; 06237F155E151F0D CRC64;

Query Match 63.8%; Score 37; DB 2; Length 731;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
Db 88 AHHHGSF 95
||| :|||
- - - - -

RESULT 9
Q83611 PRELIMINARY; PRT; 1049 AA.
ID Q83611;
AC Q83611;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

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DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE A-TYPE INCLUSION PROTEIN.

GN ATL.
 OS Ectromelia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=12643;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MP-1;
 RC Osterrieder N.;
 RA Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MP-1;
 RC Pedersen K., Hallbeck L., Arlinger J., Jahromi N., Erlandsson A.-C.;
 RA "Investigation of the potential for microbial contamination of deep
 RT granitic aquifers during drilling using molecular and culturing
 RT methods.";
 RL J. Microbiol. Methods 30:179-192(1997).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MP-1;
 RC MEDLINE=94353638; PubMed=8073633;
 RA Osterrieder N., Meyer M., Pfeiffer M.;
 RT "Characterization of the gene encoding the A-type inclusion body
 RT protein of mousepox virus";
 RL Virus Genes 8:125-135(1994).
 DR EMBL; X69325; CAA49168.1; -;
 SQ SEQUENCE 1049 AA; 122466 MW; 8CE334A695E8DFD3 CRC64;

Query Match 62.1%; Score 36; DB 12; Length 1049;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RHNGSFAY 10
 |||:|
 Db 771 RHNGSHCY 779

RESULT 10

Q90911 ID Q90911 PRELIMINARY; PRT; 105 AA.
 AC Q90911;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE HYPOTHETICAL 12.5 KDA PROTEIN.
 OS fowl adenovirus 8.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
 OX NCBI_TaxID=66295;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CFA40;
 RA Johnson M.A., Pooley C.;
 RT "Fowl adenovirus serotype 8 hypervirulent strain CFA40.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF155911; AAF17345.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 105 AA; 12478 MW; 8CAD01F3250EIF2F CRC64;

Query Match 60.3%; Score 35; DB 12; Length 105;
 Best Local Similarity 62.5%; Pred. No. 24;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 HHNGSFAY 10
 | | | : | |
 Db 23 HHMGTYAY 30

RESULT 11

Q9KRA6 ID Q9KRA6 PRELIMINARY; PRT; 233 AA.
 AC Q9KRA6;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DE ARGINYL-TRNA-PROTEIN TRANSFERASE-RELATED PROTEIN.
 GN VC1736.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406633; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004251; AAF94886.1; -;
 DT TIGR; VC1736;
 KW Transferase.
 SQ SEQUENCE 233 AA; 27350 MW; AEB6E95905EC2C3C CRC64;

Query Match 60.3%; Score 35; DB 2; Length 233;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ARNHGGS 7
 ||| | |
 Db 117 ARHRHGS 123

RESULT 12

Q24950 ID Q24950 PRELIMINARY; PRT; 272 AA.
 AC Q24950;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DE VITELLINE PROTEIN B1 PRECURSOR.
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93063029; PubMed=1435854;
 RA Rice-Ficht A.C., Dusek K.A., Kochevar G.J., Waite J.H.;
 RT "Eggshell precursor proteins of Fasciola hepatica, I. Structure and
 RL expression of vitelline protein B.";
 RL Mol. Biochem. Parasitol. 54:129-141(1992).
 DR EMBL; M93024; AAA29143.1; -;
 KW Signal.
 FT SIGNAL. 1 19 POTENTIAL.
 FT CHAIN 20 272 VITELLINE PROTEIN B1.
 SQ SEQUENCE 272 AA; 31211 MW; BFCFDBEF6736BDCA CRC64;

Query Match 60.3%; Score 35; DB 5; Length 272;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ARNHGGSF 8
 ||| | |
 Db 19 ARHPHGKE 26

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RESULT 13
Q24951 ID Q24951 PRELIMINARY; PRT; 272 AA.
AC Q24951;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE VITELLINE PROTEIN B2 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93063029; PubMed=1435854;
RA Rice-Ficht A.C., Dusek K.A., Kochevar G.J., Waite J.H.;
RT "Eggshell precursor proteins of Fasciola hepatica, I. Structure and
expression of vitelline protein B.";
RL Mol. Biochem. Parasitol. 54:129-141(1992).
DR EMBL; M93025; AAA29144.1; -.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 272 VITELLINE PROTEIN B2.
SQ SEQUENCE 272 AA; 31418 MW; 27D51230F278F6CC CRC64;

Query Match 60.3%; Score 35; DB 5; Length 272;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGFSF 8
   ||| |||
DB 19 ARHPGKPF 26

RESULT 14
Q9ZA29 ID Q9ZA29 PRELIMINARY; PRT; 282 AA.
AC Q9ZA29;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE GRA-ORF30 PROTEIN.
GN GRA-ORF30.
OS Streptomyces violaceoruber.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1935;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TU22;
RX MEDLINE=99051446; PubMed=9831526;
RA Ichinose K., Bedford D.J., Tornus D., Bechthold A., Bibb M.J.,
RA Revilli W.P., Floss H.G., Hopwood D.A.;
RT "The granaticin biosynthetic gene cluster of Streptomyces
violaceoruber Tu22: sequence analysis and expression in a heterologous
host.";
RL Chem. Biol. 5:647-659(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=TU22;
RX MEDLINE=90060034; PubMed=2583128;
RA Sherman D.H., Malpartida F., Bibb M.J., Kleser H.M., Bibb M.J.,
RA Hopwood D.A.;
RT "Structure and deduced function of the granaticin-producing polyketide
synthase gene cluster of Streptomyces violaceoruber Tu22.";
RL EMBO J. 8:2717-2725(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=TU22;
RX MEDLINE=96027933; PubMed=7476861;

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RA Bechthold A., Sohng J.K., Smith T.M., Chu X., Floss H.G.;
RT "Identification of Streptomyces violaceoruber Tu22 genes involved in
the biosynthesis of granaticin.";
RL Mol. Gen. Genet. 248:610-620(1995).
DR EMBL; AJ011500; CAA09657.1; -.
SQ SEQUENCE 282 AA; 29904 MW; A7CF6D686CFDCE8A CRC64;

Query Match 60.3%; Score 35; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HGSFAY 10
   |||||
DB 162 HGSFAY 167

RESULT 15
Q9K578 ID Q9K578 PRELIMINARY; PRT; 282 AA.
AC Q9K578;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FEZ-1 PROTEIN.
GN BLAFAZ-1.
OS Legionella gormanii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=40334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CCUG 12267;
RA Boschi L., Mercuri P.S., Riccio M.L., Amicosante G., Galleni M.,
RA Frere J.M., Rossolini G.M.;
RT "The Legionella (Fluoribacter) gormanii metallo-beta-lactamase: a new
member of the highly divergent lineage of molecular subclass B3 beta-
lactamases.";
RL Antimicrob. Agents Chemother. 44:1538-1543(2000).
DR EMBL; Y17896; CAB96921.1; -.
SQ SEQUENCE 282 AA; 31465 MW; B91A75B99A17CC5F CRC64;

Query Match 60.3%; Score 35; DB 2; Length 282;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NHGSFAY 10
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DB 15 NHGSFAY 21

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Search completed: March 28, 2001, 07:27:56
Job time: 1669 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:34 ; Search time 183.85.Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-60

Perfect score: 58

Sequence: 1 ARHNGSPAY 10

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19	W76020
2	52	89.7	10	19	W76010
3	52	89.7	117	19	W76001
4	52	89.7	117	19	W76003
5	52	89.7	117	20	Y06381
6	52	89.7	117	20	Y06387
7	52	89.7	118	20	Y06384
8	52	89.7	118	20	Y06385
9	52	89.7	118	20	Y06386
10	52	89.7	118	20	Y06383
11	52	89.7	130	20	Y06379
12	51	87.9	10	19	W76037

13	49	84.5	10	19	W76021	LM609 grafted anti
14	47	81.0	10	19	W76038	LM609 grafted anti
15	46	79.3	10	19	W76022	LM609 grafted anti
16	46	79.3	10	19	W76023	LM609 grafted anti
17	45	77.6	10	19	W76024	LM609 grafted anti
18	45	77.6	10	19	W76025	LM609 grafted anti
19	45	77.6	10	19	W76026	LM609 grafted anti
20	45	77.6	10	19	W76027	LM609 grafted anti
21	45	77.6	10	19	W76028	LM609 grafted anti
22	45	77.6	10	19	W76029	LM609 grafted anti
23	45	77.6	10	19	W76030	LM609 grafted anti
24	44	75.9	110	20	W84099	Vitronectin alpha
25	44	75.9	117	20	W84093	Murine vitronectin
26	44	75.9	117	20	W84097	Humanised anti-alp
27	43	74.1	8	20	Y06371	Murine monoclonal
28	41	70.7	10	19	W76039	LM609 grafted anti
29	41	70.7	10	19	W76040	Human IgE receptor
30	36	62.1	117	16	R79157	Human IgE receptor
31	36	62.1	117	16	R79155	Human IgE receptor
32	36	62.1	117	18	W27357	Heavy chain variab
33	36	62.1	117	18	W27526	Heavy chain variab
34	36	62.1	117	18	W27354	Heavy chain variab
35	36	62.1	239	20	W73874	Human antiFc epsll
36	36	62.1	242	20	W73876	Human antiFc epsll
37	35	60.3	286	20	Y43477	Amino acid sequenc
38	35	60.3	772	20	Y13401	Amino acid sequenc
39	34	58.6	99	20	Y29137	Amino acid sequenc
40	34	58.6	165	20	Y34655	Chlamydia pneumoni
41	34	58.6	204	19	W59609	DNA-binding/dimerl
42	34	58.6	238	21	Y70730	Klebsiella oxytoxa
43	34	58.6	349	20	Y08620	Yeast CoA thioeste
44	34	58.6	358	19	W98649	H. pylori GHPO 403
45	34	58.6	489	18	W01556	Acilavinone C-11 by

ALIGNMENTS

RESULT 1

W76020
ID W76020 standard; Protein; 10 AA.
XX
AC W76020;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49857.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 58; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSEFAY 10
 |||||
 Db 1 arnhgsefay 10

RESULT 2
 W76010
 ID W76010 standard; Protein; 10 AA.
 XX
 AC W76010;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49847.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Disclosure; Page 40; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ

Query Match 89.7%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0012;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSEFAY 10
 |||||
 Db 1 arnhgsefay 10

RESULT 3
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49820.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 1; Fig 1a; 129pp; English.
 XX
 XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;

Qy 1 ARNHGSPAY 10
 ||||:||||
 Db 97 arnygsfay 106

RESULT 4

ID W76003 standard; Protein; 117 AA.

AC W76003;

DT 02-NOV-1998 (first entry)

DE LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

OS Mus sp.

PN W09633919-A2.

XX 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;

Qy 1 ARNHGSPAY 10
 ||||:||||
 Db 97 arnygsfay 106

RESULT 5

ID Y06381 standard; Protein; 117 AA.

XX Y06381;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

PN W09929888-A1.

XX 17-JUN-1999.

PF 04-DEC-1998; 98WO-US25828.

PR 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 89.7%; Score 52; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPAY 10
 ||||:||||
 Db 97 arnygsfay 106

RESULT 6

ID Y06387 standard; Protein; 117 AA.

XX Y06387;

DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 PD
 XX
 XX 04-DEC-1998; 98WO-US25828.
 PF
 XX
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Barbas CF, Rader C;
 PI
 XX
 XX WPI; 1999-394979/33.
 DR
 XX
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX
 XX Disclosure; Page 52; 55pp; English.
 PS
 XX
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGSFAY 10
 ||||:||||
 Db 97 arnygsfay 106

RESULT 7
 Y06384
 ID Y06384 standard; Protein; 118 AA.
 XX
 AC Y06384;
 XX
 DT 06-SEP-1999 (first entry)

XX
 DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 PD
 XX
 XX 04-DEC-1998; 98WO-US25828.
 PF
 XX
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Barbas CF, Rader C;
 PI
 XX
 XX WPI; 1999-394979/33.
 DR
 XX
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX
 XX Disclosure; Page 51; 55pp; English.
 PS
 XX
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 118 AA;

Query Match 89.7%; Score 52; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGSFAY 10
 ||||:||||
 Db 98 arnygsfay 107

RESULT 8
 Y06385
 ID Y06385 standard; Protein; 118 AA.
 XX
 AC Y06385;
 XX
 DT 06-SEP-1999 (first entry)

DE Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 31..37

FT /note= "CDR1"

FT Region 52..67

FT /note= "CDR2"

FT Region 100..107

FT /note= "CDR3"

XX WO9929888-A1.

PN 17-JUN-1999.

PD 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.
XX Barbas CF, Rader C;
PI WPI; 1999-394979/33.

DR Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX Sequence 118 AA;

Query Match 89.7%; Score 52; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.017;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
|||||
Db 98 arhnygsfay 107

RESULT 9
Y06386
ID Y06386 standard; Protein; 118 AA.

XX Y06386;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 31..37

FT /note= "CDR1"

FT Region 52..67

FT /note= "CDR2"

FT Region 100..107

FT /note= "CDR3"

XX WO9929888-A1.

PN 17-JUN-1999.

PD 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

PI WPI; 1999-394979/33.

DR Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51-52; 55pp; English.

XX This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX Sequence 118 AA;

Query Match 89.7%; Score 52; DB 20; Length 118;
Best Local Similarity 90.0%; Pred. No. 0.017;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
|||||
Db 98 arhnygsfay 107

RESULT 10
Y06383
ID Y06383 standard; Protein; 118 AA.

XX Y06383;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"

XX WO9929888-A1.
 PN 17-JUN-1999.
 XX 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 PI WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX Sequence 118 AA;

Query Match 89.7%; Score 52; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. NO. 0.017;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARNHGSPAY 10
 Db 98 arnyngsfay 107
 ||||:|||||

RESULT 11
 Y06379
 ID Y06379 standard; Protein; 130 AA.
 XX
 AC Y06379;
 DT 06-SEP-1999 (first entry)
 XX
 DE Murine monoclonal antibody LM609 V kappa.
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW

KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 28..32
 FT /note= "CDR1"
 FT Region 47..63
 FT /note= "CDR2"
 FT Region 96..103
 FT /note= "CDR3"

XX WO9929888-A1.
 PN 17-JUN-1999.
 XX 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 PI WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.
 XX This sequence represents the light chain V kappa region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX Sequence 130 AA;

Query Match 89.7%; Score 52; DB 20; Length 130;
 Best Local Similarity 90.0%; Pred. NO. 0.019;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARNHGSPAY 10
 Db 94 arnyngsfay 103
 ||||:|||||

RESULT 12
 W76037
 ID W76037 standard; Protein; 10 AA.
 XX
 AC W76037;
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 XX WO9833919-A2.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX
 XX Glaser SM, Huse WD;
 PI
 XX
 XX WPI: 1998-437472/37.
 DR
 XX N-PSDB; V49874.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 43; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 87.9%; Score 51; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSFA 9
 Db | | | | | | | |
 1 arnhgsfa 9
 RESULT 13
 W76021
 ID W76021 standard; Protein; 10 AA.
 XX
 AC W76021;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX LM609 grafted antibody V-H region CDR3 protein fragment #3.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 XX Mus sp.
 OS
 XX WO9833919-A2.
 PN

XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 PA
 XX
 XX Glaser SM, Huse WD;
 PI
 XX
 XX WPI: 1998-437472/37.
 DR
 XX N-PSDB; V49858.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 84.5%; Score 49; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0043;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSFAY 10
 Db | | | | | | | |
 1 arnhgysay 10
 RESULT 14
 W76038
 ID W76038 standard; Protein; 10 AA.
 XX
 AC W76038;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX LM609 grafted antibody V-H region CDR3 protein fragment #14.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 XX Mus sp.
 OS
 XX WO9833919-A2.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX

PA (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49875.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 43; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC prevention-mediated signal transduction. This is useful in the treatment,
 CC integration and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 81.0%; Score 47; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0099;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNHGSF 8
 Db | || || || ||
 1 arnhngsf 8
 RESULT 15
 W76022
 ID W76022 standard; Protein: 10 AA.
 AC
 XX
 AC W76022;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49859.
 XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC prevention-mediated signal transduction. This is useful in the treatment,
 CC integration and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 79.3%; Score 46; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.015;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ARHNHGSFAY 10
 Db | || | : | || |
 1 arnhngsfay 10

Search completed: March 28, 2001, 06:34:35
 Job time: 515 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:10 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSPAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgnl_7/ptodata/1/iaa/5B.COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6.COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCRTUS.COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	34	58.6	204	1	US-08-591-989-4
2	34	58.6	213	2	US-08-655-821-16
3	34	58.6	231	3	US-08-926-842B-20
4	34	58.6	240	3	US-08-926-842B-21
5	34	58.6	349	1	US-08-872-784-4
6	34	58.6	349	2	US-09-100-851-4
7	34	58.6	536	2	US-08-551-211-3
8	32	55.2	36	1	US-08-053-131-84
9	32	55.2	36	1	US-08-645-641-84
10	32	55.2	36	1	US-07-853-408B-84
11	32	55.2	36	2	US-08-096-762-84
12	32	55.2	36	2	US-08-308-865-84
13	32	55.2	36	4	PCT-US92-10983-84
14	32	55.2	103	2	US-08-596-319-31
15	32	55.2	123	2	US-08-652-816A-8
16	32	55.2	384	1	US-08-707-793A-5
17	32	55.2	384	1	US-08-707-792A-5
18	32	55.2	443	1	US-07-940-245-2
19	32	55.2	443	1	US-08-226-486-2
20	32	55.2	630	2	US-08-394-177-5
21	32	55.2	630	2	US-08-596-319-2
22	32	55.2	630	3	US-08-394-312A-5
23	32	55.2	907	3	US-08-938-830-26
24	32	55.2	3033	1	US-09-020-222-26
25	32	55.2	3033	1	US-07-925-695-8
26	32	55.2	3033	1	US-07-925-695-9
27	31	53.4	14	3	US-08-956-307B-3
28	31	53.4	94	3	US-09-147-550-14

29 31 53.4 94 3 US-09-147-550-45 Sequence 45, Appl
30 31 53.4 94 3 US-09-147-550-48 Sequence 48, Appl
31 31 53.4 94 3 US-09-147-550-77 Sequence 77, Appl
32 31 53.4 94 3 US-09-147-550-84 Sequence 84, Appl
33 31 53.4 94 3 US-09-147-550-90 Sequence 90, Appl
34 31 53.4 94 3 US-09-147-550-101 Sequence 101, App
35 31 53.4 119 3 US-08-767-128-6 Sequence 6, Appl
36 31 53.4 392 3 US-08-979-917A-2 Sequence 2, Appl
37 31 53.4 393 3 US-08-979-917A-3 Sequence 3, Appl
38 31 53.4 462 1 US-08-267-092A-1 Sequence 1, Appl
39 31 53.4 462 2 US-08-540-412-1 Sequence 1, Appl
40 31 53.4 462 3 US-09-051-342-1 Sequence 1, Appl
41 31 53.4 462 3 US-08-468-161-1 Sequence 1, Appl
42 31 53.4 466 1 PCT-US95-08156-1 Sequence 1, Appl
43 31 53.4 466 1 US-08-785-066-2 Sequence 2, Appl
44 31 53.4 466 3 US-09-007-355-2 Sequence 2, Appl
45 31 53.4 466 3 US-08-913-489-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-591-989-4
; Sequence 4, Application US/08591989
; Patent No. 5795721
; GENERAL INFORMATION:
; APPLICANT: Ross S. Rabin, Sumedha Jayasena
; APPLICANT: and Larry Gold
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS OF ICP4
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,989
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX 49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-591-989-4

Query Match 58.6%; Score 34; DB 1; Length 204;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSGF 8

DB 137 APHGCSF 144

```

RESULT 2
US-08-655-821-16
; Sequence 16, Application US/08655821
; Patent No. 5846718
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ying
; APPLICANT: Scorplo, Angelo
; TITLE OF INVENTION: IDENTIFICATION OF PYRAZINAMIDE-RESISTANT
; TITLE OF INVENTION: MYCOBACTERIA AND METHODS FOR TREATING
; TITLE OF INVENTION: MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,821
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07662/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-821-16

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Query Match 58.6%; Score 34; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 NHGSFA 9

Db 57 NHGSFA 62

```

RESULT 3
US-08-926-842B-20
; Sequence 20, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
US-08-926-842B-20

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Query Match 58.6%; Score 34; DB 3; Length 231;
Best Local Similarity 62.5%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 3 HNHGSFA 10

Db 169 HSHGPFAM 176

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RESULT 4
US-08-926-842B-21
; Sequence 21, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:

```


TITLE OF INVENTION: BY USING SAID VECTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEE, Jung Joon
STREET: Hanbit Apt. 132-201, Oeun-dong, Youseong-ku
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-333
ADDRESSEE: KIM, Young Ho
STREET: Hanbit Apt. 125-1504, Oeun-dong, Youseong-ku
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-333
ADDRESSEE: HONG, Soon Kwang
STREET: #231-32 Mochung-dong
CITY: Cheongju-si
STATE: Chungcheongbuk-do
COUNTRY: Republic of Korea
ZIP: 360-140
ADDRESSEE: HONG, Young Soo
STREET: #San-1, Oeun-dong, Youseong-ku
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-333
ADDRESSEE: HWANG, Cheol Kyu
STREET: #San-1, Oeun-dong, Youseong-ku
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-333
ADDRESSEE: KIM, Hang Sub
STREET: Sindonga Apt. 11-1403, Yongjeon-dong, Dong-ku
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 300-200
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,211
FILING DATE: 31-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-1950
FILING DATE: 2-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: DT-1421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-1000
TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-211-3

Query Match 58.6%; Score 34; DB 2; Length 536;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFAY 10.

Db 193 RHGHGTLAH 201
RESULT 8
US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; PRODUCING HETEROLOGOUS ANTIBODIES
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-053-131-84

Query Match 55.2%; Score 32; DB 1; Length 36;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
Db 3 ARHYGSGSY 12

RESULT 9
US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for

;; TITLE OF INVENTION: Producing Heterologous Antibodies
;; NUMBER OF SEQUENCES: 150
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/645,641
;; FILING DATE: 20-MAY-1996
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/904,068
;; FILING DATE: 23-JUN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 14643-000913
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 84:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-645-641-84

Query Match 55.2%; Score 32; DB 1; Length 36;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
Db 3 ARHYGSGSY 12

RESULT 10
US-07-853-408B-84
; Sequence 84, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318
; CLASSIFICATION: 800

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 14643-9
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 84:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-853-408B-84

Query Match 55.2%; Score 32; DB 1; Length 36;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
Db 3 ARHYGSGSY 12

RESULT 11
US-08-096-762-84
; Sequence 84, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-096-762-84

Query Match 55.2%; Score 32; DB 2; Length 36;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
Db 3 ARHYGSGSY 12

RESULT 12
US-08-308-865-84
; Sequence 84, Application US/08308865
; Patent No. 5877397
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308.865
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/145.707
; FILING DATE:
; APPLICATION NUMBER: US 07/904.068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-308-865-84

Query Match 55.2%; Score 32; DB 2; Length 36;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10

Db 3 ARHYGSGSY 12

RESULT 13
PCT-US92-10983-84
; Sequence 84, Application PC/TUS9210983
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic Non-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10983
; FILING DATE: 19921217
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-10983-84

Query Match 55.2%; Score 32; DB 4; Length 36;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
Db 3 ARHYGSGSY 12

RESULT 14
US-08-596-319-31
; Sequence 31, Application US/08596319
; Patent No. 5981262
; GENERAL INFORMATION:
; APPLICANT: Brugge, Joan
; APPLICANT: Morgenstern, Jay
; APPLICANT: Shiue, Lily
; APPLICANT: Zydowsky, Lynne
; APPLICANT: Zoller, Mark
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: HUMAN syk
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: MA

✓
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,319
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/04540
; FILING DATE: 25-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,560
; FILING DATE: 23-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERSTEIN, David L.
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCKET NUMBER: ARIAD305A-PCT/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0400
; TELEFAX: (617) 494-0208
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-596-319-31

Query Match 55.2%; Score 32; DB 2; Length 103;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
|||:|:|:
Db 29 ARDNGSYA 37

RESULT 15
US-08-652-816A-8
; Sequence 8, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-8

Query Match 55.2%; Score 32; DB 2; Length 123;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
|||||:
Db 97 ARHHNYELY 106

Search completed: March 28, 2001, 06:39:11
Job time: 765 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:29:54 ; Search time 124.69 Seconds
(without alignments)
2.562 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	42	71.2	349	1	PHOE_KLEOX	Q01606 klebsiella
2	42	71.2	351	1	PHOE_KLEPN	P30704 klebsiella
3	39	66.1	316	1	YX12-CAEEL	Q11123 caenorhabdi
4	38	64.4	605	1	LEPA_TREPA	O83523 treponema p
5	37	62.7	282	1	OMPD_SALTY	P37592 salmonella
6	37	62.7	374	1	OMPF_SERMA	O33980 serratia ma
7	37	62.7	376	1	OMPC_SERMA	Q54471 serratia ma
8	37	62.7	377	1	OMPN_ECOLI	P77747 escherichia
9	37	62.7	383	1	OMS2_SALTY	Q56111 salmonella
10	37	62.7	789	1	LP1B_DROME	P11996 drosophila
11	36	61.0	369	1	OMPF_XENNE	O56828 xenorhabdus
12	36	61.0	394	1	OMSL_SALTY	Q56110 salmonella
13	36	61.0	602	1	LEPA_CHLPN	Q92814 chlamydia p
14	36	61.0	602	1	LEPA_CHLTR	O84067 chlamydia t
15	36	61.0	783	1	FAND_ECOLI	P12050 escherichia
16	35	59.3	536	1	YNR2_CAEEL	Q21988 caenorhabdi
17	35	59.3	1166	1	RPA2_EUPOC	P28365 euplotes oc
18	34	58.5	131	1	YRAN_ECOLI	P45465 escherichia
19	34	57.6	102	1	RNPB_PENBR	P07446 penicillium
20	34	57.6	105	1	RNF2_GIBBA	P16412 gibberella
21	34	57.6	146	1	LYC2_PIG	P12068 sus scrofa
22	34	57.6	264	1	H824_MOUSE	P20040 mus musculus
23	34	57.6	264	1	H82J_MOUSE	P18468 mus musculus
24	34	57.6	264	1	H82J_MOUSE	P18469 mus musculus
25	34	57.6	275	1	IF2A_PYRAB	Q9V0E4 pyrococcus
26	34	57.6	275	1	IF2A_PYRHO	O58655 pyrococcus
27	34	57.6	284	1	IPYR_PICPA	O13505 pichia past
28	34	57.6	286	1	IPYR_KLULA	P13998 kluyveromyc
29	34	57.6	286	1	IPYR_YEAST	P00817 saccharomyc
30	34	57.6	351	1	PHOE_CITFR	Q01605 citrobacter
31	34	57.6	360	1	MANB_BACSU	P55278 bacillus su
32	34	57.6	448	1	ASTB_PSEAE	O50175 pseudomonas
33	34	57.6	798	1	YLFN_CAEEL	Q20296 caenorhabdi

34 34 57.6 1323 1 RRPO_SMYEA P28897 strawberry
35 33.5 56.8 274 1 PK1_NPVOP O10259 orgyia pseu
36 33 55.9 65 1 CCSA_OENBE P31565 oenochera b
37 33 55.9 196 1 WBBJ_ECOLI P37750 escherichia
38 33 55.9 250 1 Y028_RICPR O05972 rickettsia
39 33 55.9 349 1 YJY9_YEAST P41093 saccharomyc
40 33 55.9 426 1 TWIN_DROME O03019 drosophila
41 33 55.9 432 1 PURA_YEAST P80210 saccharomyc
42 33 55.9 448 1 NCAB_CVHOC P33469 human coron
43 33 55.9 470 1 SYE2_RICPR Q92CT8 rickettsia
44 33 55.9 473 1 SYE_AQUAE O67271 equifex aeo
45 33 55.9 700 1 BIB_DROME P23645 drosophila

ALIGNMENTS

RESULT 1
PHOE_KLEOX
ID PHOE_KLEOX STANDARD; PRT; 349 AA.
AC Q01606;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
OS PHOE.
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K26;
RX MEDLINE; 93146376.
RA Spierings G., Ockhuijsen C., Hofstra H., Tommassen J.;
RT "Characterization of the Citrobacter freundii phoE gene and
RT development of C. freundii-specific oligonucleotides."
RL FEMS Microbiol. Lett. 78:199-204(1992).
CC -!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
CC GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS
CC PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE.
CC PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
CC SOLUTES.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC or send an email to license@isb-sib.ch).
CC EMBL; X68022; CAA48163.1; -
DR HSSP; P02932; lpho.
DR INTERPRO; IPR001702; -
DR INTERPRO; IPR001897; -
DR PFAM; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PRINTS; PR00183; ECOLIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
FT Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 349 OUTER MEMBRANE PORE PROTEIN E.
SQ SEQUENCE 349 AA; 38550 MW; D0B0A5427542B3F5 CRC64;

Query Match 71.2%; Score 42; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10


```

DR PROSITE: PS00301; EFACITOR_GTP; FALSE_NEG.
KW GTP-binding. 17 24 GTP (BY SIMILARITY).
FT NP_BIND 83 87 GTP (BY SIMILARITY).
FT NP_BIND 137 140 GTP (BY SIMILARITY).
SQ SEQUENCE 605 AA; 67622 MW; BA537DEC36FD3349 CRC64;

Query Match 64.4%; Score 38; DB 1; Length 605;
Best Local Similarity 75.0%; Pred. NO. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFDY 10
DB 470 HGYSFDY 477

RESULT 5
OMPD_SALTY STANDARD; PRT; 282 AA.
ID OMPD_SALTY
AC P37592;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORIN PROTEIN OMPD (FRAGMENT).
GN OMPD OR NMPC.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1303;
RX Hongo E., Morimyo M., Mita K., Machida I., Hama-Inaba H., Tsuji H.,
RA Ichimura S., Noda Y.;
RT "The methyl viologen-resistance-encoding gene smva of Salmonella
RL typhimurium.";
RL Gene 148:173-174(1994).
RN [2]
RP IDENTIFICATION AS OMPD.
RA Singh S.P., Miller S., Williams Y.U., Rudd K.E., Nikaido H.;
RA Unpublished observations (FEB-1996).
RL INTERPRO: IPR001702;
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC
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CC
CC EMBL; D26057; BAA05056.1;
CC HSSP; P02931; IGFN.
CC STYGENE; SG10249; OMPD.
DR INTERPRO: IPR001702;
DR PFAM; PF00267; Gram-ve_porins; 1.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin.
FT NON_TER 1
FT SEQUENCE 282 AA; 30954 MW; EE137053E7F6C6A7 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 282;
Best Local Similarity 85.7%; Pred. NO. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
DB 28 DYGSFDY 34

RESULT 6
OMPF_SERMA STANDARD; PRT; 374 AA.
ID OMPF_SERMA
AC O33980;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).
GN OMPF.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UOC-51;
RX MEDLINE; 97419518.
RA Hutsul J.A.M., Worobec E.A.;
RT "Molecular characterization of the Serratia marcescens OmpF porin,
and analysis of S. marcescens OmpF and OmpC osmoregulation.";
RL Microbiology 143:2797-2806(1997).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC
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CC
CC EMBL; U81967; AAB69103.1; ALT_INIT.
DR INTERPRO: IPR001702;
DR INTERPRO: IPR001897;
DR PFAM; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PRINTS; PR00183; ECOLIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 374 OUTER MEMBRANE PROTEIN F.
SQ SEQUENCE 374 AA; 41184 MW; BF821D385E441049 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 374;
Best Local Similarity 85.7%; Pred. NO. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
DB 108 DYGSFDY 114

RESULT 7
OMPC_SERMA STANDARD; PRT; 376 AA.
ID OMPC_SERMA
AC Q5471;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC).
GN OMPC.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UOC-51;
RX MEDLINE; 94236242.
RA Hutsul J.A.M., Worobec E.A.;
RT "Molecular characterization of a 40 kDa OmpC-like porin from Serratia
marcescens.";

```

```

RL Microbiology 140:379-387(1994).
CC -!- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE OMPc/PHOE FAMILY OF PORINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L24960; AAA26562.1; -
DR INTERPRO: IPR001702; -
DR PFAM: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 376 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 376 AA; 41440 MW; 81227FE8515B568E CRC64;

Query Match 62.7%; Score 37; DB 1; Length 376;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
Db 106 DYGSFDY 112

RESULT 8
OMPN_ECOLI
ID OMPN_ECOLI STANDARD; PRT; 377 AA.
AC P77747; P76854;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE OUTER MEMBRANE PROTEIN N PRECURSOR (PORIN OMPN).
GN OMPN.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RT Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE; 97251357.
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamanoto Y., Horiuchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]

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```

RP SEQUENCE FROM N.A., SEQUENCE OF 22-33, AND CHARACTERIZATION.
RX MEDLINE; 98317278.
RA Prilipov A., Phale P.S., Koebnik R., Widmer C., Rosenbusch J.P.;
RT "Identification and characterization of two quiescent porin genes,
RT ompC and ompN, in Escherichia coli BE.";
RL J. Bacteriol. 180:3388-3392(1998).
CC -!- FUNCTION: NON-SPECIFIC PORIN.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE OMPc/PHOE FAMILY OF PORINS.
CC -----
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CC -----
DR EMBL: AE000234; AAC74459.1; -
DR EMBL: D90775; BAA14981.1; -
DR EMBL: D90776; BAA14986.1; -
DR ECOGENE: EGI3375; OMPN.
DR INTERPRO: IPR001702; -
DR PFAM: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLIPORIN.
DR PRINTS: PR00183; ECOLIPORIN.
KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.
SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 377;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
Db 106 DYGSFDY 112

RESULT 9
OMS2_SALTI
ID OMS2_SALTI STANDARD; PRT; 383 AA.
AC Q56111;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN S2 PRECURSOR.
GN OMP52.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMSS-1;
RA Fernandez-Mora M., Calva E.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE OMPc/PHOE FAMILY OF PORINS.
CC -----
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CC -----

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DR EMBL: X89756; CAA61903.1; -
 DR INTERPRO: IPR001702; -
 DR INTERPRO: IPR001897; -
 DR PFAM: PF00267; Gram-ve-porins; 1.
 DR PRINTS: PRO0182; ECOLNEIPORIN.
 DR PRINTS: PRO0183; ECOLIPORIN.
 KW Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 383 OUTER MEMBRANE PROTEIN S2.
 SQ SEQUENCE 383 AA; 42183 MW; 47CFB6B5F6A2370F CRC64;

Query Match 62.7%; Score 37; DB 1; Length 383;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
 :|||||
 DB 106 DYGSFDY 112

RESULT 10
 LP1B_DROME STANDARD; PRT; 789 AA.
 ID LP1B_DROME
 AC P11996;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE LARVAL SERUM PROTEIN 1 BETA CHAIN PRECURSOR (HEXAMERIN 1 BETA).
 GN LSP1-B.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephyridae; Drosophilidae; Drosophila.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE; 97274657.
 RA Massey H.C. Jr., Kejzlarova-Lepesant J., Willis R.L.,
 RA Castleberry A.B., Benes H.;
 RT "The Drosophila Lsp-1 beta gene. A structural and phylogenetic
 analysis";
 RL Eur. J. Biochem. 245:199-207(1997).
 [2]
 RN SEQUENCE OF 1-100 FROM N.A.
 RP MEDLINE; 87060914.
 RX Delaney S.J., Smith D.F., McClelland A., Sunkel C., Glover D.M.;
 RT "Sequence conservation around the 5' ends of the larval serum protein
 1 genes of Drosophila melanogaster.";
 RL J. Mol. Biol. 189:1-11(1986).
 CC -1- FUNCTION: LARVAL STORAGE PROTEIN (LSP) WHICH MAY SERVE AS A STORE
 OF AMINO ACIDS FOR SYNTHESIS OF ADULT PROTEINS (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROHEXAMER, COMPOSED OF THREE SUBUNITS, ALPHA, BETA
 AND GAMMA.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: LARVAL HEMOLYMPH.
 CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
 CC
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 EMBL: U63556; AAB58821.1; -
 DR EMBL: X03873; CAA27507.1; -
 DR PIR: B27144; B27144.
 DR HSSP: P04253; IOXY.
 DR FLYBASE: FBgn0002563; Lsp1-beta.
 DR INTERPRO: IPR000896; -
 DR PFAM: PF00372; hemocyanin; 1.

DR PRINTS: PRO0187; HAEMOCYANIN
 DR PROSITE: PS00209; HEMOCYANIN_1; FALSE_NEG.
 DR PROSITE: PS00210; HEMOCYANIN_2; 1.
 KW Signal; Hemolymph; Storage protein; Glycoprotein; Multigene family.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 789 LARVAL SERUM PROTEIN 1 BETA CHAIN.
 SQ SEQUENCE 789 AA; 95995 MW; AFA3BF4855D06A5B CRC64;

Query Match 62.7%; Score 37; DB 1; Length 789;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
 :|||||
 DB 770 NYGHEDY 776

RESULT 11
 OMPF_XENNE STANDARD; PRT; 369 AA.
 ID OMPF_XENNE
 AC Q56828;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF) (OUTER MEMBRANE
 PROTEIN OPNP).
 DE OMPF OR OPNP.
 GN OMPF OR OPNP.
 OS Xenorhabdus nematophilus.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Xenorhabdus.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-AN6/1;
 RX MEDLINE; 96414477.
 RA Forst S., Waukau J., Leisman G., Exner M., Hancock R.;
 RT "Functional and regulatory analysis of the OmpF-like porin, OmpP, of
 the symbiotic bacterium Xenorhabdus nematophilus.";
 RL Mol. Microbiol. 18:779-789(1995).
 CC -1- FUNCTION: OMPF IS A PORIN THAT PASSIVE DIFFUSION PORES WHICH ALLOW
 SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER
 MEMBRANE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
 CC
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 EMBL: L40919; AAB41114.1; -
 DR INTERPRO: IPR001702; -
 DR INTERPRO: IPR001897; -
 DR PFAM: PF00267; Gram-ve-porins; 1.
 DR PRINTS: PRO0182; ECOLNEIPORIN.
 DR PRINTS: PRO0183; ECOLIPORIN.
 DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
 KW Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 369 OUTER MEMBRANE PROTEIN F.
 SQ SEQUENCE 369 AA; 40851 MW; 20E30CA680F8557A CRC64;

Query Match 61.0%; Score 36; DB 1; Length 369;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
 :|||||


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Db 107 NYGSLDY 113

RESULT 12
OMSL_SALTI STANDARD; PRT; 394 AA.
AC Q56110;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN S1 PRECURSOR.
GN OMSL1.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IMSS-1;
RX MEDLINE; 95309727.
RA Fernandez-Mora M., Oropeza R., Puente J.L., Calva E.;
RT "Isolation and characterization of ompS1, a novel Salmonella typhi
RL Gene 158:67-72(1995).
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC -----
DR EMBL; X73237; CAA51710.1; -
DR INTERPRO; IPR001702; -
DR INTERPRO; IPR001897; -
DR PFAM; PF00267; Gram-ve-porins; 1.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PRINTS; PR00183; ECOLIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
KW Signal; Outer membrane; Transmembrane; Porin.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 394 OUTER MEMBRANE PROTEIN S1.
SQ SEQUENCE 394 AA; 43253 MW; E7C8FEED424931D1 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFDY 10
| | | | |
Db 107 YGSFDY 112

RESULT 13
LEPA_CHLPN STANDARD; PRT; 602 AA.
AC Q92814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
GN LEPA OR CPN0359 OR CP0399.
OS Chlamydia pneumoniae (Chlamydia phila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CML029;
RX MEDLINE; 99206060.

Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AR39;
RX MEDLINE; 20150255.
RA Read T.D., Brunham R.C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE001620; AAD18503.1; -
DR EMBL; AE002201; AAF38244.1; -
DR TIGR; CP0399; -
DR INTERPRO; IPR000795; -
DR PFAM; PF00009; GTP_EFTU; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PROSITE; PS00301; EFACOR_GTP; FALSE_NEG.
KW GTP-binding.
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
FT NP_BIND 135 138 GTP (BY SIMILARITY).
SQ SEQUENCE 602 AA; 67285 MW; A4C110B1A10578E2 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFDY 10
| | | | |
Db 472 YGSFDY 477

RESULT 14
LEPA_CHLTR STANDARD; PRT; 602 AA.
AC O84067;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
GN LEPA OR CT064.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX;
RX MEDLINE; 9900809.
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
Science 282:754-759(1998).
RL Science 282:754-759(1998).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.

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CC -----
DR EMBL; AE001281; AAC67655.1; -
DR INTERPRO; IPR000795; -
DR INTERPRO; IPR002380; -
DR PFAM; PF00009; GTP_EFTU; 1.
DR PRINTS; PR00315; ELONGATNECT.
DR PRINTS; PR00449; RASTRNSFRNG.
DR PROSITE; PS00301; EFAPTOR_GTP; FALSE_NEG.
KW GTP-binding.
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
FT NP_BIND 135 138 GTP (BY SIMILARITY).
FT SEQUENCE 602 AA; 67435 MW; 98f67c990196EEC4 CRC64;
SQ
Query Match 61.0%; Score 36; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 37; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YGSFDY 10
Db 472 YGSFDY 477
|||||
RESULT 15
FAND_ECOLI
ID FAND_ECOLI STANDARD; PRT; 783 AA.
AC P12050;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OUTER MEMBRANE USHER PROTEIN FAND PRECURSOR.
GN FAND.
OS Escherichia coli.
OC Plasmid pPK99.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B41;
RX MEDLINE; 89160266.
RA Roosendaal B., Bakker D., de Graaf F.K.;
RT "The nucleotide sequence of the fanD gene encoding the large outer
RT membrane protein involved in the biosynthesis of K99 fimbriae.";
RL Nucleic Acids Res. 17:1263-1263(1989).
RN [2]
RP SEQUENCE OF 1-20 FROM N.A.
RA Roosendaal B., Gaastra W., de Graaf F.K.;
RT "The nucleotide sequence of the gene encoding the K99 subunit of
RT enterotoxigenic Escherichia coli.";
RL FEMS Microbiol. Lett. 22:253-258(1984).
RN [3]
RP SEQUENCE OF 770-783 FROM N.A.
RC STRAIN-B41;
RX MEDLINE; 91312125.
RA Bakker D., Vader C.E.M., Roosendaal B., Mool F.R., Oudega B.,
RA de Graaf F.K.;
RT "Structure and function of periplasmic chaperone-like proteins
RT involved in the biosynthesis of K88 and K99 fimbriae in
RT enterotoxigenic Escherichia coli.";
RL Mol. Microbiol. 5:875-886(1991).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF K99 FIMBRIAL
CC SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).

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CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
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CC -----
DR EMBL; X13560; CAA31911.1; -
DR EMBL; M35282; -; NOT_ANNOTATED_CDS.
DR EMBL; X56001; CAA39473.1; -
DR PIR; S02755; S02755.
DR INTERPRO; IPR000015; -
DR PFAM; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 783 OUTER MEMBRANE USHER PROTEIN FAND.
FT DISULFID 763 782 POTENTIAL.
FT SEQUENCE 783 AA; 87156 MW; 23BDE3923A9B7069 CRC64;
SQ
Query Match 61.0%; Score 36; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 YGSFDY 10
Db 354 YGSFDY 359
|||||
Search completed: March 28, 2001, 07:29:55
Job time: 1662 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:27:59 ; Search time 263.81 Seconds
(without alignments)
4.443 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	72.9	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	42	71.2	78	7 Q9MWT6	Q9MWT6 leopardus p
3	42	71.2	78	7 Q9MWT5	Q9MWT5 leopardus p
4	42	71.2	78	7 Q9MWT4	Q9MWT4 leopardus p
5	42	71.2	79	7 Q9L191	Q9L191 prionailuru
6	42	71.2	79	7 Q9L192	Q9L192 felis silve
7	42	71.2	79	7 Q9L380	Q9L380 felis silve
8	42	71.2	79	7 Q9L381	Q9L381 felis silve
9	42	71.2	79	7 Q9L382	Q9L382 felis silve
10	42	71.2	79	7 Q9L386	Q9L386 felis silve
11	42	71.2	79	7 Q9L397	Q9L397 felis silve
12	42	71.2	79	7 Q9L405	Q9L405 felis silve
13	42	71.2	79	7 Q9L406	Q9L406 felis silve
14	42	71.2	79	7 Q9L407	Q9L407 felis silve
15	42	71.2	79	7 Q9L408	Q9L408 felis silve
16	42	71.2	79	7 Q9L435	Q9L435 felis silve
17	42	71.2	79	7 Q9MX19	Q9MX19 leopardus p
18	42	71.2	79	7 Q9MX13	Q9MX13 leopardus p
19	42	71.2	79	7 Q9MX03	Q9MX03 leopardus p

20	42	71.2	79	7 Q9MX00	Q9MX00 leopardus p
21	42	71.2	79	7 Q9MX29	Q9MX29 leopardus p
22	42	71.2	79	7 Q9MX28	Q9MX28 leopardus p
23	42	71.2	79	7 Q9MW27	Q9MW27 leopardus p
24	42	71.2	79	7 Q9MWY9	Q9MWY9 leopardus p
25	42	71.2	79	7 Q9MWY8	Q9MWY8 leopardus p
26	42	71.2	79	7 Q9MWY6	Q9MWY6 leopardus p
27	42	71.2	79	7 Q9MWY5	Q9MWY5 leopardus p
28	42	71.2	79	7 Q9MWY4	Q9MWY4 leopardus p
29	42	71.2	79	7 Q9MWY3	Q9MWY3 leopardus p
30	42	71.2	79	7 Q9MWX6	Q9MWX6 leopardus p
31	42	71.2	79	7 Q9MWX5	Q9MWX5 leopardus p
32	42	71.2	79	7 Q9MWX4	Q9MWX4 leopardus p
33	42	71.2	79	7 Q9MWX1	Q9MWX1 leopardus p
34	42	71.2	79	7 Q9MWX0	Q9MWX0 leopardus p
35	42	71.2	79	7 Q9MMW9	Q9MMW9 leopardus p
36	42	71.2	79	7 Q9MMW7	Q9MMW7 leopardus p
37	42	71.2	79	7 Q9MMW4	Q9MMW4 leopardus p
38	42	71.2	79	7 Q9MMV9	Q9MMV9 leopardus p
39	42	71.2	79	7 Q9MMV2	Q9MMV2 leopardus p
40	42	71.2	79	7 Q9MMU4	Q9MMU4 leopardus p
41	42	71.2	79	7 Q9MMU2	Q9MMU2 leopardus p
42	42	71.2	79	7 Q9MMU1	Q9MMU1 leopardus p
43	42	71.2	79	7 Q9MMT9	Q9MMT9 leopardus p
44	42	71.2	79	7 Q9MWS7	Q9MWS7 leopardus p
45	42	71.2	79	7 Q9MWL0	Q9MWL0 leopardus w

ALIGNMENTS

RESULT 1
Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
ON NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 72.9%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

Db 274 SRHNYGSF 281

RESULT 2
Q9MWT6

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ID Q9MWT6 PRELIMINARY; PRT; 78 AA.
AC Q9MWT6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
GN LEPA-DRB.
OS Leopardus pardalis (ocelot).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057894; AAF70946.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9559 MW; 77863043708EC5B8 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 78;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 71 RHNYGVFD 78

RESULT 3
ID Q9MWT5 PRELIMINARY; PRT; 78 AA.
AC Q9MWT5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
GN LEPA-DRB.
OS Leopardus pardalis (ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057895; AAF70947.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 5076280FF45EC5A7 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 78;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 71 RHNYGVFD 78

RESULT 4
ID Q9MWT4 PRELIMINARY; PRT; 78 AA.

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AC Q9MWT4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
GN LEPA-DRB.
OS Leopardus pardalis (ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuhki N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057896; AAF70948.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9586 MW; 77863043709666B8 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 78;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 71 RHNYGVFD 78

RESULT 5
ID Q19191 PRELIMINARY; PRT; 79 AA.
AC Q19191;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCMAIR-DRB.
OS Prionailurus bengalensis iriomotensis (Iriomote cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
OX NCBI_TaxID=37030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
RT genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51546; AAB65582.1; -.
DR INTERPRO: IPR000353; -.
DR PIR: P00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9582 MW; EF9D98CA42030A7B CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 6
ID Q19192

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ID O19192 PRELIMINARY; PRT; 79 AA.
AC O19192;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCIIA-DRB.
OS Prionailurus bengalensis iriomotensis (Iriomote cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
OX NCBI_TaxID=37030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51547; AAB65533.1; -.
DR INTERPRO: IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9582 MW; EF9D98CA4F6EBCAD CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 7
O19380 PRELIMINARY; PRT; 79 AA.
AC O19380;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCIIA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51498; AAB65533.1; -.
DR INTERPRO: IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9659 MW; 79EE7526943C8A20 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

ID O19381 PRELIMINARY; PRT; 79 AA.
AC O19381;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCIIA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51499; AAB65534.1; -.
DR INTERPRO: IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9610 MW; 80C16A2749AF9E68 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 9
O19382 PRELIMINARY; PRT; 79 AA.
AC O19382;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCIIA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51500; AAB65535.1; -.
DR INTERPRO: IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9421 MW; 88CAD0EA76360AAC CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

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Db      72 RHNYGVFD 79
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RESULT 10
O19396 PRELIMINARY; PRT; 79 AA.
AC O19396;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51514; AAB65549.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9625 MW; 153A004237E3C769 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSFD 9
|||||
Db      72 RHNYGVFD 79

RESULT 11
O19397 PRELIMINARY; PRT; 79 AA.
AC O19397;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51515; AAB65550.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9641 MW; A02E404237E3C774 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;

Db      72 RHNYGVFD 79
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RESULT 12
O19405 PRELIMINARY; PRT; 79 AA.
AC O19405;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51523; AAB65558.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9590 MW; EBB33E3FEE9A4162 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSFD 9
|||||
Db      72 RHNYGVFD 79

RESULT 13
O19406 PRELIMINARY; PRT; 79 AA.
AC O19406;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97211851; PubMed=9058818;
RA Yuhki N., O'Brien S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51524; AAB65559.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9466 MW; E66144C12F413370 CRC64;

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Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 1.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
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 DB 72 RHNYGVFD 79

RESULT 14
 O19407

ID O19407 PRELIMINARY; PRT; 79 AA.
 AC O19407;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97211851; PubMed=9058818;
 RA Yuhki N., O'Brien S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51525; AAB65360.1; -;
 DR INTERPRO; IPR000353; -;
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9485 MW; 7093582FDD413365 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 1.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 ||||| ||
 DB 72 RHNYGVFD 79

RESULT 15
 O19408

ID O19408 PRELIMINARY; PRT; 79 AA.
 AC O19408;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97211851; PubMed=9058818;
 RA Yuhki N., O'Brien S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51526; AAB65361.1; -;
 DR INTERPRO; IPR000353; -;
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1

FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9496 MW; EE6144C12F412371 CRC64;

Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 1.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 ||||| ||
 DB 72 RHNYGVFD 79

Search completed: March 28, 2001, 07:27:59
 Job time: 1672 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:34:35 ; Search time 183.85 Seconds
(without alignments)
1.860 Million cell updates/sec

Title: US-09-016-061-64

Perfect score: 59

Sequence: 1 ARHNYGSFDY 10

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	19 W76022	LM609 grafted anti
2	51	86.4	10	19 W76010	LM609 grafted anti
3	51	86.4	117	19 W76001	Vitaxin antibody h
4	51	86.4	117	19 W76003	LM609 antibody hea
5	51	86.4	117	20 Y06381	Murine monoclonal
6	51	86.4	117	20 Y06387	Humanised LM609 an
7	51	86.4	118	20 Y06384	Humanised LM609 an
8	51	86.4	118	20 Y06385	Humanised LM609 an
9	51	86.4	118	20 Y06386	Humanised LM609 an
10	51	86.4	118	20 Y06383	Humanised LM609 an
11	51	86.4	130	20 Y06379	Murine monoclonal
12	50	84.7	10	19 W76023	LM609 grafted anti

13	49	83.1	117	16	R79157	Human IgE receptor
14	49	83.1	117	16	R79155	Human IgE receptor
15	49	83.1	117	18	W27357	Heavy chain variab
16	49	83.1	117	18	W27526	Heavy chain variab
17	49	83.1	117	18	W27354	Heavy chain variab
18	49	83.1	239	20	W73874	Human antiFc epsil
19	49	83.1	242	20	W73876	Human antiFc epsil
20	48	81.4	10	19	W76021	LM609 grafted anti
21	46	78.0	10	19	W76039	LM609 grafted anti
22	46	78.0	10	19	W76040	LM609 grafted anti
23	46	78.0	10	19	W76020	LM609 grafted anti
24	46	78.0	10	19	W76024	LM609 grafted anti
25	46	78.0	10	19	W76025	LM609 grafted anti
26	46	78.0	10	19	W76026	LM609 grafted anti
27	46	78.0	10	19	W76027	LM609 grafted anti
28	46	78.0	10	19	W76028	LM609 grafted anti
29	46	78.0	10	19	W76029	LM609 grafted anti
30	46	78.0	10	19	W76030	LM609 grafted anti
31	43	72.9	110	20	W84099	Vitronection alpha-
32	43	72.9	117	20	W84093	Murine vitronection
33	43	72.9	117	20	W84097	Humanised anti-alp
34	42	71.2	8	20	Y06371	Murine monoclonal
35	41	69.5	10	19	W76037	LM609 grafted anti
36	41	69.5	10	19	W76038	LM609 grafted anti
37	40	67.8	8	18	W27343	CDR3 from murine a
38	37	62.7	36	17	W03964	VDJ joint protein,
39	37	62.7	36	18	W41127	VH251 DXP'1 J6 mu
40	37	62.7	36	20	Y40395	Amino acid sequenc
41	37	62.7	111	14	R40173	Humanised IL-5 ant
42	37	62.7	111	17	R87039	MAB 39D10 heavy ch
43	37	62.7	119	19	Y86109	S. pneumoniae derl
44	37	62.7	135	14	R40175	Humanised antibody
45	37	62.7	135	14	R40177	Humanised antibody

ALIGNMENTS

RESULT 1

W76022

ID W76022 standard; Protein; 10 AA.

XX W76022;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-II region CDR3 protein fragment #4.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49859.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC angiogenesis and restenosis of alphavbeta3-mediated disease, specifically
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 59; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFDY 10
 Db ||||||||
 1 arhnygsfdy 10
 RESULT 2
 W76010
 ID W76010 standard; Protein; 10 AA.
 XX
 AC W76010;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49847.
 XX
 PT Humanised antibody, vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC angiogenesis and restenosis of alphavbeta3-mediated disease, specifically
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 86.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0078;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSFDY 10
 Db ||||||||
 1 arhnygsfdy 10
 RESULT 3
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49820.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so,are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
 |||||
 Db 97 arhnygsfay 106

RESULT 4

W76003
 ID W76003 standard; Protein; 117 AA.

XX
 AC W76003;

XX
 DT 02-NOV-1998 (first entry)

XX LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI: 1998-437472/37.

XX N-PSDB: V49822.

XX :Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 19; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
 |||||
 Db 97 arhnygsfay 106

RESULT 5

Y06381
 ID Y06381 standard; Protein; 117 AA.

XX
 AC Y06381;

XX DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX PN W09929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX WPI: 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
 |||||
 Db 97 arhnygsfay 106

RESULT 6

Y06387
 ID Y06387 standard; Protein; 117 AA.

XX
 AC Y06387;

XX

DT 06-SEP-1999 (first entry)
 XX Humanised LM609 antibody VH domain.
 DE
 XX
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 PD
 XX
 XX 04-DEC-1998; 98WO-US25828.
 PF
 XX
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Barbas CF, Rader C;
 PI
 XX
 XX WPI; 1999-394979/33.
 DR
 XX
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX
 XX Disclosure; Page 52; 55pp; English.
 PS
 XX
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX Sequence 117 AA;
 SQ

Query Match 86.4%; Score 51; DB 20; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSFDY 10
 Db 97 arhnygsfay 106
 Db
 RESULT 7
 ID Y06384
 XX Y06384 standard; Protein; 118 AA.
 XX AC Y06384;
 XX
 DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.
 DE
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 PD
 XX
 XX 04-DEC-1998; 98WO-US25828.
 PF
 XX
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Barbas CF, Rader C;
 PI
 XX
 XX WPI; 1999-394979/33.
 DR
 XX
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX
 XX Disclosure; Page 51; 55pp; English.
 PS
 XX
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX Sequence 118 AA;
 SQ

Query Match 86.4%; Score 51; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSFDY 10
 Db 98 arhnygsfay 107
 Db
 RESULT 8
 ID Y06385
 XX Y06385 standard; Protein; 118 AA.
 XX AC Y06385;
 XX
 DT 06-SEP-1999 (first entry)
 XX

DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"

XX WO9929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 XX
 XX 04-DEC-1998; 98WO-US25828.
 XX
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Barbas CF, Rader C;
 PI
 XX WPI; 1999-394979/33.
 DR
 XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.
 XX
 PS

CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX

SQ Sequence 118 AA;

Query Match 86.4%; Score 51; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 Db | | | | | | | |
 98 arhnygsfay 107

RESULT 9
 Y06386
 ID Y06386 standard; Protein; 118 AA.
 XX
 AC Y06386;
 XX
 DT 06-SEP-1999 (first entry)
 XX Humanised LM609 antibody VH domain.
 DE

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"

XX WO9929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 XX
 XX 04-DEC-1998; 98WO-US25828.
 XX
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Barbas CF, Rader C;
 PI
 XX WPI; 1999-394979/33.
 DR
 XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51-52; 55pp; English.
 XX
 PS

CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX

SQ Sequence 118 AA;

Query Match 86.4%; Score 51; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 Db | | | | | | | |
 98 arhnygsfay 107

RESULT 10
 Y06383
 ID Y06383 standard; Protein; 118 AA.
 XX
 AC Y06383;
 XX
 DT 06-SEP-1999 (first entry)
 XX Humanised LM609 antibody VH domain.
 DE

KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 XX Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"

XX PN WO9929888-A1.
 XX PD 17-JUN-1999.
 XX PF 04-DEC-1998; 98WO-US25828.
 XX PR 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies

PS Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 118 AA;

Query Match 86.4%; Score 51; DB 20; Length 118;
 Best Local Similarity 90.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 |||||
 Db 98 arhnygsfay 107

RESULT 11
 Y06379
 ID Y06379 standard; Protein; 130 AA.

XX AC Y06379;
 XX DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

XX Humanised antibody; antibody humanisation; antibody engineering;

KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers
 XX Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 28..32
 FT /note= "CDR1"
 FT Region 47..63
 FT /note= "CDR2"
 FT Region 96..103
 FT /note= "CDR3"

XX PN WO9929888-A1.
 XX PD 17-JUN-1999.
 XX PF 04-DEC-1998; 98WO-US25828.
 XX PR 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies

PS Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V kappa region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 130 AA;

Query Match 86.4%; Score 51; DB 20; Length 130;
 Best Local Similarity 90.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 |||||
 Db 94 arhnygsfay 103

RESULT 12
 W76023
 ID W76023 standard; Protein; 10 AA.

XX AC W76023;
 XX DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #5.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region..

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49860.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 84.7%; Score 50; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

Db 1 arhnygsfyy 10

RESULT 13

R79157

ID R79157 standard; peptide; 117 AA.

XX AC

XX R79157;

XX 04-MAR-1996 (first entry)

XX Human IgE receptor-binding antibody-related peptide heavy chain.

XX Immunoglobulin E; antibody; receptor; monoclonal; detection;

XX complementarity determining region.

XX OS

XX Mus sp.

XX key

XX Location/Qualifiers

XX Region

XX 31..35

XX /label= CDR1H

XX /note= "all CDR regions are claimed"

XX 50..66

XX Region

FT /label= CDR2H

FT /note= "all CDR regions are claimed"

FT 99..106

FT /label= CDR3H

FT /note= "all CDR regions are claimed"

XX JP07165799-A.

XX 27-JUN-1995.

XX 22-OCT-1993; 93JP-0264792.

XX 22-OCT-1993; 93JP-0264792.

XX (ASAK) ASahi BREWERIES LTD.

XX (NIKK-) NIKKA WHISKY KK.

XX (TORI) TORII YAHUKIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1995-261292/34.

XX N-PSDB; Q96284.

XX Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the Mab, for the specific identification
 PT of human Fc-epsilon RI

PS Claim 5; Page 14; 20pp; Japanese.

XX Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
 CC Q96280, Q96282, Q96284, Q96286 and Q96288. FR1 is a polypeptide
 CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
 CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
 CC the light chains have the general formula FR5-CDRIH-FR6-CDR2L-FR7-
 CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
 CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
 CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
 CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
 CC peptides are derived from mouse hybridoma cells and are useful in
 CC the detection of the human Fc-epsilon-RI or for the elucidation of
 CC an antigen recognising region of a monoclonal antibody against
 CC human Fc-epsilon-RI.

XX Sequence 117 AA;

Query Match 83.1%; Score 49; DB 16; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

Db 97 arhnyggmdy 106

RESULT 14

R79155

ID R79155 standard; peptide; 117 AA.

XX AC

XX R79155;

XX 04-MAR-1996 (first entry)

XX Human IgE receptor-binding antibody-related peptide heavy chain.

XX Immunoglobulin E; antibody; receptor; monoclonal; detection;

XX complementarity determining region.

XX OS

XX Mus sp.

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XX Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1H
FT /note= "all CDR regions are claimed"
FT Region 50..56
FT /label= CDR2H
FT /note= "all CDR regions are claimed"
FT Region 99..106
FT /label= CDR3H
FT /note= "all CDR regions are claimed"
XX JP07165799-A.
XX
XX 27-JUN-1995.
XX
XX 22-OCT-1993; 93JP-0264792.
XX
XX 22-OCT-1993; 93JP-0264792.
XX (ASAK ) ASahi BREWERIES LTD.
XX (NIKK-) NIKKA WHISKEY KK.
XX (TORI ) TORII YAKUHIN KK.
XX (TSUR/) TSURA T.
XX WPI: 1995-261292/34.
XX N-PSDB: Q96282.
XX Novel monoclonal antibody against human high-affinity IgE receptor -
XX and DNA fragment encoding the MAB, for the specific identification
XX of human Fc-epsilon RI
XX
XX Claim 3; Page 13; 20pp; Japanese.
XX
XX Polypeptides which specifically recognise human IgE receptor (Fc-
XX epsilon-RI) have been isolated and sequenced. The new peptides are
XX related to a monoclonal antibody against Fc-epsilon-RI and are
XX either heavy or light chain molecules. The heavy chain molecules
XX have the general formula FR1-CDRIH-FR2-CDRH-FR3-CDRH-FR4 (corresp.
XX to R79153, R79155, R79157, R79159 and R79161) and are encoded by
XX having 29-36 amino acids (aa). FR2 is a 10-16 aa polypeptide, FR3 is
XX a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
XX the light chains have the general formula FR5-CDRL-FR6-CDRL-FR7-
XX CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
XX and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
XX is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
XX 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
XX peptides are derived from mouse hybridoma cells and are useful in
XX the detection of the human Fc-epsilon-RI or for the elucidation of
XX an antigen recognising region of a monoclonal antibody against
XX human Fc-epsilon-RI.
XX
XX Sequence 117 AA;
XX
XX Query Match 83.1%; Score 49; DB 16; Length 117;
XX Best Local Similarity 80.0%; Pred. No. 0.21;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 ARHNYGSFDY 10
XX | | | | | | |
XX Db 97 arhnyggmndy 106
XX
XX RESULT 15
XX W27357
XX ID W27357 standard; Protein; 117 AA.
XX AC W27357;
XX XX
XX DT 16-DEC-1997 (first entry)
XX

```

```

DE Heavy chain variable region of chimeric human CRA2 antibody.
XX
XX Complementarity determining region; CDR: murine; mouse; human;
XX high affinity; immunoglobulin E; receptor; monoclonal antibody;
XX IgE; MAB; heavy chain; variable region; humanised; semi-chimeric;
XX chimeric; treatment; prevention; disease; allergy; CRA2.
XX
XX Chimeric - Homo sapiens.
XX Chimeric - Mus spp.
XX Synthetic.
XX JP09191886-A.
XX
XX 29-JUL-1997.
XX
XX 19-JAN-1996; 96JP-0024816.
XX
XX 19-JAN-1996; 96JP-0024816.
XX (ASAK ) ASahi BREWERIES LTD.
XX (NIKK-) NIKKA WHISKEY KK.
XX (TORI ) TORII YAKUHIN KK.
XX (TSUR/) TSURA T.
XX WPI: 1997-429186/40.
XX
XX Humanised, semi-chimeric and chimeric antibodies against human
XX high-affinity IgE receptor - useful medicinally and have low
XX antigenicity in humans
XX Claim 8; Page 15; 26pp; Japanese.
XX
XX The present sequence, the heavy chain variable region of a
XX chimeric human CRA2 antibody (Ab), comprises complementarity
XX determining regions (CDR) from a murine, anti-human high affinity
XX immunoglobulin E (IgE) receptor, monoclonal Ab (MAB). The
XX humanised chimeric MAB can be used to treat or prevent diseases,
XX specifically allergies, associated with the receptor, and has very
XX low antigenicity in humans.
XX
XX Sequence 117 AA;
XX
XX Query Match 83.1%; Score 49; DB 18; Length 117;
XX Best Local Similarity 80.0%; Pred. No. 0.21;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 ARHNYGSFDY 10
XX | | | | | | |
XX Db 97 arhnyggmndy 106
XX
XX Search completed: March 28, 2001, 06:34:35
XX Job time: 515 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:39:12 ; Search time 269.55 Seconds
(without alignments)
0.666 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgnl_7/ptodata/1/1aa/5B_COMB.pep.*
3: /cgnl_7/ptodata/1/1aa/6_COMB.pep.*
4: /cgnl_7/ptodata/1/1aa/PCITUS_COMB.pep.*
5: /cgnl_7/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	38	64.4	94	3	US-09-147-550-14	Sequence 14, Appl
2	38	64.4	94	3	US-09-147-550-45	Sequence 45, Appl
3	38	64.4	94	3	US-09-147-550-48	Sequence 48, Appl
4	38	64.4	94	3	US-09-147-550-77	Sequence 77, Appl
5	38	64.4	94	3	US-09-147-550-84	Sequence 84, Appl
6	38	64.4	94	3	US-09-147-550-90	Sequence 90, Appl
7	38	64.4	94	3	US-09-147-550-101	Sequence 101, App
8	37	62.7	36	1	US-08-053-131-84	Sequence 84, Appl
9	37	62.7	36	1	US-08-645-641-84	Sequence 84, Appl
10	37	62.7	36	1	US-07-853-408B-84	Sequence 84, Appl
11	37	62.7	36	2	US-08-096-762-84	Sequence 84, Appl
12	37	62.7	36	2	US-08-308-865-84	Sequence 84, Appl
13	37	62.7	36	4	PCT-US92-10983-84	Sequence 84, Appl
14	37	62.7	111	2	US-08-470-139-6	Sequence 6, Appl
15	37	62.7	135	2	US-08-470-139-28	Sequence 28, Appl
16	37	62.7	135	3	US-08-284-516C-36	Sequence 36, Appl
17	37	62.7	135	3	US-08-284-516C-40	Sequence 40, Appl
18	37	62.7	135	3	US-08-284-516C-46	Sequence 46, Appl
19	37	62.7	135	3	US-08-284-516C-64	Sequence 64, Appl
20	37	62.7	136	3	US-08-284-516C-56	Sequence 56, Appl
21	37	62.7	323	3	US-09-041-889-28	Sequence 28, Appl
22	37	62.7	377	3	US-09-041-889-29	Sequence 29, Appl
23	35.5	60.2	142	2	US-08-860-174A-7	Sequence 7, Appl
24	35.5	60.2	274	2	US-08-860-174A-12	Sequence 12, Appl
25	35.5	60.2	282	2	US-08-860-174A-10	Sequence 10, Appl
26	35	59.3	27	1	US-08-053-131-80	Sequence 80, Appl
27	35	59.3	27	1	US-08-645-641-80	Sequence 80, Appl
28	35	59.3	27	1	US-07-853-408B-80	Sequence 80, Appl

29 35 59.3 27 2 US-08-096-762-80 Sequence 80, Appl
30 35 59.3 27 2 US-08-308-865-80 Sequence 80, Appl
31 35 59.3 27 4 PCT-US92-10983-80 Sequence 80, Appl
32 34 57.6 94 3 US-09-147-550-39 Sequence 39, Appl
33 34 57.6 94 3 US-09-147-550-59 Sequence 59, Appl
34 34 57.6 94 3 US-09-147-550-63 Sequence 63, Appl
35 34 57.6 119 2 US-08-553-497A-8 Sequence 8, Appl
36 34 57.6 119 2 US-08-553-497A-12 Sequence 12, Appl
37 34 57.6 119 3 US-08-767-128-6 Sequence 6, Appl
38 34 57.6 254 2 US-08-207-481-20 Sequence 20, Appl
39 34 57.6 254 4 PCT-US95-02689-20 Sequence 20, Appl
40 34 57.6 286 2 US-08-809-267-3 Sequence 3, Appl
41 34 57.6 286 4 PCT-US95-13662A-3 Sequence 3, Appl
42 34 57.6 287 2 US-08-741-437-5 Sequence 5, Appl
43 34 57.6 287 2 US-09-134-593-5 Sequence 5, Appl
44 34 57.6 633 2 US-08-648-298-2 Sequence 2, Appl
45 33 55.9 94 3 US-09-147-550-55 Sequence 55, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSFD 9

|||||
80 RHNYSFD 87

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-45

Query Match 64.48; Score 38; DB 3; Length 94;
Best Local Similarity 75.08; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87
||||| 1;

RESULT 3
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-48

Query Match 64.48; Score 38; DB 3; Length 94;
Best Local Similarity 75.08; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87
||||| 1;

RESULT 4
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-77

Query Match 64.48; Score 38; DB 3; Length 94;
Best Local Similarity 75.08; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87
||||| 1;

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-84

Query Match 64.48; Score 38; DB 3; Length 94;
Best Local Similarity 75.08; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 80 RHNYGVFE 87
||||| 1;

RESULT 6
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT

ORGANISM: BOVINE
US-09-147-550-90

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSD 9
||||| |:
DB 80 RHNYGVE 87

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 64.4%; Score 38; DB 3; Length 94;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSD 9
||||| |:
DB 80 RHNYGVE 87

RESULT 8

US-08-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993

CLASSIFICATION: 800
; PRIOR APPLICATION DATA: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-84

Query Match 62.7%; Score 37; DB 1; Length 36;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 ARHNY--GSFDY 10
||| | ||:
DB 3 ARHYGSGSYDY 14

RESULT 9

US-08-645-641-84
; Sequence 84, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-645-641-84

Query Match 62.7%; Score 37; DB 1; Length 36;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 ARHNY--GSFDY 10
||| | ||:|
Db 3 ARHYGSGSYD 14

RESULT 10

US-07-853-408B-84
; Sequence 84, Application US/07853408B
; Patent No. 5789650

; GENERAL INFORMATION:

; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-853-408B-84

Query Match 62.7%; Score 37; DB 1; Length 36;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 ARHNY--GSFDY 10
||| | ||:|
Db 3 ARHYGSGSYD 14

RESULT 11

US-08-096-762-84
; Sequence 84, Application US/08096762

; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/096,762

; FILING DATE: 22-JUL-1993

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/053,131

; FILING DATE: 26-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/990,860

; FILING DATE: 16-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/904,068

; FILING DATE: 23-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/853,408

; FILING DATE: 18-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/810,279

; FILING DATE: 17-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 14643-9-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-096-762-84

Query Match 62.7%; Score 37; DB 2; Length 36;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 ARHNY--GSFDY 10
||| | ||:|
Db 3 ARHYGSGSYD 14

RESULT 12

US-08-308-865-84
; Sequence 84, Application US/08308865
; Patent No. 5877397

; GENERAL INFORMATION:

; APPLICANT: Lonberg, Nils

; APPLICANT: Kay, Robert M.

; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for

; TITLE OF INVENTION: Producing Heterologous Antibodies

;
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308.865
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/145.707
; FILING DATE:
; APPLICATION NUMBER: US 07/904.068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30.223
; REFERENCE/DOCKET NUMBER: 14643-9-1-1
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-308-865-84

Query Match 62.7%; Score 37; DB 2; Length 36;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ARHNY--GSFDY 10
||| | ||:||
Db 3 ARHYGSGSYDY 14

RESULT 13
PCT-US92-10983-84
; Sequence 84, Application PC/TUS9210983
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10983
; FILING DATE: 19921217
; CLASSIFICATION:

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30.223
; REFERENCE/DOCKET NUMBER: 14643-9-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92-10983-84

Query Match 62.7%; Score 37; DB 4; Length 36;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 ARHNY--GSFDY 10
||| | ||:||
Db 3 ARHYGSGSYDY 14

RESULT 14
US-08-470-139-6
; Sequence 6, Application US/08470139
; Patent No. 5998586
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.139
; FILING DATE: 06 JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TRUJILLO, DOREEN YATKO
; REGISTRATION NUMBER: 35.719
; REFERENCE/DOCKET NUMBER: CARP-0044
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-139-6

Query Match 62.7%; Score 37; DB 2; Length 111;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
|| | || |||
Db 91 AREYGYFDY 100

RESULT 15
US-08-470-139-28
; Sequence 28, Application US/08470139
; Patent No. 5998586
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies

NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139
FILING DATE: 06 JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-139-28

Query Match 62.7%; Score 37; DB 2; Length 135;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
|||
Db 115 AREYGYGFDY 124

Search completed: March 28, 2001, 06:39:12
Job time: 766 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:18 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-68

Perfect score: 54

Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	74.1	446	2 T19625	hypothetical prote
2	39	72.2	89	2 S38688	MHC class II histo
3	39	72.2	89	2 S38683	MHC class II histo
4	39	72.2	89	2 S38684	MHC class II histo
5	39	72.2	225	2 I47095	MHC class II OVAR-
6	36	66.7	65	2 S17441	hypothetical prote
7	36	66.7	82	2 I51106	Major histocompati
8	36	66.7	360	2 S48566	hypothetical prote
9	35	64.8	85	2 I59634	MHC class II DR-be
10	35	64.8	89	2 S38676	MHC class II histo
11	35	64.8	89	2 S38680	MHC class II histo
12	35	64.8	89	2 S57512	MHC class II histo
13	35	64.8	98	1 WMBP72	gene 7 protein - p
14	35	64.8	98	1 WMBP59	gene 7 protein - p
15	35	64.8	123	2 C25239	MHC class II histo
16	35	64.8	200	2 D32526	MHC class II histocomp
17	35	64.8	221	2 I45939	MHC cell surface g
18	35	64.8	237	2 C27060	class II histocomp
19	35	64.8	266	2 I34287	gene HLA-DRB1 prot
20	35	64.8	266	2 A27618	class II histocomp
21	35	64.8	266	2 I54295	lymphocyte antigen
22	35	64.8	313	1 A05213	cytochrome c-type
23	35	64.8	347	2 S43711	phosphatidylcholin
24	34	63.0	108	2 S26316	Ig heavy chain v r
25	34	63.0	110	2 S26317	Ig heavy chain v r
26	34	63.0	115	2 S37265	MHC class II histo
27	34	63.0	210	1 B69265	conserved hypothet
28	34	63.0	263	2 A45838	MHC class II histo
29	34	63.0	265	2 B39797	MHC class II histo

30 34 63.0 275 2 G75130 translation initia
31 34 63.0 275 2 D71087 probable translati
32 34 63.0 279 2 T05421 hypothetical prote
33 34 63.0 287 1 PWBY inorganic pyrophos
34 34 63.0 287 1 PWVKL inorganic pyrophos
35 34 63.0 723 2 F83173 outer membrane pro
36 33 61.1 80 2 I54469 MHC HLA-DR-beta-1
37 33 61.1 80 2 I68777 MHC HLA-DR beta-1
38 33 61.1 81 2 I54550 HLA DRB1*1202 - hu
39 33 61.1 87 2 S38681 major histocompati
40 33 61.1 87 2 S38682 major histocompati
41 33 61.1 87 2 S38685 major histocompati
42 33 61.1 167 2 T16454 hypothetical prote
43 33 61.1 220 2 T46055 hypothetical prote
44 33 61.1 232 2 I51220 major histocompati
45 33 61.1 232 2 B48381 MHC class II histo

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DDBB

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 74.1%; Score 40; DB 2; Length 446;
Best Local Similarity 77.8%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 51 RHNYGSHAA 59

RESULT 2

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba

C:Species: Galago senegalensis (northern lesser bushbaby)

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38688

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
|||||
Db 75 RHNYGVFES 83

RESULT 3

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 1.3;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGVFES 83

RESULT 4

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 1.3;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 75 RHNYGVFES 83

RESULT 5

MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095

R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

Anim. Genet. 24, 249-255, 1993

A:Title: Isolation, characterization and evolution of ovine major histocompatibility com

A:Reference number: I47075; MUID:94057592

A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-225 <FAB>

A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 39; DB 2; Length 225;

Best Local Similarity 77.8%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

|||||

Db 68 RHNYGVFES 76

RESULT 6

S17441

hypothetical protein (rpl2 5' region) - garden pea chloroplast (fragment)

C:Species: chloroplast Pisum sativum (garden pea)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999

C:Accession: S17441

R:Nagano, Y.; Ishikawa, H.; Matsuno, R.; Sasaki, Y.

Plant Mol. Biol. 17, 541-545, 1991

A:Title: Nucleotide sequence and expression of the ribosomal protein L2 gene in pea c

A:Reference number: S17441; MUID:91355950

A:Accession: S17441

A:Molecule type: DNA

A:Residues: 1-65 <NAG>

A:Cross-references: EMBL:X59015; NID:g12175; PIDN:CAA41754.1; PID:g388252

C:Genetics:

A:Genome: chloroplast

C:Superfamily: cytochrome c-type synthesis protein

C:Keywords: chloroplast

Query Match 66.7%; Score 36; DB 2; Length 65;

Best Local Similarity 75.0%; Pred. No. 3.7;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAS 10

|||||

Db 57 HSYGSFAS 64

RESULT 7

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 393-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 4.6;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 8

S48566

hypothetical protein YLR215c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L8167.23
C:Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Nov-1999
C:Accession: S48566
R:Pauley, A.
submitted to the EMBL Data Library, September 1994
A:Description: The sequence of S. cerevisiae cosmid 8167.
A:Reference number: S48545
A:Accession: S48566
A:Molecule type: DNA
A:Residues: 1-360 <PAU>
A:Cross-references: EMBL:U14913; NID:g544497; PIDN:AAB67444.1; PID:g544519; GSPDB:GN0001
C:Genetics:
A:Gene: MIPS:YLR215C
A:Map position: 12R
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215C

Query Match 66.7%; Score 36; DB 2; Length 360;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
||||| I
Db 304 RHNTGRFAS 312

RESULT 9
I59634
MHC class II DR-beta-1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I59634
R:Lin, Y.N.; Ren, E.C.; Chan, S.H.
Tissue Antigens 41, 204-205, 1993
A:Title: A new DR11 allele in Singaporean Chinese.
A:Reference number: I59634; MUID:93369836
A:Accession: I59634
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-85 <RES>
A:Cross-references: GB:M98436; NID:g187890; PIDN:AAA59693.1; PID:g187891
C:Genetics:
A:Gene: HLA-DRB1-11
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 85;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
||||| I
Db 75 RHNYGAVES 83

RESULT 10
S38676
MHC class II histocompatibility antigen HLA-DR-01 beta chain - Galago moholi (fragment)
C:Species: Galago moholi
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C:Accession: S38676
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38676
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27130; NID:g415801; PIDN:CAA81657.1; PID:g1132545
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
||||| I
Db 75 RHNYGAVES 83

RESULT 11
S38680
MHC class II histocompatibility antigen HLA-DR-05 beta chain - Galago moholi (fragment)
C:Species: Galago moholi
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C:Accession: S38680
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38680
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27134; NID:g415805; PIDN:CAA81661.1; PID:g1132549
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
||||| I
Db 75 RHNYGAVES 83

RESULT 12
S57512
MHC class II histocompatibility antigen HLA-DR beta 1 chain DRB1*08 precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S57512; I79647
R:Versluis, L.F.; Savelkoul, P.; van der Zwan, A.W.; van den Berg-Loonen, E.; Tilanus
submitted to the EMBL Data Library, June 1995
A:Reference number: S57512
A:Accession: S57512
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <VER>
A:Cross-references: EMBL:X88854; NID:g887451; PIDN:CAA61324.1; PID:g887452
R:Gyllenstein, U.B.; Sundvall, M.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3686-3690, 1991
A:Title: Allelic diversity is generated by intraexon sequence exchange at the DRB1 10
A:Reference number: I59196; MUID:91219437
A:Accession: I79647
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-73 <RES>
A:Cross-references: GB:M63196; NID:g181762; PIDN:AAA52321.1; PID:g181763
C:Genetics:
A:Gene: GDB:HLA-DRB1
A:Cross-references: GDB:120642
A:Map position: 6p21.3-6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
||||| I
Db 75 RHNYGAVES 83

RESULT 13

WMBP7Z

gene 7 protein - phage pZA

C:Species: phage pZA

A:Note: host Bacillus subtilis

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999

C:Accession: A24831

R:Paces, V.; Vlcek, C.; Urbanek, P.

Gene 4, 107-114, 1986

A:Title: Nucleotide sequence of the late region of Bacillus subtilis phage pZA, a close

A:Reference number: A91550; MUID:87031573

A:Accession: A24831

A:Molecule type: DNA

A:Residues: 1-98 <PAC>

A:Cross-references: GB:M11813; GB:M13904; GB:M13905; NID:g216046; PIDN:AAA88483.1; PID:g

C:Genetics:

A:Gene: 7

C:Superfamily: phage pZA gene 7 protein

C:Keywords: late protein

Query Match	64.8%	Score 35;	DB 1;	Length 98;
Best Local Similarity	77.8%	Pred. No. 8.6;		
Matches	7;	Conservative	0;	Mismatches
			2;	Indels
			0;	Gaps

QY 2 RHNYGSEAS 10
| | | | | |
Db 33 RVNYGSEVS 41

RESULT 14
WMBPF9
gene 7 protein - phage phi-29
N:Alternate names: head morphogenesis protein
C:Species: phage phi-29
A:Note: host Bacillus subtilis
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: A28923; A25816
R:Innis, C.A.; Garvey, K.J.; Ito, J.
Nucleic Acids Res. 14, 7129, 1986
A:Title: Nucleotide sequence of phage phi-29 gene 7: structure of intergenic spacer between gene 7 and gene 8
A:Reference number: A28923; MUID:87016351
A:Accession: A28923
A:Molecule type: DNA
A:Residues: 1-98 <INN>
A:Cross-references: GB:X04386; NID:g15522; PIDN:CAA27974.1; PID:g15524
R:Vicek, C.; Paces, V.
Gene 46, 215-225, 1986
A:Title: Nucleotide sequence of the late region of Bacillus phage phi-29 completes the 11.5 kb genome
A:Reference number: A25816; MUID:87106857
A:Accession: A25816
A:Molecule type: DNA
A:Residues: 1-98 <VLC>
A:Cross-references: GB:M14782; NID:g215323; PIDN:AAA32279.1; PID:g215324
C:Genetics:
A:Gene: 7
C:Superfamily: phage PZA gene 7 protein
C:Keywords: head protein; late protein

Query Match	64.8%	Score 35;	DB 1;	Length 98;
Best Local Similarity	77.8%	Pred. No. 8.6;		
Matches	7;	Conservative	0;	Mismatches
			2;	Indels
			0;	Gaps

Qy 2 RHNYGSFAS 10
Db 33 RVNYGSFVS 41

RESULT	15	beta chain precursor - human (fra
C25239	II histocompatibility antigen HLA-DR-3-MN2-2	
MHC class II		

C;Species: Homo sapiens (man)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 03-May-1996
C;Accession: C25239
R;Wu, S.; Saunders, T.L.; Bach, F.H.
Nature 324, 676-679, 1986
A;Title: Polymorphism of human Ia antigens generated by reciprocal intergenic exchange
A;Reference number: A25239; MUID: 87090380
A;Accession: C25239
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <WUS>
C;Superfamily: class II histocompatibility antigen: immunoglobulin homology

Query Match	64.8%	Score 35;	DB 2;	Length 123;
Best Local Similarity	66.7%	Pred. NO. 11;		
Matches	6;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy 2 RHNYGSFAS 10
 ||||: |
 Db 109 RHNYGAVES 117

Search completed: March 28, 2001, 07:04:19
Job time: 1057 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:34:58 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec.

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	36	66.7	65	1	CCSA_PEA	P31172 pisum sativ
2	36	66.7	328	1	CCSA_ARATH	P56770 arabidopsis
3	35	64.8	98	1	VG7_BPPH2	P13848 bacterioph
4	35	64.8	98	1	VG7_BPPZA	P07533 bacterioph
5	35	64.8	313	1	CCSA_TORAC	P12216 nicotiana t
6	34	63.0	275	1	IF2A_PYPAB	Q9v0e4 pyrococcus
7	34	63.0	275	1	IF2A_PYRHO	Q58655 pyrococcus
8	34	63.0	284	1	IPYR_PICPA	O13505 pichia past
9	34	63.0	286	1	IPYR_KLULA	P13998 kluyveromyc
10	34	63.0	286	1	IPYR_YEAST	P00817 saccharomyc
11	33	61.1	266	1	HB2D_CANFA	P18470 canis fami
12	33	61.1	322	1	FATB_VIBAN	P11460 vibrio angu
13	33	61.1	398	1	PF21_ARATH	Q04088 arabidopsis
14	33	61.1	448	1	NCAP_CVHOC	P33469 human coron
15	33	61.1	470	1	SYE2_RICPR	Q9zct8 rickettsia
16	33	61.1	473	1	SYE_AQUAE	O67271 aquifex aeo
17	33	61.1	639	1	Y119_MYCTU	Q50614 mycobacteri
18	33	61.1	682	1	VG50_BPMLS	Q05262 mycobacteri
19	33	61.1	1254	1	MDR3_CAEEL	P34713 caenorhabd
20	32	59.3	65	1	CCSA_OENBE	P31565 oenothera b
21	32	59.3	196	1	WBBJ_ECOLI	P37750 escherichia
22	32	59.3	198	1	HB2G_HUMAN	P01911 homo sapien
23	32	59.3	213	1	PNCA_ECOLI	P21369 escherichia
24	32	59.3	251	1	SAST_ANAPL	P00633 anas platyr
25	32	59.3	266	1	HB2A_HUMAN	P01913 homo sapien
26	32	59.3	266	1	HB2B_HUMAN	P01912 homo sapien
27	32	59.3	266	1	HB2C_HUMAN	P01914 homo sapien
28	32	59.3	266	1	HB2D_HUMAN	P13759 homo sapien
29	32	59.3	266	1	HB2E_HUMAN	P04229 homo sapien
30	32	59.3	266	1	HB2F_HUMAN	P13758 homo sapien
31	32	59.3	266	1	HB2H_HUMAN	P13760 homo sapien
32	32	59.3	266	1	HB2I_HUMAN	P20039 homo sapien
33	32	59.3	266	1	HB2J_HUMAN	P13761 homo sapien

34	32	59.3	321	1	CCSA_MAIZE	P46659 zea mays (m
35	32	59.3	321	1	CCSA_ORISA	P12215 oryza sativ
36	32	59.3	349	1	YJY9_YEAST	P41903 saccharomyc
37	32	59.3	528	1	PR12_YEAST	P20457 saccharomyc
38	32	59.3	629	1	KSYK_RAT	Q64725 rattus norv
39	32	59.3	649	1	GPDM_SCHPO	O14400 schizosacch
40	32	59.3	1267	1	VL3_REOVL	P17378 reovirus (c
41	32	59.3	1267	1	VL3_REOVL	P17376 reovirus (c
42	31	57.4	93	1	RT19_MARPO	P26874 marchantia
43	31	57.4	201	1	PRCG_HUMAN	P49721 homo sapien
44	31	57.4	201	1	PRCG_MOUSE	Q9rip3 mus musculu
45	31	57.4	201	1	PRCG_RAT	P40307 rattus norv

ALIGNMENTS

RESULT 1.			
CCSA_PEA	STANDARD;	PRT;	65 AA.
ID CCSA_PEA			
AC P31172;			
DT 01-JUL-1993 (Rel. 26, Created)			
DT 01-JUL-1993 (Rel. 26, Last sequence update)			
DT 01-NOV-1997 (Rel. 35, Last annotation update)			
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).			
GN CCSA.			
OS Pisum sativum (Garden pea).			
OG Chloroplast.			
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1;			
OC Fabales; Fabaceae; Papilionoideae; Pisum.			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CV. ALASKA;			
RX MEDLINE; 91355950.			
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;			
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene			
RT in pea chloroplasts.";			
RL Plant Mol. Biol. 17:541-545(1991).			
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF			
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CC -----			
DR EMBL; X59015; CA441754.1; -			
DR PIR; S17441; S17441.			
KW Cytochrome c-type biogenesis; Chloroplast.			
FT NON_TER 1			
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;			
Query Match 66.7%; Score:36; DB 1; Length 65;			
Best Local Similarity 75.0%; Pred. No. 1;			
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY 3 HNYGSPAS 10			
Db 57 HSYGSPTS 64			
RESULT 2			
CCSA_ARATH	STANDARD;	PRT;	328 AA.
ID CCSA_ARATH			
AC P56770;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsids.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
 RT "Complete structure of the chloroplast genome of Arabidopsis
 thaliana.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCL1/NRFE/CCSA FAMILY.
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 CC -----
 DR EMBL; AF000423; BAA84436.1; -;
 DR INTERPRO; IPR002541; -;
 DR PFAM; PF01578; CytC_asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 66.7%; Score 36; DB 1; Length 328;
 Best Local Similarity 75.0%; Pred. No. 5.8;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAS 10
 DB 320 HSYGSFAS 327
 RESULT 3
 VG7_BPPH2
 ID VG7_BPPH2 STANDARD; PRT; 98 AA.
 AC PI3848;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
 GN 7.
 OS Bacteriophage phi-29.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87106857.
 RA Vitek C., Paces V.;
 RT "Nucleotide sequence of the late region of Bacillus phage phi 29
 completes the 19,285-bp sequence of phi 29 genome. Comparison with
 the homologous sequence of phage PZA.";
 RL Gene 46:215-225(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87016351.
 RA Innis C.A., Garvey K.J., Ito J.;
 RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
 spacer between the major early and late genes.";
 RL Nucleic Acids Res. 14:7129-7129(1986).
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 CC -----
 DR EMBL; M14782; AAA32279.1; -;
 DR EMBL; X04386; CAA27974.1; -;
 DR PIR; A28923; WMBP79.
 KW Late protein.
 SQ SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 2.5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 DB 33 RVNYGSFVS 41
 RESULT 4
 VG7_BPPZA
 ID VG7_BPPZA STANDARD; PRT; 98 AA.
 AC P07533;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
 GN 7.
 OS Bacteriophage PZA.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87031573.
 RA Paces V., Vitek C., Urbanek P.;
 RT "Nucleotide sequence of the late region of Bacillus subtilis phage
 PZA, a close relative of phi 29.";
 RL Gene 44:107-114(1986).
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 CC -----
 DR EMBL; M11813; AAA88483.1; -;
 DR PIR; A24831; WMBP72.
 KW Late protein.
 SQ SEQUENCE 98 AA; 11281 MW; 444408C39B606A25 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 2.5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 DB 33 RVNYGSFVS 41
 RESULT 5
 CCSA_TOBAC
 ID CCSA_TOBAC STANDARD; PRT; 313 AA.
 AC P12216;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Nicotiana tabacum (Common tobacco).

OG Chloroplast.
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 CC Solanales; Solanaceae; Nicotiana.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=CV. BRIGHT YELLOW 4;
 RA Suglura M.;
 RL Submitted (AUG-1986) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP COMPLETE GENOME.
 RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
 RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
 RA Yamaguchi-Shinozaki K., Ohno C., Torazawa K., Meng B.Y., Sugita M.,
 RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
 RA Tohdoh N., Shimada H., Suglura M.;
 RA "The complete nucleotide sequence of the tobacco chloroplast genome:
 RT its gene organization and expression.";
 RL EMOB J. 5:2043-2049(1986).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLL/NRFE/CCSA FAMILY.
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 CC -----
 CC EMBL; 200044; CAA77395.1; -
 DR PIR; A05213; A05213.
 DR INTERPRO; IPR002541; -
 DR PFAM; PF01578; CytC.asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 313 AA; 35358 MW; 0C93417F79C47A96 CRC64;
 Query Match 64.8%; Score 35; DB 1; Length 313;
 Best Local Similarity 75.0%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAS 10
 Db 303 HSYGSFSP 310
 RESULT 6
 ID IF2A_PVRAB STANDARD; PRT; 275 AA.
 AC Q9Y0E4;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PAB0568.
 OS Pyrococcus abyssi.
 CC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORSAY;
 RA Hellig R.;
 RA "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -----
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 CC -----
 CC EMBL; 200044; BAA30058.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 Db 23 HNYGAF 28
 RESULT 7
 ID IF2A_PVRHO STANDARD; PRT; 275 AA.
 AC Q58655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 CC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE; 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
 CC -----
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 CC -----
 CC EMBL; 200044; BAA30058.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

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 CC -----
 CC EMBL; AJ248285; CAB49760.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83
 SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;
 Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 Db 23 HNYGAF 28
 RESULT 7
 ID IF2A_PVRHO STANDARD; PRT; 275 AA.
 AC Q58655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 CC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE; 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AP000004; BAA30058.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DB 23 HNYGAF 28

RESULT 8

ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC OI3505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 13-JUL-1998 (Rel. 36, Last sequence update)
 DT 13-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRRL Y-11430;
 RX MEDLINE: 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
 RT HIS3 genes";
 RL Yeast 14:861-867(1998).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -!- MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ001000; CAA04453.1; -
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolyase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 30AD27970D7775D6 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DB 91 HNYGAF 96

RESULT 9

ID IPYR_KLUJA STANDARD; PRT; 286 AA.
 AC PI3998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E.COLI AND YEAST PPASES.
 RX MEDLINE; 90234161.
 RA Lahti R., Koliakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -!- MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X14230; CAA32446.1; -
 DR PIR; S07894; PWKLI.
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolyase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DB 91 HNYGAF 96

RESULT 10

ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomyces.

RP [1].
RC SEQUENCE FROM N.A.
RX STRAIN=X2180;
RA MEDLINE; 89083474.
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=S288C;
RX MEDLINE; 95203288.
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a *Saccharomyces cerevisiae* protein
RT database";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE; 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT *Saccharomyces cerevisiae*";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE; 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase.";
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyttia T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of *Saccharomyces cerevisiae*
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]

RP SIMILARITY TO E. COLI AND K. LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihtinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and *E. coli*
RT inorganic pyrophosphatases";
RL Biochim. Biophys. Acta 1038:338-345(1990).
RC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
CC EMBL; X13253; CA31629.1; -;
DR EMBL; Z35880; CAAB4949.1; -;
DR PIR; S45864; PWB.
DR PDB; 1PY; 15-OCT-91.
DR PDB; 1YPP; 07-DEC-96.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1WGU; 19-NOV-97.
DR PDB; 1HUK; 08-APR-98.
DR PDB; 1HUK; 08-APR-98.
DR PDB; 117E; 23-DEC-98.
DR PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -;
DR SGD; S0000215; IPPL.
DR INTERPRO; IPR001596; -;
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolyase; Magnesium; 3D-structure.
FT INIT_MET 0 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT STRAND 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197

FT STRAND 203 203
 FT HELIX 205 207
 FT STRAND 210 210
 FT HELIX 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DB 91 HNYGAF 96

RESULT 11
 HB2D_CANFA STANDARD; PRT; 266 AA.
 AC P18470;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE DLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN PRECURSOR.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90316610.
 RA Sarmiento U.M., Storb R.;
 RT "Nucleotide sequence of a dog DRB cDNA clone.";
 RL Immunogenetics 31:396-399(1990).
 CC -----
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 CC -----
 CC EMBL; M29611; AAA30874.1; -
 CC PIR; A45844; A45844.
 CC HSP; P13760; 25EB.
 CC INTERPRO; IPR000353; -
 CC INTERPRO; IPR000495; -
 CC INTERPRO; IPR003006; -
 CC PFAM; PF00969; MHC_II_beta; 1.
 CC PRAM; PF00047; Ig; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 266
 FT DLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
 FT DR-1 BETA CHAIN.
 FT EXTRACELLULAR BETA-1.
 FT EXTRACELLULAR BETA-2.
 FT CYTOPLASMIC TAIL.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 266 AA; 30151 MW; 4E8297BBF1ACDD67 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 266;
 Best Local Similarity 66.7%; Pred. No. 18;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 HNYGSFAS 10
 DB 109 HNYGVIES 117

RESULT 12
 FATB_VIBAN STANDARD; PRT; 322 AA.
 AC P11460;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE FERRIC ANGUIBACTIN-BINDING PROTEIN PRECURSOR.
 GN FATB
 OS Vibrio anguillarum.
 OG Plasmid pJMI.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-775;
 RX MEDLINE; 88139336.
 RA Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
 RT "Genetic and molecular characterization of essential components of
 the Vibrio anguillarum plasmid-mediated iron-transport system.";
 RL J. Biol. Chem. 263:2853-2860(1988).
 RN [2]
 RP SEQUENCE OF 1-154 FROM N.A.
 RC STRAIN-775;
 RX MEDLINE; 92084677.
 RA Koester W.L., Actis L.A., Waldbeser L.S., Tolmasky M.E., Crosa J.H.;
 RT "Molecular characterization of the iron transport system mediated by
 the pJMI plasmid in Vibrio anguillarum 775.";
 RL J. Biol. Chem. 266:23829-23833(1991).
 CC -!- FUNCTION: BINDS FERRIC ANGUIBACTIN; PART OF THE BINDING-PROTEIN-
 CC DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIC ANGUIBACTIN.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE INNER MEMBRANE BY A LIPID
 CC ANCHOR (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 CC PROTEIN FAMILY 8.
 CC -----
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 CC -----
 CC EMBL; J03529; AAA91380.1; -
 CC EMBL; M74068; AAA25643.1; ALT_INIT.
 CC PIR; A29928; A29928.
 CC INTERPRO; IPR002491; -
 CC PFAM; PF01497; Peripla_BP_2; 1.
 CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 CC TRANSPOSIT; Iron transport; Signal; Inner membrane; Lipoprotein;
 CC Plasmid.
 FT SIGNAL -1 22 POTENTIAL.
 FT CHAIN 23 322 FERRIC ANGUIBACTIN-BINDING PROTEIN.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 322 AA; 35635 MW; FB8674EED5CF3F7 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 322;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAS 10
 DB 203 HNYGSFSS 210

```

RESULT 13
PF21_ARATH
ID PF21_ARATH STANDARD; PRT; 398 AA.
AC Q04088;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE POSSIBLE TRANSCRIPTION FACTOR POSF21.
GN POSF21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ZURICH; TISSUE=LEAF;
RX MEDLINE; 93251100.
RA Aeschbacher R.A., Schrott M., Potrykus I., Saul M.W.;
RT "Isolation and molecular characterization of PosF21, an Arabidopsis
RT thaliana gene which shows characteristics of a b-zip class
RT transcription factor.";
RL Plant J. 1:303-316(1991).
CC -1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR WITH AN ACTIVATORY
CC ROLE.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY AT A LOW LEVEL IN
CC -1- YOUNG SEEDLINGS AND IN ROOTS, STEMS AND LEAVES OF MATURE
CC ARABIDOPSIS PLANTS.
CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X61031; CAA43366.1; -
DR INTERPRO; IPR001871; -
DR PFAM; PF00170; BZIP; 1.
DR PROSITE; PS00036; BZIP_BASIC; FALSE_NEG.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 203 222
FT DOMAIN 229 264 BASIC MOTIF.
FT DOMAIN 340 364 LEUCINE-ZIPPER.
FT DOMAIN 354 372 POLY-GLN.
FT DOMAIN 354 372 POLY-GLN.
SQ SEQUENCE 398 AA; 44689 MW; 2DAA9EC9B9C14D11 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 398;
Best Local Similarity 85.7%; Pred. NO. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGFSAS 10
Db 305 NYGFSGS 311

RESULT 14
NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE POSSIBLE TRANSCRIPTION FACTOR POSF21.
GN POSF21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ZURICH; TISSUE=LEAF;
RX MEDLINE; 93251100.
RA Aeschbacher R.A., Schrott M., Potrykus I., Saul M.W.;
RT "Isolation and molecular characterization of PosF21, an Arabidopsis
RT thaliana gene which shows characteristics of a b-zip class
RT transcription factor.";
RL Plant J. 1:303-316(1991).
CC -1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR WITH AN ACTIVATORY
CC ROLE.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY AT A LOW LEVEL IN
CC -1- YOUNG SEEDLINGS AND IN ROOTS, STEMS AND LEAVES OF MATURE
CC ARABIDOPSIS PLANTS.
CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
CC -----
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CC -----
DR EMBL; X61031; CAA43366.1; -
DR INTERPRO; IPR001871; -
DR PFAM; PF00170; BZIP; 1.
DR PROSITE; PS00036; BZIP_BASIC; FALSE_NEG.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 203 222
FT DOMAIN 229 264 BASIC MOTIF.
FT DOMAIN 340 364 LEUCINE-ZIPPER.
FT DOMAIN 354 372 POLY-GLN.
FT DOMAIN 354 372 POLY-GLN.
SQ SEQUENCE 398 AA; 44689 MW; 2DAA9EC9B9C14D11 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 398;
Best Local Similarity 85.7%; Pred. NO. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGFSAS 10
Db 305 NYGFSGS 311

RESULT 15
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2)
DE GLTX2 OR RP623.
GN Rickettsia prowazekii.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ235272; CAA15066.1; -
DR HSP; P27000; IGLN.
DR INTERPRO; IPR000924; -
DR INTERPRO; IPR001412; -
DR PFAM; PF00749; trna-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSK" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFCE50A20B8A9FD CRC64;

Query Match 61.1%; Score 33; DB 1; Length 470;

```

```

RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR INTERPRO; IPR001218; -
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193ABIAE0D75626 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. NO. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 103 RHNRGSF 109

RESULT 15
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2)
DE GLTX2 OR RP623.
GN Rickettsia prowazekii.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -
DR HSP; P27000; IGLN.
DR INTERPRO; IPR000924; -
DR INTERPRO; IPR001412; -
DR PFAM; PF00749; trna-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSK" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFCE50A20B8A9FD CRC64;

Query Match 61.1%; Score 33; DB 1; Length 470;

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Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | |
Db 31 ARHNGKF 38

Search completed: March 28, 2001, 07:35:00
Job time: 137 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:02 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	79.6	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	41	75.9	89	7 Q19495	Q19495 gallus gall
3	40	74.1	446	5 O62086	O62086 caenorhabdi
4	39	72.2	39	7 P79474	P79474 cervus elap
5	39	72.2	39	7 P79477	P79477 cervus elap
6	39	72.2	39	7 P79478	P79478 cervus elap
7	39	72.2	39	7 P79479	P79479 cervus elap
8	39	72.2	76	7 Q9TPC2	Q9TPC2 macaca mula
9	39	72.2	82	7 Q30606	Q30606 macaca mula
10	39	72.2	82	7 Q30608	Q30608 macaca mula
11	39	72.2	82	7 Q30637	Q30637 macaca mula
12	39	72.2	82	7 Q30638	Q30638 macaca mula
13	39	72.2	82	7 Q30658	Q30658 macaca mula
14	39	72.2	82	7 Q30659	Q30659 macaca mula
15	39	72.2	82	7 Q30666	Q30666 macaca mula
16	39	72.2	82	7 Q30667	Q30667 macaca mula
17	39	72.2	82	7 Q30668	Q30668 macaca mula
18	39	72.2	82	7 Q19287	Q19287 macaca mula
19	39	72.2	82	7 Q19288	Q19288 macaca mula

20	39	72.2	82	7 Q9TPC9	Q9TPC9 callicebus
21	39	72.2	82	7 Q9MXN1	Q9MXN1 macaca mula
22	39	72.2	83	6 Q9TSS5	Q9TSS5 bos indicus
23	39	72.2	83	7 Q98002	Q98002 ovis aries
24	39	72.2	85	7 Q30796	Q30796 ovis aries
25	39	72.2	85	7 Q30800	Q30800 ovis aries
26	39	72.2	85	7 Q30803	Q30803 ovis aries
27	39	72.2	85	7 Q30812	Q30812 ovis aries
28	39	72.2	85	7 P79966	P79966 capra aegag
29	39	72.2	85	7 P79967	P79967 capra aegag
30	39	72.2	85	7 P79968	P79968 capra aegag
31	39	72.2	86	7 Q30326	Q30326 bos taurus
32	39	72.2	89	7 Q19210	Q19210 capra hircu
33	39	72.2	89	7 Q19212	Q19212 capra hircu
34	39	72.2	89	7 Q30521	Q30521 galago sene
35	39	72.2	89	7 Q30522	Q30522 galago sene
36	39	72.2	89	7 Q30526	Q30526 galago sene
37	39	72.2	89	7 Q30217	Q30217 homo sapien
38	39	72.2	89	7 Q9MXW8	Q9MXW8 aotus nancy
39	39	72.2	89	7 Q9MXW4	Q9MXW4 aotus nancy
40	39	72.2	89	7 Q9MXW3	Q9MXW3 aotus nancy
41	39	72.2	89	7 Q9MXV8	Q9MXV8 aotus nancy
42	39	72.2	89	7 Q9MXV7	Q9MXV7 aotus nancy
43	39	72.2	89	7 Q9MXV5	Q9MXV5 aotus nancy
44	39	72.2	89	7 Q9MXU6	Q9MXU6 aotus nancy
45	39	72.2	89	7 Q9MXU5	Q9MXU5 aotus nancy

ALIGNMENTS

RESULT 1

Q9LIE5
ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AF001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 79.6%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

Db 274 SRHNYGSF 281

RESULT 2

Q19495

ID O19495 PRELIMINARY; PRT; 89 AA.
 AC O19495;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15.15I-5; TISSUE=BURSA;
 RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
 RL Immunogenetics 47:350-354(1998).
 DR EMBL; U91532; AAC15813.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEBI379 CRC64;

 Query Match 75.9%; Score 41; DB 7; Length 89;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 RHNYGSFAS 10
 ID 75 RHNYGDFES 83
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE C31H5 6 PROTEIN.
 GN C31H5.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans".
 RL Nature 368:32-38(1994).
 DR EMBL; Z93778; CAB07846.1; -.
 DR INTERPRO; IPR000379; -.
 DR INTERPRO; IPR002925; -.
 DR PFAM; PF01738; DLH; 2.
 SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 74.1%; Score 40; DB 5; Length 446;
 Best Local Similarity 77.8%; Pred. No. 7.3;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNYGSFAS 10
 ID 51 RHNYGSHAA 59
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.89;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 RHNYGSFAS 10
 ID 25 RHNYGVFES 33
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3CID CRC64;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.89;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 RHNYGSFAS 10

```

Db      25 RHNYGVFES 33
      ||||| | |
RESULT  6
ID      P79478      PRELIMINARY;      PRT;      39 AA.
AC      P79478;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DE      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE      01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE      MHC CLASS II DRB (FRAGMENT).
OS      Cervus elaphus (Red deer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC      Cervidae; Cervinae; Cervus.
OX      NCBI_TaxID=9860;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Swarbrick P.A., Crawford A.M.;
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U63081; AAB37781.1; -.
KW      MHC.
FT      NON_TER      1
FT      NON_TER      39
SQ      SEQUENCE      39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match      72.2%; Score 39; DB 7; Length 39;
Best Local Similarity      77.8%; Pred. No. 0.89;
Matches      7; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      2 RHNYGSFAS 10
      ||||| | |
Db      25 RHNYGVFES 33

RESULT  7
ID      P79479      PRELIMINARY;      PRT;      39 AA.
AC      P79479;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DE      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE      01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE      MHC CLASS II DRB (FRAGMENT).
OS      Cervus elaphus (Red deer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC      Cervidae; Cervinae; Cervus.
OX      NCBI_TaxID=9860;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Swarbrick P.A., Crawford A.M.;
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U63082; AAB37782.1; -.
KW      MHC.
FT      NON_TER      1
FT      NON_TER      39
SQ      SEQUENCE      39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match      72.2%; Score 39; DB 7; Length 39;
Best Local Similarity      77.8%; Pred. No. 0.89;
Matches      7; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      2 RHNYGSFAS 10
      ||||| | |
Db      25 RHNYGVFES 33

RESULT  8
Q9TPC2
ID      Q9TPC2      PRELIMINARY;      PRT;      76 AA.

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AC      Q9TPC2;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE      MHC CLASS II ANTIGEN (FRAGMENT).
GN      MAMU-DRB1.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Saueremann U., Khazand M., Nagy M., Peiberg C.;
RT      "Mhc-DQ-DRB-haplotype analysis in the rhesus macaque: evidence for a
RT      number of different haplotypes displaying a low allelic
RT      polymorphism.";
RL      Tissue Antigens 0:0-0(1999).
DR      EMBL; AF175315; AAF07040.1; -.
DR      INTERPRO; IPR000353; -.
DR      PFAM; PF00969; MHC_II_beta; 1.
KW      MHC.
FT      NON_TER      1
FT      NON_TER      76
SQ      SEQUENCE      76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match      72.2%; Score 39; DB 7; Length 76;
Best Local Similarity      77.8%; Pred. No. 1.8;
Matches      7; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      2 RHNYGSFAS 10
      ||||| | |
Db      67 RHNYGVFES 75

RESULT  9
Q30606
ID      Q30606      PRELIMINARY;      PRT;      82 AA.
AC      Q30606;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE      MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
GN      MHC-DRB.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97152405; PubMed=8995183;
RA      Knapp L.A., Cadavid L.F., Eberle M.E., Knechtle S.J., Bontrop R.E.,
RA      Watkins D.I.;
RT      "Identification of new mamu-DRB alleles using DGGE and direct
RT      sequencing.";
RL      Immunogenetics 45:171-179(1997).
DR      EMBL; U57948; AAC50981.1; -.
DR      INTERPRO; IPR000353; -.
DR      PFAM; PF00969; MHC_II_beta; 1.
KW      MHC.
FT      NON_TER      1
FT      NON_TER      82
SQ      SEQUENCE      82 AA; 9921 MW; CC75FCF5EB35EEC2 CRC64;

Query Match      72.2%; Score 39; DB 7; Length 82;
Best Local Similarity      77.8%; Pred. No. 1.9;
Matches      7; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      2 RHNYGSFAS 10
      ||||| | |

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Db 73 RHNYGVFES 81

RESULT 10
Q30608 ID Q30608 PRELIMINARY; PRT; 82 AA.
AC Q30608;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
GN MHC-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152405; PubMed=8995183;
RA Knapp L.A., Cadavid L.F., Eberle M.E., Knechtie S.J., Bontrop R.E.,
RA Watkins D.I.;
RT "Identification of new manu-DRB alleles using DGGE and direct
RT sequencing.";
RL Immunogenetics 45:171-179(1997).
DR EMBL; U57950; AAC50983.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9880 MW; C16CA448A7EF9148 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 11
Q30637 ID Q30637 PRELIMINARY; PRT; 82 AA.
AC Q30637;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1KM; TISSUE=BLOOD;
RX MEDLINE=93123123; PubMed=1478892;
RA Slierendregt B.L.; van Noort J.T.; Bakas R.M., Otting N., Jonker M.,
RA Bontrop R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
RT complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=1KL; TISSUE=BLOOD;
RX Slierendregt B.L.;
RL Submitted (Sep-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26141; CAA81142.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9953 MW; FB1B03E5209CD316 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 12
Q30638 ID Q30638 PRELIMINARY; PRT; 82 AA.
AC Q30638;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1KL; TISSUE=BLOOD;
RX MEDLINE=93123123; PubMed=1478892;
RA Slierendregt B.L.; van Noort J.T., Bakas R.M., Otting N., Jonker M.,
RA Bontrop R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
RT complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=1KL; TISSUE=BLOOD;
RX Slierendregt B.L.;
RL Submitted (Sep-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26141; CAA81142.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9953 MW; FB1B03E5209CD316 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 13
Q30658 ID Q30658 PRELIMINARY; PRT; 82 AA.
AC Q30658;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 10024 MW; FAAB1152D09CD306 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 12
Q30638 ID Q30638 PRELIMINARY; PRT; 82 AA.
AC Q30638;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1KL; TISSUE=BLOOD;
RX MEDLINE=93123123; PubMed=1478892;
RA Slierendregt B.L.; van Noort J.T., Bakas R.M., Otting N., Jonker M.,
RA Bontrop R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
RT complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=1KL; TISSUE=BLOOD;
RX Slierendregt B.L.;
RL Submitted (Sep-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26141; CAA81142.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9953 MW; FB1B03E5209CD316 CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
Db 73 RHNYGVFES 81

RESULT 13
Q30658 ID Q30658 PRELIMINARY; PRT; 82 AA.
AC Q30658;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1KL; TISSUE=BLOOD;
 RX MEDLINE=93123123; PubMed=1478892;
 RA Slierendregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
 Bontrop R.E.;
 RT "Evolutionary stability of transspecies major histocompatibility
 complex class II DRB lineages in humans and rhesus monkeys.";
 RL Hum. Immunol. 35:29-39(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1KL; TISSUE=BLOOD;
 RA Slierendregt B.L.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 226161; CA81162.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 82
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 9964 MW; 8AF2C663B1B4D4ED CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 1.9;
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QY 2 RHNYGSFAS 10
 DB 73 RHNYGVFES 81
 RESULT 14
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 ID Q30659 PRELIMINARY; PRT; 82 AA.
 AC Q30659;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
 GN MHC DR-BETA 5.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
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 RC STRAIN=1ME; TISSUE=BLOOD;
 RX MEDLINE=93123123; PubMed=1478892;
 RA Slierendregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
 Bontrop R.E.;
 RT "Evolutionary stability of transspecies major histocompatibility
 complex class II DRB lineages in humans and rhesus monkeys.";
 RL Hum. Immunol. 35:29-39(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1ME; TISSUE=BLOOD;
 RA Slierendregt B.L.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 226162; CA81163.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 82
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 9940 MW; CC81E33E81B8D69A CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;

Best Local Similarity 77.8%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNYGSFAS 10
 DB 73 RHNYGVFES 81
 RESULT 15
 Q30666
 ID Q30666 PRELIMINARY; PRT; 82 AA.
 AC Q30666;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
 GN MHC DR-BETA.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1MP; TISSUE=BLOOD;
 RX MEDLINE=93123123; PubMed=1478892;
 RA Slierendregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
 Bontrop R.E.;
 RT "Evolutionary stability of transspecies major histocompatibility
 complex class II DRB lineages in humans and rhesus monkeys.";
 RL Hum. Immunol. 35:29-39(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1MP; TISSUE=BLOOD;
 RA Slierendregt B.L.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 226170; CA81171.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 82
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 9881 MW; A0661E28A7F36AFB CRC64;

Query Match 72.2%; Score 39; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 DB 73 RHNYGVFES 81

Search completed: March 28, 2001, 07:53:02
 Job time: 495 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:46 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-68

Perfect score: 54

Sequence: 1 ARHNYGSFAS 10

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BLOSUM62

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	100.0	10	19 W76024	LM609 grafted anti
2	51	94.4	10	19 W76025	LM609 grafted anti
3	51	94.4	10	19 W76030	LM609 grafted anti
4	50	92.6	10	19 W76026	LM609 grafted anti
5	50	92.6	10	19 W76027	LM609 grafted anti
6	50	92.6	10	19 W76028	LM609 grafted anti
7	50	92.6	10	19 W76029	LM609 grafted anti
8	50	92.6	10	19 W76010	LM609 grafted anti
9	50	92.6	117	19 W76001	Vitaxin antibody h
10	50	92.6	117	19 W76003	LM609 antibody hea
11	50	92.6	117	20 Y06381	Murine monoclonal
12	50	92.6	117	20 Y06387	Humanised LM609 an

13	50	92.6	118	20 Y06384	Humanised LM609 an
14	50	92.6	118	20 Y06385	Humanised LM609 an
15	50	92.6	118	20 Y06386	Humanised LM609 an
16	50	92.6	118	20 Y06383	Murine monoclonal
17	50	92.6	130	20 Y06379	LM609 grafted anti
18	49	90.7	10	19 W76037	LM609 grafted anti
19	48	88.9	10	19 W76040	LM609 grafted anti
20	47	87.0	10	19 W76021	LM609 grafted anti
21	46	85.2	10	19 W76039	LM609 grafted anti
22	46	85.2	10	19 W76022	LM609 grafted anti
23	46	85.2	10	19 W76023	LM609 grafted anti
24	45	83.3	10	19 W76020	LM609 grafted anti
25	43	79.6	10	19 W76038	LM609 grafted anti
26	42	77.8	110	20 W84099	Vitronectin alpha-
27	42	77.8	117	20 W84093	Murine vitronectin
28	42	77.8	117	20 W84097	Humanised anti-alp
29	41	75.9	8	20 Y06371	Murine monoclonal
30	37	68.5	119	19 Y86109	S. pneumoniae deri
31	36	66.7	117	16 R79157	Human IgE receptor
32	36	66.7	117	16 R79155	Human IgE receptor
33	36	66.7	117	18 W27357	Heavy chain variab
34	36	66.7	117	18 W27526	Heavy chain variab
35	36	66.7	117	18 W27354	Heavy chain variab
36	36	66.7	119	18 W01578	Lead binding Mab 8
37	36	66.7	239	20 W73874	Human antiFc epsil
38	36	66.7	242	20 W73876	Human antiFc epsil
39	35	64.8	89	17 Y14338	Protein encoded by
40	35	64.8	89	17 Y14306	Protein encoded by
41	35	64.8	89	17 Y14307	Protein encoded by
42	35	64.8	954	21 Y80092	Vitamin B12 transp
43	34	63.0	30	21 Y81870	Yeast IPPI protein
44	33	61.1	80	12 R13396	HLA-DRW12a antigen
45	33	61.1	80	12 R13397	HLA-DRW12b antigen

ALIGNMENTS

```
RESULT 1
W76024
ID W76024 standard; Protein; 10 AA.
XX
XX W76024;
AC
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX W09833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX N-PSDB; V49861.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
```

PT integrin - and related grafted antibodies based on murine monoclonal
 CC LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNYGSPAS 10
 Db 1 arhnygsfas 10
 |||||||||
 1 arhnygsfas 10
 RESULT 2
 W76025
 ID W76025 standard; Protein; 10 AA.
 XX
 AC W76025;
 XX
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #7.
 DE
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 XX WPI: 1998-437472/37.
 DR N-PSDB; V49862.
 XX
 XX Humanised antibody, vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 CC LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 94.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0043;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNYGSPAS 10
 Db 1 arhnygsfas 10
 |||||||||
 1 arhnygsfas 10
 RESULT 3
 W76030
 ID W76030 standard; Protein; 10 AA.
 XX
 AC W76030;
 XX
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #12.
 DE
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 XX WPI: 1998-437472/37.
 DR N-PSDB; V49867.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 CC LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 94.4%; Score 51; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0043;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAS 10
 Db 1 arhnygsfaa 10
 |||||

RESULT 4

W76026
 ID W76026 standard; Protein; 10 AA.

XX AC

XX AC

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #8.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

RESULT 5

W76027
 ID W76027 standard; Protein; 10 AA.

XX AC

XX AC

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||

```

Db      1 arhnygsfa 9
RESULT      6
W76028
ID      W76028 standard; Protein; 10 AA.
AC      W76028;
XX
XX      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #10.
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX      LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX      macular degeneration; osteoporosis; primer; V-H region; CDR;
XX      complementarity determining region.
XX
XX      Mus sp.
XX
XX      WO9833919-A2.
XX
XX      06-AUG-1998.
XX
XX      30-JAN-1998; 98WO-US01826.
XX
XX      30-JAN-1997; 97US-0791391.
XX
XX      (IXSY-) IXSYS INC.
XX
XX      Glaser SM, Huse WD;
XX
XX      WPI; 1998-437472/37.
XX
XX      N-PSDB; V49865.
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX      integrin - and related grafted antibodies based on murine monoclonal
XX      LM609, also related nucleic acid, used to treat, prevent or diagnose
XX      angiogenesis or restenosis
XX
XX      Claim 62; Page 41; 129pp; English.
XX
XX      W76007-W76040 are protein fragments of the grafted monoclonal antibody
XX      LM609 heavy and light chain variable region. LM609 and the antibody
XX      vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX      inhibit binding of alphavbeta3 to a ligand and thus block
XX      integrin-mediated signal transduction. This is useful in the treatment,
XX      prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
XX      arthritis, macular degeneration, osteoporosis etc.). The antibodies
XX      contain non-murine framework regions so are suitable for use in humans.
XX      Enhanced types of LM609 have affinity more than 90 times greater than
XX      that of parent the parent antibody.
XX
XX      Sequence 10 AA;
XX
XX      Query Match      92.6%; Score 50; DB 19; Length 10;
XX      Best Local Similarity 100.0%; Pred. No. 0.0065;
XX      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 ARHNYGSFA 9
XX      Db      1 arhnygsfa 9
XX
XX      RESULT      7
XX      W76029
XX      ID      W76029 standard; Protein; 10 AA.
XX
XX      Query Match      92.6%; Score 50; DB 19; Length 10;
XX      Best Local Similarity 100.0%; Pred. No. 0.0065;
XX      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 ARHNYGSFA 9
XX      Db      1 arhnygsfa 9
XX
XX      RESULT      8
XX      W76010
XX      ID      W76010 standard; Protein; 10 AA.
XX
XX      AC      W76010;
XX
XX      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

```

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 XX
 XX PD 06-AUG-1998.
 XX
 XX PF 30-JAN-1998; 98WO-US01826.
 XX
 XX PR 30-JAN-1997; 97US-0791391.
 XX
 XX PA (IXSY-) IXSYS INC.
 XX
 XX PI Glaser SM, Huse WD;
 XX
 XX DR WPI: 1998-437472/37.
 XX
 XX DR N-PSDB; V49847.
 XX
 XX PS Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 XX LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 XX
 XX PS Disclosure; Page 40; 129pp; English.
 XX
 XX CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
 XX inhibit binding of alphavbeta3 to a ligand and thus block
 XX integrin-mediated signal transduction. This is useful in the treatment,
 XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
 XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 XX arthritis, macular degeneration, osteoporosis etc.). The antibodies
 XX contain non-murine framework regions so are suitable for use in humans.
 XX Enhanced types of LM609 have affinity more than 90 times greater than
 XX that of parent the parent antibody.
 XX
 XX SO Sequence 10 AA;

 Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

 RESULT 9
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 XX AC W76001;
 XX
 XX DT 02-NOV-1998 (first entry)
 XX
 XX DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 XX OS Mus sp.
 XX
 XX PN WO9833919-A2.
 XX
 XX PD 06-AUG-1998.
 XX
 XX PF 30-JAN-1998; 98WO-US01826.
 XX
 XX PR 30-JAN-1997; 97US-0791391.
 XX
 XX PA (IXSY-) IXSYS INC.
 XX
 XX PI Glaser SM, Huse WD;
 XX
 XX DR WPI: 1998-437472/37.
 XX
 XX DR N-PSDB; V49847.
 XX
 XX PS Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 XX LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 XX
 XX PS Claim 1; Fig 1a; 129pp; English.
 XX
 XX CC This sequence represents a fragment of the vitaxin antibody variable
 XX heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 XX integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 XX to a ligand and thus block integrin-mediated signal transduction. This is
 XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 XX disease, specifically angiogenesis and restenosis (but also e.g.
 XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 XX osteoporosis etc.). The antibodies contain non-murine framework regions
 XX so are suitable for use in humans. Enhanced types of LM609 have affinity
 XX more than 90 times greater than that of parent the parent antibody.
 XX
 XX SQ Sequence 117 AA;

 Query Match 92.6%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

 RESULT 10
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX
 XX AC W76003;
 XX
 XX DT 02-NOV-1998 (first entry)
 XX
 XX DE LM609 antibody heavy chain variable region protein fragment.
 XX
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 XX OS Mus sp.
 XX
 XX PN WO9833919-A2.
 XX
 XX PD 06-AUG-1998.
 XX
 XX PF 30-JAN-1998; 98WO-US01826.
 XX
 XX PR 30-JAN-1997; 97US-0791391.
 XX
 XX PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 DR N-PSDB; V49822.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 43; Fig 2a; 129pp; English.
 PS This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX Sequence 117 AA;

Query Match 92.6%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 97 arnygsfa 105
 |||||

RESULT 11
 Y06381
 ID Y06381 standard; Protein; 117 AA.

AC Y06381;

DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

OS WO9929888-A1.

PN 17-JUN-1999.

PD 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI: 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 92.6%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 97 arnygsfa 105
 |||||

RESULT 12

Y06387

ID Y06387 standard; Protein; 117 AA.

AC Y06387;

DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..2

FT /note= "vector-encoded residues"

FT Region 31..35

FT /note= "CDR1"

FT Region 50..66

FT /note= "CDR2"

FT Region 107..117

FT /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI: 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX
 SQ Sequence 117 AA;

Query Match 92.6%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

RESULT 13
 Y06384
 ID Y06384 standard; Protein; 118 AA.

XX AC Y06384;

XX DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VH domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Homo sapiens.
 XX OS Synthetic.

Key	Location/Qualifiers
FT Peptide	1..2
FT Region	/note= "vector-encoded residues"
FT Region	31..37
FT Region	/note= "CDR1"
FT Region	52..67
FT Region	/note= "CDR2"
FT Region	100..107
FT Region	/note= "CDR3"

XX PN W09929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 51; 55pp; English.

XX CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX
 SQ Sequence 118 AA;

Query Match 92.6%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 98 arhnygsfa 106
 |||||

RESULT 14

Y06385
 ID Y06385 standard; Protein; 118 AA.

XX AC Y06385;

XX DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VH domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Homo sapiens.
 XX OS Synthetic.

Key	Location/Qualifiers
FT Peptide	1..2
FT Region	/note= "vector-encoded residues"
FT Region	31..37
FT Region	/note= "CDR1"
FT Region	52..67
FT Region	/note= "CDR2"
FT Region	100..107
FT Region	/note= "CDR3"

XX PN W09929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 51; 55pp; English.

XX CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 118 AA;

Query Match 92.6%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 98 arhnygsfa 106

RESULT 15
Y06386
ID Y06386 standard; Protein; 118 AA.
XX AC Y06386;
XX DT 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX LM609; monoclonal antibody; complementarity determining region;
XX CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Peptide 1..2
XX FT /note= "vector-encoded residues"
XX FT Region 31..37
XX FT /note= "CDR1"
XX FT Region 52..67
XX FT /note= "CDR2"
XX FT Region 100..107
XX FT /note= "CDR3"
XX PN WO9929888-A1.
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX DR WPI; 1999-394979/33.
XX PT Production of humanized mouse monoclonal antibodies
XX PS Disclosure; Page 51-52; 55pp; English.
XX CC This sequence represents the heavy chain variable region of a
XX humanised antibody. LM609 is directed to human integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 118 AA;

Query Match 92.6%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 98 arhnygsfa 106

Search completed: March 28, 2001, 06:59:47
Job time: 1383 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:54 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-68

Perfect score: 54

Sequence: 1 ARHNYGSFAS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgnl_7/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgnl_7/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgnl_7/ptodata/1/iaa/6-COMB.pep.*
- 4: /cgnl_7/ptodata/1/iaa/PCTUS-COMB.pep.*
- 5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	72.2	94	3	US-09-147-550-14
2	39	72.2	94	3	US-09-147-550-45
3	39	72.2	94	3	US-09-147-550-48
4	39	72.2	94	3	US-09-147-550-77
5	39	72.2	94	3	US-09-147-550-84
6	39	72.2	94	3	US-09-147-550-90
7	39	72.2	94	3	US-09-147-550-101
8	36	66.7	119	3	US-08-767-128-6
9	35	64.8	94	3	US-09-147-550-39
10	35	64.8	94	3	US-09-147-550-59
11	35	64.8	94	3	US-09-147-550-63
12	34	63.0	94	3	US-09-147-550-55
13	34	63.0	94	3	US-09-147-550-62
14	34	63.0	94	3	US-09-147-550-87
15	34	63.0	94	3	US-09-147-550-108
16	34	63.0	286	2	US-08-809-267-3
17	34	63.0	286	4	PCT-US95-13662A-3
18	34	63.0	287	2	US-08-741-437-5
19	34	63.0	287	2	US-09-134-593-5
20	33	61.1	94	3	US-09-147-550-19
21	33	61.1	94	3	US-09-147-550-30
22	33	61.1	94	3	US-09-147-550-83
23	33	61.1	94	3	US-09-147-550-85
24	33	61.1	94	3	US-09-147-550-91
25	33	61.1	94	3	US-09-147-550-93
26	33	61.1	94	3	US-09-147-550-106
27	33	61.1	94	3	US-09-147-550-109
28	32	59.3	15	1	US-08-618-464-7

Sequence 7, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 1, Appl
Sequence 30, Appl
Sequence 17, Appl
Sequence 23, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl

29 32 59.3 15 3 US-09-107-615-7
30 32 59.3 25 2 US-08-480-190-44
31 32 59.3 25 2 US-08-488-379-44
32 32 59.3 25 4 PCT-US93-07545-44
33 32 59.3 36 1 US-08-053-131-84
34 32 59.3 36 1 US-08-645-641-84
35 32 59.3 36 1 US-07-853-408B-84
36 32 59.3 36 2 US-08-096-762-84
37 32 59.3 36 2 US-08-308-865-84
38 32 59.3 36 4 PCT-US92-10983-84
39 32 59.3 80 1 US-08-264-250A-1
40 32 59.3 89 1 US-08-025-038-30
41 32 59.3 89 1 US-08-039-137-17
42 32 59.3 90 2 US-08-485-133-23
43 32 59.3 94 3 US-09-147-550-12
44 32 59.3 94 3 US-09-147-550-13
45 32 59.3 94 3 US-09-147-550-15

ALIGNMENTS

RESULT 1
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 80 RHNYGVFES 88
|||||

RESULT 2
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
DB 80 RHNYGVFES 88

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE

US-09-147-550-48

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
DB 80 RHNYGVFES 88

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45
; LENGTH: 94

; TYPE: PRT

; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
DB 80 RHNYGVFES 88

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 84
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE

US-09-147-550-84

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
| | | | | | | |
DB 80 RHNYGVFES 88

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 90
; LENGTH: 94

; TYPE: PRT

ORGANISM: BOVINE
US-09-147-550-90

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 |||||

DB 80 RHNYGVFES 88

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 72.2%; Score 39; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 |||||

DB 80 RHNYGVFES 88

RESULT 8

US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079 West Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-6

Query Match 66.7%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||:|:|

DB 97 ARHNYGYA 105

RESULT 9

US-09-147-550-39
; Sequence 39, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-39

Query Match 64.8%; Score 35; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
| | | | |
Db 80 RHNYGGMES 88

RESULT 10
US-09-147-550-59
; Sequence 59, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-59

Query Match 64.8%; Score 35; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
| | | | |
Db 80 RHNYGGMES 88

RESULT 11
US-09-147-550-63
; Sequence 63, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-63

Query Match 64.8%; Score 35; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
| | | | |
Db 80 RHNYGGMES 88

RESULT 12
US-09-147-550-55
; Sequence 55, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-55

Query Match 63.0%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
| | | | |
Db 80 RHNYGGVES 88

RESULT 13
US-09-147-550-62
; Sequence 62, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-62

Query Match 63.0%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
| | | | |

Db 80 RHNYGVS 88

RESULT 14

US-09-147-550-87
; Sequence 87, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-87

Query Match 63.0%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

Db 80 RHNYGVS 88

RESULT 15

US-09-147-550-108
; Sequence 108, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-108

Query Match 63.0%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

Db 80 RHNYGVS 88

Search completed: March 28, 2001, 07:01:54
Job time: 1333 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:19 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSFAT 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	446	2	TI19625
2	37	67.3	448	1	nucleocapsid prote
3	36	65.5	82	2	Major Histocompati
4	36	65.5	89	2	MHC class II histo
5	36	65.5	89	2	MHC class II histo
6	36	65.5	89	2	MHC class II histo
7	36	65.5	225	2	MHC class II OVAR-
8	35	63.6	31	2	hypothetical prote
9	35	63.6	201	1	multicatalytic end
10	35	63.6	201	2	translation initia
11	35	63.6	262	2	phosphatidylcholin
12	35	63.6	347	2	hypothetical prote
13	35	63.6	1101	2	Ig heavy chain V r
14	34	61.8	108	2	Ig heavy chain V r
15	34	61.8	110	2	conserved hypothet
16	34	61.8	210	1	translation initia
17	34	61.8	275	2	probable translati
18	34	61.8	275	2	inorganic pyrophos
19	34	61.8	287	1	inorganic pyrophos
20	34	61.8	287	1	ars binding protei
21	34	61.8	527	2	hypothetical prote
22	34	61.8	548	2	outer membrane pro
23	34	61.8	723	2	hypothetical prote
24	33	60.0	65	2	MHC HLA-DR-beta-1
25	33	60.0	80	2	MHC HLA-DR-beta-1
26	33	60.0	80	2	HLA DRB1*1202 - hu
27	33	60.0	81	2	MHC class II DR-be
28	33	60.0	85	2	MHC class II histo
29	33	60.0	89	2	MHC class II histo

30	33	60.0	89	2	S38680	MHC class II histo
31	33	60.0	89	2	S57512	MHC class II histo
32	33	60.0	123	2	C25239	hypothetical prote
33	33	60.0	167	2	T16454	class II histocomp
34	33	60.0	200	2	D32526	hypothetical prote
35	33	60.0	220	2	T46055	class II histocomp
36	33	60.0	237	2	C27060	gene HLA-DRE1 prot
37	33	60.0	266	2	I54287	class II histocomp
38	33	60.0	266	2	A27618	lymphocyte antigen
39	33	60.0	266	2	I54295	hypothetical prote
40	33	60.0	279	2	T05421	hypothetical prote
41	33	60.0	297	2	T32719	hypothetical prote
42	33	60.0	360	2	S48566	secreted glycoprot
43	33	60.0	383	2	S58179	L2 protein - human
44	33	60.0	467	1	P2WL33	glutamate--tRNA L1
45	33	60.0	470	2	H71667	

ALIGNMENTS

RESULT 1

TI19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: TI19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: TI19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Map position: 1
A:Gene: CESP:C31H5.6
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHYNGSFA 9

DB 51 RHYNGSHA 58

RESULT 2

A60003
nucleocapsid protein - human coronavirus (strain OC43)
C:Species: human coronavirus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999
C:Accession: A60003
R:Kamahora, T.; Soe, L.H.; Lai, M.M.C.
Virus Res. 12, 1-9, 1989
A:Title: Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus O
C:Reference number: A60003; MUID:89243809
A:Accession: A60003
A:Molecule type: genomic RNA
A:Residues: 1-448 <KAM>
C:Genetics:
A:Gene: N
C:Superfamily: coronavirus nucleocapsid protein

C:Keywords: glycoprotein; nucleocapsid
F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 67.3%; Score 37; DB 1; Length 448;

Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
| | | | | | |
Db 103 RHNRGSFAT 111

RESULT 3
151106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <FIG>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | | | |
Db 75 RHNYGVF 81

RESULT 4
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | | | |
Db 75 RHNYGVF 81

RESULT 5
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA

A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | | | |
Db 75 RHNYGVF 81

RESULT 6
S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | | | |
Db 75 RHNYGVF 81

RESULT 7
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility complex class II genes
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAAL6562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | | | |
Db 68 RHNYGVF 74

RESULT 8
S00685
hypothetical protein 3 - phase P1

C:Species: phage p1
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C:Accession: S00685
R:Eliason, J.L.; Sternberg, N.
J. Mol. Biol. 198, 281-293, 1987
A:Title: Characterization of the binding sites of cl repressor of bacteriophage P1. Evid
A:Reference numbers: S00684; MUID:88118929
A:Accession: S00685
A:Molecule type: not shown
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-31 <ELI>
A:Cross-references: EMBL:X06561; NID:g15128; PIDN:CAA29805.1; PID:g15130

Query Match 63.6%; Score 35; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
||||| :|
Db 18 RHNYGFHST 26

RESULT 9
S55040
multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain C7-I - human
N:Alternate names: proteasome beta-2; proteasome chain C7-I
C:Species: Homo sapiens (man)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 16-Jun-2000
C:Accession: S55040; PC2323; S50148
R:Nothwang, H.G.; Tamura, T.; Tanaka, K.; Ichihara, A.
Biochim. Biophys. Acta 1219, 361-368, 1994
A:Title: Sequence analyses and inter-species comparisons of three novel human proteasome
A:Reference number: S50147; MUID:95002149
A:Accession: S55040
A:Molecule type: mRNA
A:Residues: 1-201 <NOT>
A:Cross-references: GB:D26599; NID:g565648; PIDN:BAA05646.1; PID:g565649
R:Kristensen, P.; Johnsen, A.H.; Uerkvitz, W.; Tanaka, K.; Hendil, K.B.
Biochem. Biophys. Res. Commun. 205, 1785-1789, 1994
A:Title: Human proteasome subunits from 2-dimensional gels identified by partial sequenc
A:Reference number: PC2315; MUID:95110324
A:Accession: PC2323
A:Molecule type: protein
A:Residues: 72-85 <KRI>
A:Experimental source: placenta
C:Comment: The proteasome consists of subunits of 21K-30K arranged in 4 stacked rings.
C:Genetics:
A:Gene: GDB:PSMB2; HC7-I
A:Cross-references: GDB:567222
C:Superfamily: human multicatalytic endopeptidase complex beta chain C7
C:Keywords: hydrolase; proteinase

Query Match 63.6%; Score 35; DB 1; Length 201;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
||| |||||
Db 130 AAHGCGAFLT 139

RESULT 10
S38725
multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain C7-I - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S38726
R:Nishimura, C.; Tamura, T.; Tokunaga, F.; Tanaka, K.; Ichihara, A.
FEBS Lett. 332, 52-56, 1993
A:Title: cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PRE1 essential
A:Reference number: S38725; MUID:94009687

A:Accession: S38725
A:Molecule type: mRNA
A:Residues: 1-201 <NIS>
A:Cross-references: GB:D21799; NID:g436780; PIDN:BAA04823.1; PID:g436781
A:Accession: S38726
A:Molecule type: protein
A:Residues: 42-62; 69, 'L', 71-80, 'V', 82-90, 'P', 92-98, 'G', 100-119, 'X', 121-122, 'X', 124; 12
C:Superfamily: human multicatalytic endopeptidase complex beta chain C7
C:Keywords: hydrolase

Query Match 63.6%; Score 35; DB 2; Length 201;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
||| |||||
Db 130 AAHGCGAFLT 139

RESULT 11
G69040
translation initiation factor eIF-2, alpha subunit - Methanobacterium thermoautotroph
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C:Accession: G69040
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwanl,
J. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A:Reference number: A69000; MUID:98037514
A:Accession: G69040
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-262 <MTH>
A:Cross-references: GB:AE000895; GB:AE000666; NID:g2622403; PIDN:AAB85786.1; PID:g262
C:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1308
A:Start codon: GTG
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.6%; Score 35; DB 2; Length 262;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFAT 10
|||||
Db 27 NYGAFAT 33

RESULT 12
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misiden
C:Species: Synecococcus sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189
A:Accession: S43771
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:g488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 63.6%; Score 35; DB 2; Length 347;
 Best Local Similarity 77.8%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 334 AEHNYISFA 342

RESULT 13
 T16840
 hypothetical protein T10E10.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 R:Geisel, C.
 submitted to the EMBL Data Library, October 1995
 A:Description: The sequence of C. elegans cosmid T10E10.
 A:Reference number: Z18588
 A:Accession: T16840
 A:Status: preliminary; translated from CB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1101 <GEI>
 A:Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E10
 A:Experimental source: strain Bristol N2
 C:Genetics:

A:Gene: CESP-T10E10.4
 A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 63.6%; Score 35; DB 2; Length 1101;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
 |||||
 Db 32 RHNPSTAT 40

RESULT 14
 S26316
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26316
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26316
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <STA>
 A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 84 ARGNYGNYA 92

RESULT 15
 S26317
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protei
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:Cross-references: EMBL:X59186
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 110;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 86 ARGNYGNYA 94

Search completed: March 28, 2001, 07:04:21
 Job time: 1059 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:00 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNGSFAT 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	67.3	448	1	NCAP_CVHOC
2	35	63.6	201	1	PRCG_HUMAN
3	35	63.6	201	1	PRCG_MOUSE
4	35	63.6	201	1	PRCG_RAT
5	35	63.6	262	1	IF2A_METH
6	34	61.8	275	1	IF2A_PYPAB
7	34	61.8	275	1	IF2A_PYRHO
8	34	61.8	284	1	IPYR_PICPA
9	34	61.8	286	1	IPYR_KLULA
10	34	61.8	286	1	IPYR_YEAST
11	33	60.0	65	1	CCSA_PEA
12	33	60.0	328	1	CCSA_ARATH
13	33	60.0	467	1	VL2_HPV33
14	33	60.0	470	1	SYE2_RICPR
15	33	60.0	473	1	SYE_AQAE
16	33	60.0	512	1	PNTA_HAEN
17	33	60.0	625	1	TRF5_YEAST
18	33	60.0	682	1	VG50_BPML5
19	32	58.2	65	1	CCSA_OENB
20	32	58.2	98	1	VG7_BPPH2
21	32	58.2	98	1	VG7_BPP2A
22	32	58.2	196	1	WBBJ_ECOLI
23	32	58.2	198	1	HB2J_HUMAN
24	32	58.2	214	1	DPOL_ADET1
25	32	58.2	266	1	HB2A_HUMAN
26	32	58.2	266	1	HB2B_HUMAN
27	32	58.2	266	1	HB2C_HUMAN
28	32	58.2	266	1	HB2D_CANFA
29	32	58.2	266	1	HB2D_HUMAN
30	32	58.2	266	1	HB2E_HUMAN
31	32	58.2	266	1	HB2F_HUMAN
32	32	58.2	266	1	HB2H_HUMAN
33	32	58.2	266	1	HB2I_HUMAN

34 32 58.2 266 1 HB2J_HUMAN
35 32 58.2 313 1 CCSA_TOBAC
36 32 58.2 321 1 CCSA_MAIZE
37 32 58.2 321 1 CCSA_ORISA
38 32 58.2 347 1 SCA3_HUMAN
39 32 58.2 349 1 SCA3_MOUSE
40 32 58.2 349 1 YJY9_YEAST
41 32 58.2 364 1 ERG3_CANGA
42 32 58.2 365 1 ERG3_YEAST
43 32 58.2 528 1 PRI2_YEAST
44 32 58.2 609 1 GPII_YEAST
45 32 58.2 629 1 KSVK_RAT

P13761, homo sapien
P12216, nicotiana t
P46659, zea mays (m
P12215, oryza sativ
O14828, homo sapien
O35609, mus musculu
P41303, saccharomyc
P50860, candida gla
P32353, saccharomyc
P20457, saccharomyc
P53306, saccharomyc
Q64725, rattus norv

ALIGNMENTS

RESULT 1

NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.

OS Human coronavirus (strain OC43).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

OC Coronaviridae; Coronavirus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 89243809.

RA Kamahora T., Soe L.H., Lai M.M.C.;

RT "Sequence analysis of nucleocapsid gene and leader RNA of human

RT coronavirus OC43";

RL Virus Res. 12:1-9(1989).

DR PIR; A60003; A60003.

DR INTERPRO; IPR001218; "

DR PFAM; PF00937; Corona_nucleoca; 1.

KW Nucleocapsid.

SQ SEQUENCE 448 AA; 49316 MW; 5193ABIAE0D75626 CRC64;

Query Match 67.3%; Score 37; DB 1; Length 448;

Best Local Similarity 77.8%; Pred. No. 6.1;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAT 10

Db 103 RHNGSFAT 111

RESULT 2

PRCG_HUMAN
ID PRCG_HUMAN STANDARD; PRT; 201 AA.
AC P49721; P31145;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE PROTEASOME COMPONENT C7-I (EC 3.4.99.46) (MACROPAIN SUBUNIT C7-I)

DE (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C7-I).

GN PSMB2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95002149.

RA Nothwang H.G., Tamura T., Tanaka K., Ichihara A.;

RT "Sequence analyses and inter-species comparisons of three novel human

RT proteasomal subunits, HsN3, HsC7-I and HsC10-II, confine potential

RT proteolytic active-site residues.";

RL Biochim. Biophys. Acta 1219:361-368(1994).


```

RN  [2]
RP  SEQUENCE OF 172-177 AND 186-193.
RC  TISSUE=KERATINOCYTES;
RX  MEDLINE; 93162043.
RA  Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA  Vandekerckhove J.;
RT  "Microsequences of 145 proteins recorded in the two-dimensional gel
RL  Electrophoresis 13:960-969(1992).
CC  -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC  WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC  ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC  NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC  PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE
CC  ACTIVITY.
CC  -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC  SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC  -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC  ALSO IN THE NUCLEUS.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE
CC  PROTEASOME B-TYPE FAMILY. C7-I SUBFAMILY.
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; D26599; BAA05646.1; -.
CC  AARHUS/GHENT-2DPAGE; 2120; IEF.
CC  MIM; 602175; -.
CC  INTERPRO; IPR000243; -.
CC  IPFAM; PF00227; proteasome; 1.
CC  PROSITE; PS00854; PROTEASOME_B; 1.
CC  Proteasome; Hydrolase; Protease.
CC  SEQUENCE 201 AA; 22836 MW; 04D085D7BAA76130 CRC64;
CC  -----
CC  Query Match 63.6%; Score 35; DB 1; Length 201;
CC  Best Local Similarity 60.0%; Pred. No. 6.4;
CC  Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC  QY 1 ARHNYGSFAT 10
CC  | | | | |
CC  Db 130 AAHGYGAFLT 139
CC  -----
RESULT 3
PRCG_MOUSE
ID PRCG_MOUSE STANDARD; PRT; 201 AA.
AC Q9R1P3;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEASOME COMPONENT C7-I (EC 3.4.99.46) (MACROPAIN SUBUNIT C7-I)
DE (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C7-I).
GN PSMB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.BR;
RX MEDLINE; 99367391.
RA Elenich L.A., Nandi D., Kent E.A., McCluskey T.S., Cruz M., Iyer M.N.,
RA Woodward E.C., Conn C.W., Ochoa A.L., Ginsburg D.B., Monaco J.J.;
RT "The complete primary structure of mouse 20S proteasomes.";
RL Immunogenetics 49:835-842(1999).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH

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CC  ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC  NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC  PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE
CC  ACTIVITY.
CC  -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC  SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC  -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC  ALSO IN THE NUCLEUS.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE
CC  PROTEASOME B-TYPE FAMILY. C7-I SUBFAMILY.
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CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AF060090; AAD50535.1; -.
CC  MGD; MGI:1347045; PSMB2.
CC  INTERPRO; IPR000243; -.
CC  INTERPRO; IPR001353; -.
CC  IPFAM; PF00227; proteasome; 1.
CC  PROSITE; PS00854; PROTEASOME_B; 1.
CC  Proteasome; Hydrolase; Protease.
CC  SEQUENCE 201 AA; 22906 MW; E9B3121974777958 CRC64;
CC  -----
CC  Query Match 63.6%; Score 35; DB 1; Length 201;
CC  Best Local Similarity 60.0%; Pred. No. 6.4;
CC  Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC  QY 1 ARHNYGSFAT 10
CC  | | | | |
CC  Db 130 AAHGYGAFLT 139
CC  -----
RESULT 4
PRCG_RAT
ID PRCG_RAT STANDARD; PRT; 201 AA.
AC P40307;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROTEASOME COMPONENT C7-I (EC 3.4.99.46) (MACROPAIN SUBUNIT C7-I)
DE (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C7-I).
GN PSMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=LIVER;
RX MEDLINE; 94009687.
RA Nishimura C., Tamura T., Tokunaga F., Tanaka K., Ichihara A.;
RT "cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast
RL PRE1 essential for chymotrypsin-like activity.";
RL FEBS Lett. 332:52-56(1993).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE
CC ACTIVITY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC ALSO IN THE NUCLEUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE
CC PROTEASOME B-TYPE FAMILY. C7-I SUBFAMILY.
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 CC -----

DR EMBL: D21799; BAA04823.1; -
 DR PIR: S38725; S38725.
 DR INTERPRO: IPR000243; -
 DR INTERPRO: IPR001353; -
 DR PFAM: PF00227; proteasome; 1.
 DR PROSITE: PS00854; PROTEASOME_B: 1.
 DR KEGG: proteasome; Hydrolase; Protease.
 FT CONFLICT 70 70 R -> L (IN AA SEQUENCE).
 FT CONFLICT 81 81 A -> V (IN AA SEQUENCE).
 FT CONFLICT 91 91 C -> P (IN AA SEQUENCE).
 SQ SEQUENCE 201 AA; 22912 MW; E9AC021972B76528 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 201;
 Best Local Similarity 60.0%; Pred. NO. 6.4;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
 Db 130 AAHGYGAFLT 139

RESULT 5
 IF2A_METH STANDARD; PRT; 262 AA.
 ID IF2A_METH
 AC 027363;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR MTH1308.

OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacterium.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE; 98037514.
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Kagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Nollig J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT delta: functional analysis and comparative genomics";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).

CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
 CC -----

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DR EMBL: AE000895; AAB85786.1; -
 DR INTERPRO: IPR003029; -

DR PFAM: PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 11 86 S1 MOTIF.
 SQ SEQUENCE 262 AA; 29780 MW; D7324B76DAFD5AA7 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 262;
 Best Local Similarity 85.7%; Pred. NO. 8.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFAT 10
 Db 27 NYGAFAT 33

RESULT 6
 IF2A_PYRAB STANDARD; PRT; 275 AA.
 ID IF2A_PYRAB
 AC Q9V0E4;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PAB0568.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ORSAY;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
 CC -----

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 CC -----

DR EMBL: AJ248285; CAB49760.1; -
 DR INTERPRO: IPR003029; -
 DR PFAM: PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. NO. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 Db 23 HNYCAF 28

RESULT 7
 IF2A_PYRHO STANDARD; PRT; 275 AA.
 ID IF2A_PYRHO
 AC 058655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE; 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 Sakai M., Ogura K., Otsuka K., Nakazawa H., Takamiya M., Ohfuku Y.,
 Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
 Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 Masuchi Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 RL DNA Res. 5:55-76(1998).
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
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 CC -----
 CC EMBL; AP000004; BAA30058.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;
 Query Match 61.8%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 23 HNYGAF 28
 RESULT 8
 IPYR_PICPA
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC Q13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RA "Cloning and sequence analysis of the Pichia pastoris TRP1 and
 RT HIS3 genes";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.

CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ001000; CAA04453.1; -
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0
 FT ACT_SITE 56 56
 FT BINDING 78 78
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD2790D7775D6 CRC64;
 Query Match 61.8%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 RESULT 9
 IPYR_KLUJA
 ID IPYR_KLUJA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RA "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E.COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 Cooperman B.S.;
 RA "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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EMBL: X14230; CAA32446.1; -
 PIR: S07894; PWVKL.
 HSSP: P00817; IWGI.
 INTERPRO: IPR001596; -
 PFAM: PF00719; Pyrophosphatase: 1.
 PROSITE: PS00387; PPASE; 1.
 Hydrolase: Magnesium.
 INIT_MET 0 BY SIMILARITY.
 ACT_SITE 56 PROBABLE.
 BINDING 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DQ 91 HNYGAF 96

RESULT 10
 IPYR_YEAST
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN=S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database.";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]
 SEQUENCE OF 239-249.
 RC STRAIN=ATCC 38531 / Y41;

RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT *Saccharomyces cerevisiae*.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohn W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyttia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of *Saccharomyces cerevisiae*
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RL implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E. COLI AND K. LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heikinheimo J., Vihtonen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*
 RT inorganic pyrophosphatases.";
 RL Blochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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DR PDB; 8PRK; 23-DEC-98.
 DR SWISS-2DPAGE; P00817; YEAST.
 DR YEPD; 7305; -.
 DR SGD; S0000215; IPPI.
 DR INTERPRO; IPR001596; -.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium; 3D-structure.
 FT INIT_MET 0 0
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
 FT CONFLICT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 71 71 D -> N (IN REF. 3).
 FT CONFLICT 74 74 MISSING (IN REF. 3).
 FT CONFLICT 123 123 E -> Q (IN REF. 3).
 FT CONFLICT 136 136 Q -> E (IN REF. 3).
 FT CONFLICT 186 186 N -> D (IN REF. 3).
 FT CONFLICT 224 224 D -> N (IN REF. 3).
 FT CONFLICT 266 266 L -> P (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 16 20
 FT STRAND 25 25
 FT TURN 28 30
 FT TURN 38 41
 FT STRAND 45 45
 FT STRAND 55 55
 FT STRAND 79 79
 FT TURN 97 98
 FT TURN 111 112
 FT STRAND 121 123
 FT TURN 131 132
 FT STRAND 135 135
 FT STRAND 138 146
 FT STRAND 151 158
 FT TURN 160 161
 FT TURN 165 167
 FT HELIX 172 175
 FT TURN 176 177
 FT TURN 179 180
 FT HELIX 182 197
 FT STRAND 203 203
 FT HELIX 205 207
 FT STRAND 210 210
 FT HELIX 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 Db 91 HNYGAF 96
 |||||

RESULT 11
 CCSA_PEA
 ID CCSA_PEA STANDARD; PRT; 65 AA.
 AC P31172;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
 GN CCSA.
 OS Pisum sativum (Garden pea).
 OG Chloroplast.

CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 CC Fabales; Fabaceae; Papilionoideae; Pisum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ALASKA;
 RX MEDLINE; 9135950.
 RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
 RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
 in pea chloroplasts";
 RL Plant Mol. Biol. 17:541-545(1991).
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCIL/NRFE/CCSA FAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X59015; CAA41754.1; -.
 DR PIR; S17441; S17441.
 KW Cytochrome c-type biogenesis; Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 60.0%; Score 33; DB 1; Length 65;
 Best Local Similarity 62.5%; Pred. No. 4.7;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAT 10
 Db 57 HSYGSFST 64
 |||||

RESULT 12
 CCSA_ARATH
 ID CCSA_ARATH STANDARD; PRT; 328 AA.
 AC P56770;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 CC Brassicales; Brassicaceae; Arabidopsids.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
 RT "Complete structure of the chloroplast genome of Arabidopsis
 thaliana";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDAJ databases.
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCIL/NRFE/CCSA FAMILY.
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 CC
 DR EMBL; AP000423; BAA84436.1; -.

```

DR INTERPRO: IPR002541; -.
DR PFAM: PF01578; Cyt_casm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 60.0%; Score 33; DB 1; Length 328;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAT 10
Db 320 HSYGSFTS 327

RESULT 13
VL2_HPV33
ID VL2_HPV33 STANDARD; PRT; 467 AA.
AC P06418;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MINOR CAPSID PROTEIN L2.
GN L2.
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86200464.
RA Cole S.T., Streeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus type 33, which is associated with cervical cancer.";
RL J. Virol. 58:991-995(1986).
CC -----
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CC -----
CC EMBL: M12732; AAA5963.1; -.
DR PIR: A03650; P2WL33.
DR INTERPRO: IPR000784; -.
DR PFAM: PF00513; Late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 467 AA; 50595 MW; B70DC4ADFEB21957 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 467;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
Db 378 QHSYSTFAT 386

RESULT 14
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCTB;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae;
RN [1]

SEQUENCE FROM N.A.
STRAIN-MADRID E;
RX MEDLINE: 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL: AJ235272; CAA15066.1; -.
DR HSP: P27000; IGLN.
DR INTERPRO: IPR000924; -.
DR INTERPRO: IPR001412; -.
DR PFAM: PF00749; TRNA-synt_lc; 1.
DR PRINTS: PR00987; TRNASYNTHGLU.
DR PROSITE: PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 60.0%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSP 8
Db 31 ARHNGKF 38

RESULT 15
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
DE GLTX OR AQ_1221.
GN Aquifex aeolicus.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
RX MEDLINE: 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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 CC -----
 DR EMBL: AE000729; AAC07230.1; -.
 DR INTERPRO: IPR000924; -.
 DR INTERPRO: IPR001412; -.
 DR PFAM: PF00749; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTHGLU.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 10 20 "HIGH" REGION.
 FT SIMILAR 242 246 "KMSKS" REGION.
 FT BINDING 245 245 ATP (BY SIMILARITY).
 SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 60.0%; Score 33; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 |||||
 Db 31 ARHNGGF 38

Search completed: March 28, 2001, 07:35:01
 Job time: 138 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:02 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSFAT 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	78.2	839	10	Q9LIE5
2	39	70.9	446	5	O62086
3	38	69.1	89	7	O19495
4	36	65.5	39	7	P79474
5	36	65.5	39	7	P79477
6	36	65.5	39	7	P79478
7	36	65.5	39	7	P79479
8	36	65.5	74	6	Q9TTM4
9	36	65.5	76	7	Q9TPC2
10	36	65.5	78	6	Q97835
11	36	65.5	78	6	Q97839
12	36	65.5	78	6	Q97844
13	36	65.5	78	6	Q97968
14	36	65.5	78	7	Q9MWT6
15	36	65.5	78	7	Q9MWT5
16	36	65.5	78	7	Q9MWT4
17	36	65.5	79	7	O19191
18	36	65.5	79	7	O19192
19	36	65.5	79	7	O19380

20	36	65.5	79	7	O19381	O19381 felis silve
21	36	65.5	79	7	O19382	O19382 felis silve
22	36	65.5	79	7	O19396	O19396 felis silve
23	36	65.5	79	7	O19397	O19397 felis silve
24	36	65.5	79	7	O19405	O19405 felis silve
25	36	65.5	79	7	O19406	O19406 felis silve
26	36	65.5	79	7	O19407	O19407 felis silve
27	36	65.5	79	7	O19408	O19408 felis silve
28	36	65.5	79	7	O19435	O19435 felis silve
29	36	65.5	79	7	Q9MX19	Q9MX19 leopardus p
30	36	65.5	79	7	Q9MX13	Q9MX13 leopardus p
31	36	65.5	79	7	Q9MX03	Q9MX03 leopardus p
32	36	65.5	79	7	Q9MX00	Q9MX00 leopardus p
33	36	65.5	79	7	Q9MW29	Q9MW29 leopardus p
34	36	65.5	79	7	Q9MW28	Q9MW28 leopardus p
35	36	65.5	79	7	Q9MW27	Q9MW27 leopardus p
36	36	65.5	79	7	Q9MWY9	Q9MWY9 leopardus p
37	36	65.5	79	7	Q9MWY8	Q9MWY8 leopardus p
38	36	65.5	79	7	Q9MWY6	Q9MWY6 leopardus p
39	36	65.5	79	7	Q9MWY5	Q9MWY5 leopardus p
40	36	65.5	79	7	Q9MWY4	Q9MWY4 leopardus p
41	36	65.5	79	7	Q9MWY3	Q9MWY3 leopardus p
42	36	65.5	79	7	Q9MWX6	Q9MWX6 leopardus p
43	36	65.5	79	7	Q9MWX5	Q9MWX5 leopardus p
44	36	65.5	79	7	Q9MWX4	Q9MWX4 leopardus p
45	36	65.5	79	7	Q9MWX1	Q9MWX1 leopardus p

ALIGNMENTS

RESULT 1

ID Q9LIE5 PRELIMINARY; PRT; 839 AA.

AC Q9LIE5:

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)

DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE

DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;

RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.

RT Sequence features of the regions of 4,251,695 bp covered by ninety PL,

RT TAC and BAC clones."

RL DNA Res. 7:217-221(2000).

DR EMBL; AP001306; BAB03065.1; -.

SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 78.2%; Score 43; DB 10; Length 839;

Best Local Similarity 87.5%; Pred. No. 4;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8

Db 274 SRHNYGSF 281

RESULT 2
O62086

ID O62086 PRELIMINARY; PRT; 446 AA.
 AC O62086;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE C31H5.6 PROTEIN.
 GN C31H5.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wellstock L., Wilkinson-Sproat J., Womland P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: Z93778; CAB07846.1; -;
 DR INTERPRO: IPR000379; -;
 DR INTERPRO: IPR002925; -;
 DR PFAM: PF01738; DLH; 2.
 SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 70.9%; Score 39; DB 5; Length 446;
 Best Local Similarity 87.3%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
 Db 51 RHNYGSHA 58
 |||||

RESULT 3
 ID O19495 PRELIMINARY; PRT; 89 AA.
 AC O19495;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15.151-5; TISSUE=BURSA;
 RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
 RL Immunogenetics 47:350-354(1998).
 DR EMBL: U91532; AAC15813.1; -;
 DR INTERPRO: IPR000353; -;
 DR PFAM: PF00969; MHC_II_beta; 1.
 KW MHC.-;
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 69.1%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 3.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 75 RHNYGDF 81
 |||||

RESULT 4
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U63077; AAB37777.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 25 RHNYGVF 31
 |||||

RESULT 5
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U63080; AAB37780.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3CID CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db 25 RHNYGVF 31
|||||

RESULT 6

P79478 ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 25 RHNYGVF 31

RESULT 7

P79479 ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 25 RHNYGVF 31

RESULT 8

Q9TTM4 ID Q9TTM4 PRELIMINARY; PRT; 74 AA.

AC Q9TTM4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MHC (BOLA) CLASS II DR-BETA CHAIN (FRAGMENT).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAPANESE BLACK;
RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033388; BAA85470.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
DR NON_TER 1 1
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 74;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 68 RHNYGVF 74

RESULT 9

Q9TPC2 ID Q9TPC2 PRELIMINARY; PRT; 76 AA.
AC Q9TPC2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN MAMU-DRB1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Saueremann U., Khazand M., Nagy M., Peiberg C.;
RT "Mhc-DQ-DRB-haplotype analysis in the rhesus macaque: evidence for a
RT number of different haplotypes displaying a low allelic
RT polymorphism.";
RL Tissue Antigens 0:0-0(1999).
DR EMBL; AF15315; AAF07040.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
DR MHC.
KW NON_TER 1 1
FT NON_TER 76 76
SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 76;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
|||||
Db 67 RHNYGVF 73

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RESULT 10
O97835 PRELIMINARY; PRT; 78 AA.
AC O97835;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9677 MW; 653346CE7D1E1388 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 11
O97839 PRELIMINARY; PRT; 78 AA.
AC O97839;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017212; BAA36769.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9430 MW; AFA08B7E34B6832 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 72 RHNYGVF 78

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RESULT 12
O97844 PRELIMINARY; PRT; 78 AA.
AC O97844;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017220; BAA36777.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9645 MW; 505346CE7D0860CF CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 13
O97968 PRELIMINARY; PRT; 78 AA.
AC O97968;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N21.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017231; BAA36788.1; -.
DR EMBL; AB017204; BAA36761.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9436 MW; 72907E039EC167B2 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 72 RHNYGVF 78

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Db 72 RHNYGVF 78

RESULT 14

Q9MWT6 PRELIMINARY; PRT; 78 AA.
 AC Q9MWT6;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
 GN LEPA-DRB.
 OS Leopardus pardalis (ocelot).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
 OX NCBI_TaxID=32538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
 RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
 RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
 RT pardalis) and Margay (Leopardus wiedii).";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF057894; AAF70946.1; -
 KW MHC.
 FT NON_TER 1
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 9559 MW; 77863043708EC5B8 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 78;

Best Local Similarity 85.7%; Pred. No. 7.6;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

Db 71 RHNYGVF 77

RESULT 15

Q9MWT5 PRELIMINARY; PRT; 78 AA.
 AC Q9MWT5;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
 GN LEPA-DRB.
 OS Leopardus pardalis (ocelot).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
 OX NCBI_TaxID=32538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
 RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
 RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
 RT pardalis) and Margay (Leopardus wiedii).";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF057895; AAF70947.1; -
 KW MHC.
 FT NON_TER 1
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 9559 MW; 5076280FF45EC5A7 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 78;

Best Local Similarity 85.7%; Pred. No. 7.6;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

Db 71 RHNYGVF 77

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:47 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNYGSFAT 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT:*
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- 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	19 W76025	LM609 grafted anti
2	51	92.7	10	19 W76024	LM609 grafted anti
3	50	90.9	10	19 W76026	LM609 grafted anti
4	50	90.9	10	19 W76027	LM609 grafted anti
5	50	90.9	10	19 W76028	LM609 grafted anti
6	50	90.9	10	19 W76029	LM609 grafted anti
7	50	90.9	10	19 W76030	LM609 grafted anti
8	50	90.9	10	19 W76010	LM609 grafted anti
9	50	90.9	117	19 W76001	Vitaxin antibody h
10	50	90.9	117	19 W76003	LM609 antibody hea
11	50	90.9	117	20 Y06381	Murine monoclonal
12	50	90.9	117	20 Y06387	Humanised LM609 an

13	50	90.9	118	20 Y06384	Humanised LM609 an
14	50	90.9	118	20 Y06385	Humanised LM609 an
15	50	90.9	118	20 Y06386	Humanised LM609 an
16	50	90.9	118	20 Y06383	Humanised LM609 an
17	50	90.9	130	20 Y06379	Murine monoclonal
18	47	85.5	10	19 W76021	LM609 grafted anti
19	46	83.6	10	19 W76037	LM609 grafted anti
20	46	83.6	10	19 W76039	LM609 grafted anti
21	46	83.6	10	19 W76040	LM609 grafted anti
22	46	83.6	10	19 W76022	LM609 grafted anti
23	46	83.6	10	19 W76023	LM609 grafted anti
24	45	81.8	10	19 W76020	LM609 grafted anti
25	42	76.4	110	20 W84099	Vitronectin alpha-
26	42	76.4	117	20 W84093	Murine vitronectin
27	42	76.4	117	20 W84097	Humanised anti- α lp
28	41	74.5	8	20 Y06371	Murine monoclonal
29	41	74.5	10	19 W76038	LM609 grafted anti
30	37	67.3	119	19 Y86109	S. pneumoniae deri
31	36	65.5	117	16 R79157	Human IgE receptor
32	36	65.5	117	16 R79155	Human IgE receptor
33	36	65.5	117	18 W27357	Heavy chain variab
34	36	65.5	117	18 W27356	Heavy chain variab
35	36	65.5	117	18 W27354	Heavy chain variab
36	36	65.5	119	18 W01578	Lead binding Mab 8
37	36	65.5	239	20 W73874	Human antiFc epsil
38	36	65.5	242	20 W73876	Human antiFc epsil
39	35	63.6	573	21 Y74962	Neisseria meningit
40	34	61.8	30	21 Y81870	Yeast IPPI protein
41	34	61.8	505	15 R47463	Ced-3. Caenorhabd
42	33	60.0	80	12 R13396	HLA-DRW12a antigen
43	33	60.0	80	12 R13397	HLA-DRW12b antigen
44	33	60.0	89	17 Y14338	Protein encoded by
45	33	60.0	89	17 Y14306	Protein encoded by

ALIGNMENTS

RESULT 1

ID W76025 standard; Protein; 10 AA.

AC W76025;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX Vitaxin; antibody; variable region; heavy chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
| | | | | | | | | |
Db 1 arhnygsfat 10

RESULT 2
W76024
ID W76024 standard; Protein; 10 AA.
XX
AC W76024;
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
XX
XX N-PSDB; V49861.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 92.7%; Score 51; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0049;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
| | | | | | | | | |
Db 1 arhnygsfas 10

RESULT 3
W76026
ID W76026 standard; Protein; 10 AA.
XX
AC W76026;
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
XX
XX N-PSDB; V49863.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
XX LM609 heavy and light chain variable region. LM609 and the antibody
XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
XX inhibit binding of alphavbeta3 to a ligand and thus block
XX integrin-mediated signal transduction. This is useful in the treatment,
XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

```

Db      1 arhnygsfa 9

RESULT      6
W76029
ID      W76029 standard; Protein; 10 AA.
AC      W76029;
XX
XX      02-NOV-1998 (first entry)
DT
DE      LM609 grafted antibody V-H region CDR3 protein fragment #11.
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
XX      Mus sp.
OS
XX      WO9833919-A2.
PN
XX      06-AUG-1998.
PD
XX      30-JAN-1998; 98WO-US01826.
PF
XX      30-JAN-1997; 97US-0791391.
PR
XX      (IXSY-) IXSYS INC.
PA
XX      Glaser SM, Huse WD;
PI
XX      WPI; 1998-437472/37.
DR
XX      N-PSDB; V49866.
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
XX      Claim 62; Page 41; 129pp; English.
PS
XX      W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC      LM609 heavy and light chain variable region. LM609 and the antibody
CC      vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC      inhibit binding of alphavbeta3 to a ligand and thus block
CC      integrin-mediated signal transduction. This is useful in the treatment,
CC      prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC      arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC      contain non-murine framework regions so are suitable for use in humans.
CC      Enhanced types of LM609 have affinity more than 90 times greater than
CC      that of parent the parent antibody.
XX
XX      Sequence 10 AA;

Query Match      90.9%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSFA 9
        |||||
Db      1 arhnygsfa 9

RESULT      8
W76010
ID      W76010 standard; Protein; 10 AA.
XX
XX      W76010;
AC
XX      02-NOV-1998 (first entry)
DT
XX      LM609 grafted antibody V-H region CDR3 protein fragment #1.
DE
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW

```


KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 DR
 XX N-PSDB; V49847.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PT
 XX
 XX Disclosure; Page 40; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ

 Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0072;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

 RESULT 9
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 XX Vitaxin antibody heavy chain variable region protein fragment.
 DE
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 DR
 XX N-PSDB; V49847.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PT
 XX
 XX Claim 1; Fig 1a; 129pp; English.
 XX
 XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 XX Sequence 117 AA;
 SQ

 Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

 RESULT 10
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX
 AC W76003;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 XX LM609 antibody heavy chain variable region protein fragment.
 DE
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 PI
 XX WPI: 1998-437472/37.
 DR
 XX N-PSDB; V49847.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PT
 XX
 XX Claim 1; Fig 1a; 129pp; English.
 XX
 XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 XX Sequence 117 AA;
 SQ

XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 DR N-PSDB; V49822.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 43; Fig 2a; 129pp; English.
 PS This sequence represents the LM609 antibody variable heavy chain region.
 XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 XX Sequence 117 AA;
 SQ

Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

RESULT 11
 Y06381
 ID Y06381 standard; Protein; 117 AA.
 AC Y06381;
 XX
 XX 06-SEP-1999 (first entry)
 DT
 XX Murine monoclonal antibody LM609 VH region.
 DE
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.
 XX
 XX WO9929888-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX 04-DEC-1998; 98WO-US25828.
 XX
 XX 05-DEC-1997; 97US-0986016.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 DR
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX Disclosure; Page 52-53; 55pp; English.
 PS
 XX This sequence represents the heavy chain variable region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX Sequence 117 AA;
 SQ

Query Match 90.9%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

RESULT 12
 Y06387
 ID Y06387 standard; Protein; 117 AA.
 AC Y06387;
 XX
 XX 06-SEP-1999 (first entry)
 DT
 XX Humanised LM609 antibody VH domain.
 DE
 XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX 04-DEC-1998; 98WO-US25828.
 XX
 XX 05-DEC-1997; 97US-0986016.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 DR
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX Disclosure; Page 52; 55pp; English.
 PS
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;
 SQ

Query Match 90.9%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 97 arhnygsfa 105

RESULT 13

Y06384
 ID Y06384 standard; Protein; 118 AA.

XX AC Y06384;

XX DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VH domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;

XX KW LM609; monoclonal antibody; complementarity determining region;

XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX KW cancer; therapy; diagnosis.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key

XX FT Peptide

XX FT 1..2

XX FT Location/Qualifiers

XX FT /note= "vector-encoded residues"

XX FT Region

XX FT 31..37

XX FT /note= "CDR1"

XX FT Region

XX FT 52..67

XX FT /note= "CDR2"

XX FT Region

XX FT 100..107

XX FT /note= "CDR3"

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 51; 55pp; English.

XX CC This sequence represents the heavy chain variable region of a

XX CC humanised LM609 antibody. LM609 is directed to human integrin

XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 118 AA;
 SQ

Query Match 90.9%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

RESULT 14

Y06385

ID Y06385 standard; Protein; 118 AA.

XX AC Y06385;

XX DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VH domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;

XX KW LM609; monoclonal antibody; complementarity determining region;

XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX KW cancer; therapy; diagnosis.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key

XX FT Peptide

XX FT 1..2

XX FT Location/Qualifiers

XX FT /note= "vector-encoded residues"

XX FT Region

XX FT 31..37

XX FT /note= "CDR1"

XX FT Region

XX FT 52..67

XX FT /note= "CDR2"

XX FT Region

XX FT 100..107

XX FT /note= "CDR3"

XX PN WO9929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 51; 55pp; English.

XX CC This sequence represents the heavy chain variable region of a

XX CC humanised LM609 antibody. LM609 is directed to human integrin

XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular

XX CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 98 arhnygsfa 106
|||||

RESULT 15
Y06386
ID Y06386 standard; Protein; 118 AA.
XX AC Y06386;
XX
DT 06-SEP-1999 (first entry)
XX
DE Humanised LM609 antibody VH domain.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..2
FT FT /note= "vector-encoded residues"
FT Region 31..37
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..107
FT /note= "CDR3"
XX
PN WO929888-A1.
XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
XX
XX Disclosure; Page 51-52; 55pp; English.
XX
CC This sequence represents the heavy chain variable region of a
CC humanised antibody. LM609 is directed to human integrin
CC alpha v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 98 arhnygsfa 106
|||||

Search completed: March 28, 2001, 06:59:47
Job time: 1383 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:54 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNYGSFAT 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgnl_7/ptodata/1/iaa/5A-COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B-COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6-COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCTUS-COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	65.5	94	3	US-09-147-550-14
2	36	65.5	94	3	US-09-147-550-45
3	36	65.5	94	3	US-09-147-550-48
4	36	65.5	94	3	US-09-147-550-77
5	36	65.5	94	3	US-09-147-550-84
6	36	65.5	94	3	US-09-147-550-90
7	36	65.5	94	3	US-09-147-550-101
8	36	65.5	119	3	US-08-767-128-6
9	34	61.8	286	2	US-08-809-267-3
10	34	61.8	286	4	PCT-US95-13662A-3
11	34	61.8	287	2	US-08-741-437-5
12	34	61.8	287	2	US-09-134-593-5
13	34	61.8	503	3	US-08-258-287B-36
14	34	61.8	503	3	US-08-368-704C-36
15	34	61.8	505	2	US-08-394-189B-5
16	34	61.8	505	4	PCT-US93-05701-20
17	34	61.8	505	4	PCT-US93-05705-5
18	32	58.2	15	1	US-08-618-464-7
19	32	58.2	15	3	US-09-107-615-7
20	32	58.2	25	2	US-08-480-190-44
21	32	58.2	25	2	US-08-488-379-44
22	32	58.2	25	4	PCT-US93-07545-44
23	32	58.2	36	1	US-08-053-131-84
24	32	58.2	36	1	US-08-645-641-84
25	32	58.2	36	1	US-07-853-408B-84
26	32	58.2	36	2	US-08-096-762-84
27	32	58.2	36	2	US-08-308-865-84
28	32	58.2	36	4	PCT-US92-10983-84

Sequence 1, Appl
Sequence 30, Appl
Sequence 17, Appl
Sequence 23, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

ALIGNMENTS

RESULT 1
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 2
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

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; EARLIER FILING DATE: 1997-03-28
;
; NUMBER OF SEQ ID NOS: 115
;
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

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Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels

Qy 2 RHNYSF 8
Dp 80 RHNYSF 86

RESULT 3
US-09-147-550-48
: Sequence 48. Application US/09147550

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Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels

QY 2 RHNYSF 8
D6 80 RHNYSF 86

RESULT 4
US-09-147-550-77
: Sequence 77, Application US/09147550

; GENERAL INFORMATION :
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 ; CURRENT APPLICATION NUMBER: US/09/147,550
 ; CURRENT FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: PCT/JP97/02485
 ; EARLIER FILING DATE: 1997-07-17
 ; EARLIER APPLICATION NUMBER: JP 8-190933
 ; EARLIER FILING DATE: 1996-07-19
 ; EARLIER APPLICATION NUMBER: JP 9-77979
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

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Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6: Conservative 0; Mismatches 1: Indels

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550

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? GENERAL INFORMATION:
?
? APPLICANT: Aida, Yoko
?
? TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
? TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
?
? FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
?
? CURRENT APPLICATION NUMBER: US/09/147,550
?
? CURRENT FILING DATE: 1999-04-23
?
? EARLIER APPLICATION NUMBER: PCT/JP97/02485
?
? EARLIER FILING DATE: 1997-07-17
?
? EARLIER APPLICATION NUMBER: JP 8-190933
?
? EARLIER FILING DATE: 1996-07-19
?
? EARLIER APPLICATION NUMBER: JP 9-77979
?
? EARLIER FILING DATE: 1997-03-28
?
? NUMBER OF SEQ ID NOS: 115
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? SOFTWARE: PatentIn Ver. 2.0
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? SEQ ID NO 84
?
? LENGTH: 94
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? TYPE: PRT
?
? ORGANISM: BOVINE
?
? US-09-147-550-84

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Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6: Conservative 0; Mismatches 1; Indels

QY	2	RHNYGSF	8
Db	80	RHNYGVF	86

RESULT 6
US-09-147-550-90
; Sequence 90. Application US/09147550

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: GENERAL INFORMATION:
: APPLICANT: Aida, Yoko
: TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
: TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
: FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
: CURRENT APPLICATION NUMBER: US/09/147,550
: CURRENT FILING DATE: 1999-04-23
: EARLIER APPLICATION NUMBER: PCT/JP97/02485
: EARLIER FILING DATE: 1997-07-17
: EARLIER APPLICATION NUMBER: JP 8-190933
: EARLIER FILING DATE: 1996-07-19
: EARLIER APPLICATION NUMBER: JP 9-77979
: EARLIER FILING DATE: 1997-03-28
: NUMBER OF SEQ ID NOS: 115
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 90
: LENGTH: 94
: TYPE: PRT

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ORGANISM: BOVINE
US-09-147-550-90

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8

US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-6

Query Match 65.5%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | |
Db 97 ARHHGYGA 105

RESULT 9

US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,267

; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 433
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662
; FILING DATE: 25-OCT-1994
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-809-267-3

Query Match 61.8%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 10
PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: Slatko, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids

; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US95-13662A-3

Query Match 61.8%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 11
US-08-741-437-5
; Sequence 5, Application US/08741437
; Patent No. 5843665
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
; US-08-741-437-5

Query Match 61.8%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 12

US-09-134-593-5
 ; Sequence 5, Application US/09134593
 ; Patent No. 5981232
 ; GENERAL INFORMATION:
 ; APPLICANT: Hawkins, Phillip R.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/134,593
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/741,437
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0148 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 855-0555
 ; TELEFAX: (415) 845-4166
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 287 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 4199
 ; US-09-134-593-5

Query Match 61.8%; Score 34; DB..2; Length 287;
 Best Local Similarity 83.3%; Pred. No. 66;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3..HNYGSF 8
 Db 92 HNYGAF 97

RESULT 13
 US-08-258-287B-36
 ; Sequence 36, Application US/08258287B
 ; Patent No. 6083735
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuan, Junying
 ; APPLICANT: Miura, Masayuki
 ; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/258,287B
 ; FILING DATE: 10-JUN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/080,850
 ; FILING DATE: 24-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bugalsky, Lawrence B.
 ; REGISTRATION NUMBER: 35,086
 ; REFERENCE/DOCKET NUMBER: 0609.3920001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; TELEX: 248636 SSK
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 503 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: both
 ; US-08-258-287B-36

Query Match 61.8%; Score 34; DB 3; Length 503;
 Best Local Similarity 77.8%; Pred. No. 11e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAT 10
 Db 162 RHNYMSAAT 170

RESULT 14
 US-08-368-704C-36
 ; Sequence 36, Application US/08368704C
 ; Patent No. 6087160
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuan, Junying
 ; APPLICANT: Miura, Masayuki
 ; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
 ; NUMBER OF SEQUENCES: 95
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/368,704C
 ; FILING DATE: 4-JAN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/258,287
 ; FILING DATE: 10-JUN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/080,850
 ; FILING DATE: 24-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bugalsky, Lawrence B.
 ; REGISTRATION NUMBER: 35,086
 ; REFERENCE/DOCKET NUMBER: 0609.3920002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-368-704C-36

Query Match 61.8%; Score 34; DB 3; Length 503;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RHNYGSFAT 10
||| | ||
Db 162 RHNYMSAAT 170

RESULT 15
US-08-394-189B-5
; Sequence 5, Application US/08394189B
; Patent No. 5962301
; GENERAL INFORMATION:
; APPLICANT: Horvitz, Robert
; APPLICANT: Yuan, Junying
; APPLICANT: Shaham, Shai
; TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1
; TITLE OF INVENTION: BETA CONVERTASE GENE TO A C. ELEGANS CELL DEATH
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,189B
; FILING DATE: 24-FEB-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/282,211
; FILING DATE: 12-JUL-1994
; APPLICATION NUMBER: 07/984,182
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: 07/897,788
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/211001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-394-189B-5

Query Match 61.8%; Score 34; DB 2; Length 505;

Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 RHNYGSFAT 10
||| | ||
Db 164 RHNYMSAAT 172

Search completed: March 28, 2001, 07:01:55
Job time: 1334 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:21 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSPAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	71.4	210	1 B69265	conserved hypothet
2	39	69.6	446	2 T19625	hypothetical prote
3	38	67.9	464	2 T70828	hypothetical prote
4	37	66.1	275	2 T04480	acyl-CoA oxidase h
5	36	64.3	82	2 I51106	Major Histocompati
6	36	64.3	89	2 S38688	MHC class II histo
7	36	64.3	89	2 S38683	MHC class II histo
8	36	64.3	89	2 S38684	MHC class II histo
9	36	64.3	225	2 I47095	MHC class II OVAR-
10	36	64.3	581	1 A37913	serine/threonine-s
11	36	64.3	723	2 F83173	outer membrane pro
12	36	64.3	731	1 J24654	probable copper-tr
13	35	62.5	232	2 G69080	conserved hypothet
14	35	62.5	243	2 D72098	serine esterase.p
15	35	62.5	275	2 G75130	translation initia
16	35	62.5	275	2 D71087	probable translati
17	35	62.5	347	2 S43771	phosphatidylcholin
18	35	62.5	520	2 T78502	paired box transcr
19	35	62.5	538	2 T28874	hypothetical prote
20	35	62.5	682	2 J00420	beta-1,3-glucanase
21	35	62.5	743	2 T15062	hypothetical prote
22	34	60.7	108	2 S26316	Ig heavy chain v r
23	34	60.7	110	2 S26317	Ig heavy chain v r
24	34	60.7	287	1 PWBX	inorganic pyrophos
25	34	60.7	287	1 PWBKL	inorganic pyrophos
26	34	60.7	309	2 T41494	zinc finger, ADP-r
27	34	60.7	372	2 T51082	hypothetical prote
28	34	60.7	407	2 H71857	pyruvate ferredoxi
29	34	60.7	407	2 F64658	pyruvate synthase

30	34	60.7	442	2 G69264	conserved hypothet
31	34	60.7	453	2 A05139	serum albumin - mo
32	34	60.7	514	2 T10559	hypothetical prote
33	34	60.7	1263	2 T00649	hypothetical prote
34	33.5	59.8	818	2 F82173	collagenase VC1650
35	33	58.9	80	2 S25050	Ig heavy chain v r
36	33	58.9	80	2 I54469	MHC HLA-DR-beta-1
37	33	58.9	80	2 I68777	MHC HLA-DR-beta-1
38	33	58.9	81	2 I54550	HLA DRB1*1202 - hu
39	33	58.9	85	2 I59634	MHC class II DR-be
40	33	58.9	89	2 S38676	MHC class II histo
41	33	58.9	89	2 S38680	MHC class II histo
42	33	58.9	89	2 S57512	MHC class II histo
43	33	58.9	102	2 S25025	Ig heavy chain - m
44	33	58.9	106	2 S25036	Ig heavy chain v r
45	33	58.9	111	2 S25052	Ig heavy chain v r

ALIGNMENTS

RESULT 1
B69265
conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: B69265
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: B69265
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <KLE>
A:Cross-references: GB:AE001098; GB:AE000782; NID:92689421; PIDN:AAB91117.1; PID:9265
C:Superfamily: conserved hypothetical protein AF0119

Query Match 71.4%; Score 40; DB 1; Length 210;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSPAD 10
DB 128 RHAYGSPVD 136

RESULT 2
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 69.6%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
| | | | |
DB 51 RHNYGSHA 58

RESULT 3
B70828
Hypothetical protein Rv0462 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70828
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: B70828
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-464 <COL>
A:Cross-references: GB:AL021933; GB:AL123456; NID:g3261529; PIDN:CAAL17417.1; PID:g290953
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0462
C:Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
F:7-450/Domain: dihydrolipoamide dehydrogenase homology <LDD>

Query Match 67.9%; Score 38; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
| | | | |
DB 110 HNYGTFAD 117

RESULT 4
T04480
acyl-CoA oxidase homolog - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04480
R:Grossi, M.; Gulli, M.; Stanca, A.M.; Cattivelli, L.
Plant Sci. 105, 71-80, 1995
A:Title: Characterization of two barley genes that respond rapidly to dehydration stress
A:Reference number: Z15371
A:Accession: T04480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-275 <GRO>
A:Cross-references: EMBL:X84055; NID:g642243; PIDN:CAA58874.1; PID:g642244
A:Experimental source: cv. Arda, leaf
C:Genetics:
A:Gene: cdr29

Query Match 66.1%; Score 37; DB 2; Length 275;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNYGSFAD 10
| | | | |
DB 1 ANNYGSFAD 10

RESULT 5
151106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: 151106
R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
A:Reference number: 151103; MUID:94245280
A:Accession: 151106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

QY 2 RHNYGSF 8
| | | | |
DB 75 RHNYGVF 81

Query Match 64.3%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

QY 2 RHNYGSF 8
| | | | |
DB 75 RHNYGVF 81

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushba
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

QY 2 RHNYGSFAD 10
| | | | |
DB 1 ANNYGSFAD 10

Qy 2 RHNYGSF 8
 |||||
 Db 75 RHNYGVF 81

RESULT 8

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38684

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from

A:Reference number: S38684

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FTC>

A:Cross-references: EMBL:Z27154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 6.6;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 9

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000

C:Accession: I47095

R:Fabb, S.A.; Maddox, J.F.; Gogollin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

Anim. Genet. 24, 249-255, 1993

A>Title: Isolation, characterization and evolution of ovine major histocompatibility com

A:Reference number: I47075; MUID:94057592

A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-225 <FAB>

A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F;98-163/Domain: immunoglobulin homology <IMW>

Query Match

Best Local Similarity 64.3%; Score 36; DB 2; Length 225;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

|||||

Db 68 RHNYGVF 74

RESULT 10

A37913

serine/threonine-specific protein kinase (EC 2.7.1.-) mkl - fission yeast (Schizosaccha

N:Alternate names: mitosis inhibitor protein kinase

C:Species: Schizosaccharomyces pombe

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999

C:Accession: A37913; T40626

R:Lundgren, K.; Walworth, N.; Boother, R.; Dembski, M.; Kirschner, M.; Beach, D.

Cell 64, 1111-1122, 1991

A>Title: mkl and weel cooperate in the inhibitory tyrosine phosphorylation of cdc2.

A:Reference number: A37913; MUID:91168259

A:Accession: A37913
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-581 <LUN>
 A:Cross-references: GB:M60834; NID:g173413; PIDN:AAA91278.1; PID:g1213637
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
 submitted to the EMBL Data Library, December 1998
 A:Reference number: Z21941

A:Accession: T40626

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-581 <LYN>

A:Cross-references: EMBL:AL034563; PIDN:CAA22534.1; GSPDB:GN00067; SPDB:SPBC660.14

C:Experimental source: strain 972h-; cosmid c660

C:Genetics:

A:Gene: SPBC660.14

A:Map position: 2

A:Introns: 403/3

C:Superfamily: fission yeast mkl protein; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:287-558/Domain: protein kinase homology <KIN>

Query Match 64.3%; Score 36; DB 1; Length 581;

Best Local Similarity 70.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10

|||||

Db 463 ASHNYGKPAD 472

RESULT 11

F83173

outer membrane protein OprC PA3790 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000

C:Accession: F83173

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950

A:Accession: F83173

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-723 <STO>

A:Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AAG07177.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: oprC; PA3790

Query Match

Best Local Similarity 64.3%; Score 36; DB 2; Length 723;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAD 10

|||||

Db 407 HNYGAFGE 414

RESULT 12

JC2464

probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.

C:Species: Enterobacteriaceae spp.

C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999

C:Accession: JC2464

R:Trenor III., C.; Lin, W.; Andrews, N.C.

Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994

A>Title: Novel bacterial p-type ATPases with histidine-rich heavy-metal-associated se

A:Reference number: JC2464; MUID:95110304

A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <TRE>
 A:Cross-references: GB:U16658; NID:9643612; PIDN:AAA62113.1; PID:9643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
 C:KeyWords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembr
 F:7-92/Region: His-rich
 F:135-477/Domain: ATPase transduction domain homology <ATP>
 F:544-685/Domain: ATPase nucleotide-binding domain homology <ATP>
 F:287/Active site: Glu #status predicted
 F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 64.3%; Score 36; DB 1; Length 731;
 Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 | | | | |
 Db 88 AHHHGSFKD 97

RESULT 13
 G69080
 conserved hypothetical protein MTH1600 - Methanobacterium thermoautotrophicum (strain De
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
 C:Accession: G69080
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514
 A:Accession: G69080
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-232 <MTH>
 A:Cross-references: GB:AE000919; GB:AE000666; NID:92622717; PIDN:AAB86073.1; PID:9262272
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1600
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1634

Query Match 62.5%; Score 35; DB 2; Length 232;
 Best Local Similarity 62.5%; Pred. No. 27;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 | | | | |
 Db 154 HNFEGGTD 161

RESULT 14
 D72098
 serine esterase, probable CP0488 [imported] - Chlamydomophila pneumoniae (strains CWL029 a
 N:Alternate names: lysophospholipase esterase
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: D72098; A81572
 R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606
 A:Accession: D72098
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-243 <ARN>
 A:Cross-references: GB:AE001162; GB:AE001363; NID:94376541; PIDN:AAD18420.1; PID:9437654
 A:Experimental source: strain CWL029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
 , C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
 A:Reference number: A81500; MUID:20150255
 A:Accession: A81572
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-243 <REA>
 A:Cross-references: GB:AE002210; GB:AE002161; NID:97189400; PIDN:AAF38318.1; PID:9718
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CPn0271; CP0488

Query Match 62.5%; Score 35; DB 2; Length 243;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 | | | | |
 Db 32 HNYGSLAD 39

RESULT 15
 G75130
 translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyss
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: G75130
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
 A:Reference number: A75001
 A:Accession: G75130
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <KAW>
 A:Cross-references: GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CAB49760.1; PID:9545
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: aif2A; PAB0568
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 62.5%; Score 35; DB 2; Length 275;
 Best Local Similarity 62.5%; Pred. No. 32;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
 | | | | |
 Db 23 HNYGAFLE 30

Search completed: March 28, 2001, 07:04:23
 Job time: 1061 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:01 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSFAD 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	64.3	581	1 MKL1_SCHPO	P30290 schizosach
2	35	62.5	275	1 IF2A_PYRAB	Q9V0E4 pyrococcus
3	35	62.5	275	1 IF2A_PYRHO	O58655 pyrococcus
4	35	62.5	520	1 PAX7_HUMAN	P23759 homo sapien
5	35	62.5	682	1 E13B_BACCI	P23903 bacillus ci
6	34	60.7	284	1 IPYR_PICPA	O13505 pichia past
7	34	60.7	286	1 IPYR_KLULA	P13998 kluyveromyc
8	34	60.7	286	1 IPYR_YEAST	P00817 saccharomyc
9	34	60.7	608	1 ALBU_MOUSE	P07724 mus musculus
10	33.5	59.8	587	1 COLA_VIBPA	Q56696 vibrio para
11	33	58.9	448	1 NCAP_CVHOC	P33469 human coron
12	33	58.9	470	1 SYE2_RICPR	Q92CT8 rickettsia
13	33	58.9	473	1 SYE2_AQUAE	O67271 aquifex aeo
14	33	58.9	608	1 ALBU_RAT	P02770 rattus norv
15	33	58.9	682	1 VG50_BPML5	Q05262 mycobacteri
16	32	57.1	65	1 CCSA_OENBE	P31565 oenothera b
17	32	57.1	65	1 CCSA_PEA	P31172 pisum sativ
18	32	57.1	196	1 HB2J_ECOLI	P37750 escherichia
19	32	57.1	198	1 HB2G_HUMAN	P01911 homo sapien
20	32	57.1	227	1 PRRA_RAT	P03320 rattus norv
21	32	57.1	246	1 YAFK_ECOLI	Q47148 escherichia
22	32	57.1	255	1 CBPM_STRAL	P00733 streptomyce
23	32	57.1	266	1 HB2A_HUMAN	P01913 homo sapien
24	32	57.1	266	1 HB2B_HUMAN	P01912 homo sapien
25	32	57.1	266	1 HB2C_HUMAN	P01914 homo sapien
26	32	57.1	266	1 HB2D_CANFA	P18470 canis fami
27	32	57.1	266	1 HB2D_HUMAN	P13759 homo sapien
28	32	57.1	266	1 HB2E_HUMAN	P04229 homo sapien
29	32	57.1	266	1 HB2F_HUMAN	P13758 homo sapien
30	32	57.1	266	1 HB2H_HUMAN	P13760 homo sapien
31	32	57.1	266	1 HB2I_HUMAN	P20039 homo sapien
32	32	57.1	266	1 HB2J_HUMAN	P13761 homo sapien
33	32	57.1	298	1 MTRE_METKA	Q49606 methanopyru

34	32	57.1	313	1 CCSA_TOBAC	P12216 nicotiana t
35	32	57.1	315	1 VC04_VACCV	P17370 vaccinia vi
36	32	57.1	316	1 VC04_VACCC	P21038 vaccinia vi
37	32	57.1	321	1 CCSA_MAIZE	P46659 zea mays (m
38	32	57.1	321	1 CCSA_ORISA	P12215 oryza sativ
39	32	57.1	328	1 CCSA_ARATH	P56770 arabidopsis
40	32	57.1	349	1 VJY9_YEAST	P41903 saccharomyc
41	32	57.1	466	1 GSHR_MOUSE	P47791 mus musculu
42	32	57.1	502	1 YM40_MARPO	P38478 marchantia
43	32	57.1	528	1 PRI2_YEAST	P20457 saccharomyc
44	32	57.1	561	1 DIM_ARATH	Q39085 arabidopsis
45	32	57.1	567	1 DIM_PEA	P93472 pisum sativ

ALIGNMENTS

```
RESULT 1
MIK1_SCHPO
ID MIK1_SCHPO STANDARD; PRT; 581 AA.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MITOSIS INHIBITOR PROTEIN KINASE MIK1 (EC 2.7.1.-).
GN MIK1.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91169259.
RA Lundgren K., Walworth N., Booher R., Dembski M., Kirschner M.,
RA Beach D.;
RT "mik1 and weel cooperate in the inhibitory tyrosine phosphorylation
of cdc2.";
RL Cell 64:1111-1122(1991).
CC -! FUNCTION: PROTEIN KINASE THAT ACTS BOTH ON SERINES AND ON
TYROSINES. IT ACTS AS A NEGATIVE REGULATOR OF ENTRY INTO MITOSIS
(G2 TO M TRANSITION). PHOSPHORYLATES AND INHIBITS CDC2.
CC -! SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES. HIGHLY SIMILAR TO S.POMBE WEE1.
CC -----
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CC -----
CC EMBL: M60834; AAA91278.1; -.
CC PIR: A37913; A37913.
CC INTERPRO: IPR00719; -.
CC INTERPRO: IPR002290; -.
CC PFAM: PF00069; pkinase.1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC Mitosis; Transferase; Serine/threonine-protein kinase;
KW Tyrosine-protein kinase; ATP-binding.
FT DOMAIN 289 561 PROTEIN_KINASE.
FT NP_BIND 295 303 ATP (BY SIMILARITY).
FT BINDING 320 320 ATP (BY SIMILARITY).
FT ACT_SITE 417 417 BY SIMILARITY.
SQ SEQUENCE 581 AA; 65933 MW; 371E0CEBD2CAlCE3 CRC64;
```

Query Match 64.3%; Score 36; DB 1; Length 581;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10

```

Db 463 ASHNYGKPAD 472
1 1111 11
RESULT 2
ID IF2A_PVRAB STANDARD; PRT; 275 AA.
AC Q9V0B4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
(CY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
CC
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CC -----
DR EMBL: AJ248285; CAB49760.1; -
DR INTERPRO: IPR003029; -
DR PFAM: PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879BAF CRC64;

Query Match 62.5%; Score 35; DB 1; Length 275;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSEAD 10
DB 23 HNYGAFLE 30

RESULT 3
ID IF2A_PVRHO STANDARD; PRT; 275 AA.
AC Q58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OF3.";
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
(CY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
CC
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CC -----
DR EMBL: AP000004; BAA30058.1; -
DR INTERPRO: IPR003029; -
DR PFAM: PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 275;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSEAD 10
DB 23 HNYGAFLE 30

RESULT 4
ID PAX7_HUMAN STANDARD; PRT; 520 AA.
AC P23759;
DT 01-NOV-1991 (Rel. 20, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PAIRED BOX PROTEIN PAX-7 (HUP1).
GN PAX7 OR HUP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE; 97480728.
RA Vorobyov E., Mertsalov I., Dockhorn-Dworniczak B., Dworniczak B.,
Horst J.;
" The genomic organization and full coding region of the human PAX7
gene.";
RL Genomics 45:168-174(1997).
RN [2]
RP SEQUENCE FROM N.A. (LONG FORM).
RA Heath P.;
"Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 1-467 FROM N.A. (LONG FORM).
RX MEDLINE; 95075634.
RA Schaefer B.W., Czerny T., Bernasconi M., Genini M., Busslinger M.;
" Molecular cloning and characterization of a human PAX-7 CDNA
expressed in normal and neoplastic myocytes.";
RL Nucleic Acids Res. 22:4574-4582(1994).
RN [4]
RP SEQUENCE OF 30-195 FROM N.A. (SHORT FORM).
RX MEDLINE; 89305521.

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RA Burfi M., Tromvoukis Y., Bopp D., Erigerio G., Noll M.;
 RT "Conservation of the paired domain in metazoans and its structure in
 three isolated human genes."
 RL EMBO J. 8:1183-1190(1989).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN
 MYOGENESIS.
 CC -1- SUBUNIT: CAN BIND AS A HETERODIMER WITH PAX3.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE), AND
 CC A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: RHABDYOYOSARCOMA-2 (RMS2) IS CHARACTERIZED BY A
 CC CHROMOSOMAL TRANSLOCATION T(1;13)(P36;Q14) WHICH INVOLVES PAX7 AND
 CC FOXO1A. THE RESULTING PROTEIN IS A TRANSCRIPTIONAL ACTIVATOR.
 CC -1- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
 CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
 CC -----
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 CC -----
 DR EMBL; X96743; CAA65520.1; .
 DR EMBL; X96744; CAA65521.1; .
 DR EMBL; X15042; CAA65521.1; JOINED.
 DR EMBL; X15250; CAA65521.1; JOINED.
 DR EMBL; X15251; CAA65521.1; JOINED.
 DR EMBL; X96745; CAA65521.1; JOINED.
 DR EMBL; X96746; CAA65521.1; JOINED.
 DR EMBL; X96747; CAA65521.1; JOINED.
 DR EMBL; X96748; CAA65521.1; JOINED.
 DR EMBL; X15042; CAA65522.1; .
 DR EMBL; X15042; CAA65522.1; JOINED.
 DR EMBL; X15250; CAA65522.1; JOINED.
 DR EMBL; X15251; CAA65522.1; JOINED.
 DR EMBL; X96745; CAA65522.1; JOINED.
 DR EMBL; X96746; CAA65522.1; JOINED.
 DR EMBL; X96747; CAA65522.1; JOINED.
 DR EMBL; X96748; CAA65522.1; JOINED.
 DR EMBL; AL021528; CAA16432.1; .
 DR EMBL; Z35141; CAA84513.1; .
 DR PIR; S06959; S06959.
 DR HSSP; P06601; 1FJL.
 DR TRANSPAC; T00396; .
 DR MM; 167410; .
 DR INTERPRO; IPR001356; .
 DR INTERPRO; IPR001523; .
 DR PFAM; PF00292; PAX; 1.
 DR PFAM; PF00046; homeobox; 1.
 DR PRINTS; PR00027; PAIREDBOX.
 DR PROSITE; PS00027; HOMEOBOX_1; 1.
 DR PROSITE; PS00071; HOMEOBOX_2; 1.
 DR PROSITE; PS00034; PAIRED_BOX; 1.
 KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
 KW Developmental protein; Paired box; Chromosomal translocation;
 KW Proto-oncogene; Alternative splicing.
 FT DOMAIN 34 161 PAIRED BOX.
 FT DNA_BIND 217 276 HOMEOBOX.
 FT DOMAIN 340 346 POLY-ALA.
 FT VARSPLIC 151 152 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 520 AA; 56896 MW; 3B0F8CC99D656599C CRC64;

Query Match 62.5%; Score 35; DB 1; Length 520;
 Best Local Similarity 50.0%; Pred. No. 21;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSPAD 10
 |||:|:|
 Db 354 ARHSSFSYSYSD 363

RESULT 5
 E13B_BACCI STANDARD; PRT; 682 AA.
 ID E13B_BACCI
 AC P23903;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39) ((1->3)-
 DE BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE A1).
 GN GLCA.
 OS Bacillus circulans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 39-52.
 RC STRAIN-WL-12;
 RX MEDLINE; 90185240.
 RA Yahata N., Watanabe T., Nakamura Y., Yamamoto Y., Kamimiya S.,
 RA Tanaka H.;
 RT "Structure of the gene encoding beta-1,3-glucanase A1 of Bacillus
 RT circulans WL-12";
 RL Gene 86:113-117(1990).
 CC -1- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
 CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
 CC IN 1,3-BETA-D-GLUCANS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 DR EMBL; M34503; AAA22474.1; .
 DR PIR; JQ0420; JQ0420.
 DR HSSP; P23904; 1AJQ.
 DR INTERPRO; IPR000757; .
 DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
 KW Cell wall; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 38
 FT CHAIN 39 682 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1.
 FT ACT_SITE 552 552 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 557 557 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 682 AA; 75465 MW; 8C4F407E34D4ADD5 CRC64;
 Query Match 62.5%; Score 35; DB 1; Length 682;
 Best Local Similarity 62.5%; Pred. No. 28;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 HNYGSPAD 10
 ||:|:|
 Db 227 HNFQOPTD 234
 RESULT 6
 IPYR_PICPA STANDARD; PRT; 284 AA.
 ID IPYR_PICPA
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-NRRL Y-11430;
RX MEDLINE; 99034033.
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ001000; CA04453.1; -.
CC HSSP; P00817; IWGI.
CC INTERPRO; IPR001596; -.
CC PFAM; PF00719; Pyrophosphatase; 1.
CC PROSITE; PS00387; PPASE; 1.
CC KW Hydrolase; Magnesium.
CC FT INIT_MET 0 BY SIMILARITY.
CC FT ACT_SITE 56 56 PROBABLE.
CC FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
CC SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96
|||||
RESULT 7
IPYR_KLUJLA STANDARD; PRT; 286 AA.
AC F13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IP1 OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E.COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Coogerman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

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CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X14230; CAA32446.1; -.
CC PIR; S07894; PWKVL.
CC HSSP; P00817; IWGI.
CC INTERPRO; IPR001596; -.
CC PFAM; PF00719; Pyrophosphatase; 1.
CC PROSITE; PS00387; PPASE; 1.
CC KW Hydrolase; Magnesium.
CC FT INIT_MET 0 BY SIMILARITY.
CC FT ACT_SITE 56 56 PROBABLE.
CC FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
CC SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96
|||||
RESULT 8
IPYR_YEAST STANDARD; PRT; 286 AA.
AC P00817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IP1 OR PP1 OR PPA OR YBR011C OR YBR0202.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-X2180;
RX MEDLINE; 89083474.
RA Kolakowski L.F. Jr., Schloesser M., Coogerman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN-S288C;

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DR PFAM: PF01752; Peptidase_M9; 1.
DR PRINTS; PR00031; MICOLPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; zymogen; signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 587 MICROBIAL COLLAGENASE.
FT METAL 435 435 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 436 436 BY SIMILARITY.
FT METAL 439 439 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 587 AA; 66003 MW; 8A94D83E3D2A2BD1 CRC64;

Query Match 59.8%; Score 33.5; DB 1; Length 587;
Best Local Similarity 72.7%; Pred. No. 46;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ARHN-YGSFAD 10
Db 1 111111
443 ARFNQYGSFSD 453

RESULT 11
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RL Virus Res. 12:1-9(1989).
DR PIR: A60003; A60003.
DR INTERPRO; IPR001218; -.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 103 RHNRGSF 109

RESULT 12
SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE; 99039499.

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Scharitz-Ponten T., Alsmark U.C.M., Bodowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC 1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC 1- SUBUNIT: MONOMER (BY SIMILARITY).
CC 1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC 1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -.
DR HSSP; P27000; IGLN.
DR INTERPRO; IPR000924; -.
DR INTERPRO; IPR001412; -.
DR PFAM; PF00749; TRNA-synt_1c; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 58.9%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db 31 ARHNGKF 38

RESULT 13
SYE_AQUAE STANDARD; PRT; 473 AA.
AC Q67271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC 1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC 1- SUBUNIT: MONOMER (BY SIMILARITY).
CC 1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC 1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
 CC EMBL; A000729; AAC07230.1; -
 CC INTERPRO: IPR000924; -
 CC INTERPRO: IPR001412; -
 CC PFAM; PF00749; tRNA-synt_1c; 1.
 CC PRINTS; PR00987; TRNASYNTHGLU.
 CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 CC KW Aminocacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 CC SIMILAR 10 20 "HIGH" REGION.
 CC FT SIMILAR 242 246 "KMSKS" REGION.
 CC FT BINDING 245 245 ATP (BY SIMILARITY).
 CC SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 58.9%; Score 33; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ARHNYGSF 8
 Db 31 ARHNGGF 38

RESULT 14
 ALBU_RAT STANDARD; PRT; 608 AA.
 ID ALBU_RAT
 AC P02770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SERUM ALBUMIN PRECURSOR.
 GN ALB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 8123722.
 RA Sargent T.D., Yang M., Bonner J.;
 RT "Nucleotide sequence of cloned rat serum albumin messenger RNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
 RN [2]
 RP SEQUENCE OF 1-38, AND PROCESSING.
 RX MEDLINE; 77249657.
 RA Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
 RT "Rat liver pre-proalbumin: complete amino acid sequence of the pre-
 RT piece. Analysis of the direct translation product of albumin
 RT messenger RNA.";
 RL J. Biol. Chem. 252:6846-6855(1977).
 RN [3]
 RP SEQUENCE OF 25-222.
 RX MEDLINE; 78109429.
 RA Isemura S., Ikenaka T.;
 RT "Amino acid sequences of fragments I and II obtained by cyanogen
 RT bromide cleavage of rat serum albumin.";
 RL J. Biochem. 83:35-48(1978).
 RN [4]
 RP SEQUENCE OF 223-288 AND 572-608.
 RX MEDLINE; 76260153.
 RA Isemura S., Ikenaka T.;
 RT "Fragmentation of rat serum albumin by cyanogen bromide cleavage and
 RT the amino acid sequences of four fragments.";
 RL J. Biochem. 79:1183-1196(1976).
 RN [5]
 RP COPPER BINDING.
 RX MEDLINE; 79001617.
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Copper(II)-binding ability of human alpha-fetoprotein.";

RL Cancer Res. 38:3483-3486(1978).
 CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
 CC BINDING CAPACITY FOR WATER, CA⁺⁺, NA⁺, K⁺, FATTY ACIDS, HORMONES,
 CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
 CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -----
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CC EMBL; V01222; CAA24532.1; -
 CC PIR; A03233; ABRTS.
 CC HSP; P02768; LUOR.
 CC INTERPRO: IPR000264; -
 CC PFAM; PF00273; transport_prot; 3.
 CC PRINTS; PR00802; SERUMALBUMIN.
 CC PROSITE; PS00212; ALBUMIN; 3.
 CC Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
 KW Copper.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 608 SERUM ALBUMIN.
 FT REPEAT 28 202 1.
 FT REPEAT 221 394 2.
 FT REPEAT 413 592 3.
 FT METAL 27 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 FT VARIANT 262 262 V -> L.
 SQ SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 608;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAD 10
 Db 105 RDNYGELAD 113
 RESULT 15
 VG50_BPML5 STANDARD; PRT; 682 AA.
 ID VG50_BPML5
 AC Q05262;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
 DE (EC 1.17.4.2) (GP50).

```

GN 50.
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -I- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
OXIDIZED THIOREDIXIN + H(2)O = RIBONUCLEOSIDE TRIPHOSPHATE +
REDUCED THIOREDIXIN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z18946; CAA79426.1; -.
DR PIR; S30995; S30995.
DR INTERPRO; IPR000788; -.
DR PFAM; PF00317; ribonucleo_red; 1.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 311 AKEGYGSFA 319

```

Search completed: March 28, 2001, 07:35:02
Job time: 139 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:03 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSFAD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	87.5	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	40	71.4	210	1 Q30115	Q30115 archaeboglob
3	39	69.6	162	2 O08236	O08236 ixodes scap
4	39	69.6	162	2 O52253	O52253 rickettsia
5	39	69.6	446	5 O62086	O62086 caenorhabdi
6	39	69.6	707	2 O52307	O52307 prevotella
7	38	67.9	89	7 O19495	O19495 gallus gall
8	38	67.9	464	2 O53747	O53747 mycobacteri
9	37	66.1	275	10 Q43476	Q43476 hordeum vul
10	37	66.1	625	10 Q9MB96	Q9MB96 oryza sativ
11	37	66.1	685	5 Q9V6C3	Q9V6C3 drosophila
12	36	64.3	39	7 P79474	P79474 cervus elap
13	36	64.3	39	7 P79477	P79477 cervus elap
14	36	64.3	39	7 P79478	P79478 cervus elap
15	36	64.3	39	7 P79479	P79479 cervus elap
16	36	64.3	74	6 Q9TWM4	Q9TWM4 bos taurus
17	36	64.3	76	7 Q9TPC2	Q9TPC2 macaca mula
18	36	64.3	78	6 O97835	O97835 ovnis aries
19	36	64.3	78	6 O97839	O97839 ovnis aries

20	36	64.3	78	6	O97844	O97844 ovnis aries
21	36	64.3	78	6	O97968	O97968 ovnis aries
22	36	64.3	78	7	O9MWT6	O9MWT6 leopardus p
23	36	64.3	78	7	O9MWT5	O9MWT5 leopardus p
24	36	64.3	78	7	O9MWT4	O9MWT4 leopardus p
25	36	64.3	79	7	O19191	O19191 prionalluru
26	36	64.3	79	7	O19192	O19192 prionalluru
27	36	64.3	79	7	O19380	O19380 fellis silve
28	36	64.3	79	7	O19381	O19381 fellis silve
29	36	64.3	79	7	O19382	O19382 fellis silve
30	36	64.3	79	7	O19396	O19396 fellis silve
31	36	64.3	79	7	O19397	O19397 fellis silve
32	36	64.3	79	7	O19405	O19405 fellis silve
33	36	64.3	79	7	O19406	O19406 fellis silve
34	36	64.3	79	7	O19407	O19407 fellis silve
35	36	64.3	79	7	O19408	O19408 fellis silve
36	36	64.3	79	7	O19435	O19435 fellis silve
37	36	64.3	79	7	O9MX19	O9MX19 leopardus p
38	36	64.3	79	7	O9MX13	O9MX13 leopardus p
39	36	64.3	79	7	O9MX03	O9MX03 leopardus p
40	36	64.3	79	7	O9MX00	O9MX00 leopardus p
41	36	64.3	79	7	O9MW29	O9MW29 leopardus p
42	36	64.3	79	7	O9MW28	O9MW28 leopardus p
43	36	64.3	79	7	O9MW27	O9MW27 leopardus p
44	36	64.3	79	7	O9MWY9	O9MWY9 leopardus p
45	36	64.3	79	7	O9MWY8	O9MWY8 leopardus p

ALIGNMENTS

RESULT 1
Q9LIE5 PRELIMINARY; PRT; 839 AA.
ID Q9LIE5
AC Q9LIE5
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AF001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 87.5%; Score 49; DB 10; Length 839;
Best Local Similarity 80.0%; Pred. No. 0.34;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10

Db 274 SRHNYGSFCD 283

RESULT 2

O30115


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QY      1 ARHNGSFAD 10
      | : : | : | |
Db      144 AHDFGAFAD 153

RESULT  4
O52253  PRELIMINARY; PRT; 162 AA.
ID      O52253;
AC      AC
DT      01-JUN-1998 (TrEMBLrel. 06, Created)
DT      01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT      01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE      190 KDA ANTIGEN (FRAGMENT).
OS      Rickettsia cooley.
OC      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC      Rickettsiaceae; Rickettsiae; Rickettsia.
OX      NCBI_TaxID=69410;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Billings A.N., Teltow G.J., Walker D.H.;
RL      Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF031535; AAB95268.1;
FT      NON_TER
FT      NON_TER 162
SQ      SEQUENCE 162 AA; 16230 MW; 8DF06E97A8478E54 CRC64;

Query Match          69.6%; Score 39; DB 2; Length 162;
Best Local Similarity 60.0%; Pred. No. 4.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 ARHNGSFAD 10
      | : : | : | |
Db      144 AHDFGAFAD 153

RESULT  5
O62086  PRELIMINARY; PRT; 446 AA.
ID      O62086;
AC      AC
DT      01-AUG-1998 (TrEMBLrel. 07, Created)
DT      01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE      01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE      C31H5.6 PROTEIN.
GN      C31H5.6.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kershaw J.;
RL      Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94150718; PubMed=7906398;
RA      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA      Bonfield J., Burton J., Conneil M., Copsey T., Cooper J., Coulson A.,
RA      Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA      Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA      Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA      Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA      Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA      Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA      Watson A., Weinstock L., Wilkinson-Sprout J., Wohldman P.;
RT      *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT      elegans";
RL      Nature 368:32-38(1994).
DR      EMBL: Z93778; CAB07846.1;
DR      INTERPRO: IPR00379;
DR      INTERPRO: IPR002925;
DR      PFAM: PF01738; DLH: 2.

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SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 69.6%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSFA 9
| | | | |
DB 51 RHNYGSHA 58

RESULT 6

Q52307 PRELIMINARY; PRT; 707 AA.
AC Q52307;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE XYLANASE.
OS Prevotella ruminicola (Bacteroides ruminicola).
OC Bacteria; CFB group; Bacteroidaceae; Prevotella.
OX NCBI_TaxID=839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D31D;
RA Whitehead T.R.;
RT "Cloning and comparison of xylanase genes from ruminal and colonic
Bacteroides species."
RL Curr. Microbiol. 23:15-19(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D31D;
RX MEDLINE=97201063; PubMed=9048892;
RA Flint H.J., Whitehead T.R., Martin J.C., Gasparic A.;
RT "Interrupted catalytic domain structures in xylanases from two
distinctly related strains of Prevotella ruminicola."
RL Biochim. Biophys. Acta 1337:161-165(1997).
DR EMBL; U53926; AAB81559.1; -;
DR HSSP; P56588; 1BG4.
DR INTERPRO; IPR000583; -;
DR INTERPRO; IPR001000; -;
DR PFAM; PF00331; Glyco_hydro_10; 2.
DR PRINTS; PR00134; GLHYDRLASE10.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN1.
KW Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 707 AA; 78252 MW; 8484E75C60869DB5 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 707;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 RHNYGSFAD 10
| | | | |
DB 694 KHTYGGFAD 702

RESULT 7

O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -;
DR INTERPRO; IPR000353; -;
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 67.9%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
| | | | |
DB 75 RHNYGDF 81

RESULT 8

O53747 PRELIMINARY; PRT; 464 AA.
AC O53747;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE PUTATIVE DIHYDROLIPOAMIDE DEHYDROGENASE.
GN RV0462 OR MTV038.06.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."
RL Nature 393:537-544(1998).
CC -1- COFACTOR: FAD FLAVOPROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULPHIDE
CC OXIDOREDUCTASES CLASS-I.
DR EMBL; AL021933; CAAL7417.1; -;
DR HSSP; P11959; 1EBD.
DR TUBERCULIST; RV0462; -;
DR INTERPRO; IPR000205; -;
DR INTERPRO; IPR001100; -;
DR INTERPRO; IPR001327; -;
DR PFAM; PF00070; pyr_redox; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRDTASEI.
DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
KW Redox-active center; Oxidoreductase; Flavoprotein; FAD.
SQ SEQUENCE 464 AA; 49239 MW; DD93D95DC6F76B22 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNYGSFAD 10
| | | | |

Db 110 HGYGTFAD 117

RESULT 9

Q43476

ID Q43476 PRELIMINARY; PRT; 275 AA.

AC Q43476

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE MAMMALIAN ACYL COA OXIDASE HOMOLOGOUS (FRAGMENT).

GN CDR29.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. ARDA; TISSUE=GREEN LEAF;

RA Grossi M., Gullii M., Stanca A.M., Cattivelli L.;

RL Plant Sci. 105:71-80(1995).

DR ENBL: X84055; CAA58874.1; -

DR MENDEL; 12863; Horvu; 2063; 12863.

DR INTERPRO: IPR002655; -

DR PFAM: PF01756; ACOX; 1.

FT NON_TER 1

SQ SEQUENCE 275 AA; 30689 MW; 332811FD05827472 CRC64;

Query Match 66.1%; Score 37; DB 10; Length 275;

Best Local Similarity 70.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSGFAD 10

Db 1 ANHNSGSFLD 10

RESULT 10

Q9MB96

ID Q9MB96 PRELIMINARY; PRT; 625 AA.

AC Q9MB96

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE OSGAI.

GN OSGAI.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Ogawa M., Kusano T., Katsumi M., Sano H.;

RT "Rice gibberellin-insensitive gene homolog, OSGAI, encodes a nuclear-

RT localized protein capable of gene activation at transcriptional

RT level."

RL Gene 245:21-29(2000).

DR ENBL: AB030956; BAA90749.1; -

SQ SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;

Query Match 66.1%; Score 37; DB 10; Length 625;

Best Local Similarity 70.0%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSGFAD 10

Db 481 ANHNSGSFLD 490

RESULT 11

P79474

AC P79474;

ID P79474

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

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ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

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AC P79474;

PRELIMINARY; PRT; 39 AA.

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P79474

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AC P79474;

PRELIMINARY; PRT; 39 AA.

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AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

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AC P79474;

PRELIMINARY; PRT; 39 AA.

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AC P79474;

PRELIMINARY; PRT; 39 AA.

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AC P79474;

PRELIMINARY; PRT; 39 AA.

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AC P79474;

PRELIMINARY; PRT; 39 AA.

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PRELIMINARY; PRT; 39 AA.

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PRELIMINARY; PRT; 39 AA.

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PRELIMINARY; PRT; 39 AA.

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PRELIMINARY; PRT; 39 AA.

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PRELIMINARY; PRT; 39 AA.

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PRELIMINARY; PRT; 39 AA.

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AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

ID P79474

AC P79474;

PRELIMINARY; PRT; 39 AA.

RESULT 12

P79474

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*
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 13
P79477
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 14
P79478
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;

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OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 15
P79479
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

Search completed: March 28, 2001, 07:53:05
Job time: 498 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:47 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-72
Perfect score: 56
Sequence: 1 ARHNYCSPAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*
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21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	19	W76026
2	52	92.9	10	19	W76027
3	50	89.3	10	19	W76024
4	50	89.3	10	19	W76025
5	50	89.3	10	19	W76028
6	50	89.3	10	19	W76029
7	50	89.3	10	19	W76030
8	50	89.3	10	19	W76010
9	50	89.3	117	19	W76001
10	50	89.3	117	19	W76003
11	50	89.3	117	20	Y06381
12	50	89.3	117	20	Y06387

13	50	89.3	118	20	Y06384	Humanised LM609 an
14	50	89.3	118	20	Y06385	Humanised LM609 an
15	50	89.3	118	20	Y06386	Humanised LM609 an
16	50	89.3	118	20	Y06383	Humanised LM609 an
17	50	89.3	130	20	Y06379	Murine monoclonal
18	47	83.9	10	19	W76021	LM609 grafted anti
19	46	82.1	10	19	W76039	LM609 grafted anti
20	46	82.1	10	19	W76040	LM609 grafted anti
21	46	82.1	10	19	W76022	LM609 grafted anti
22	46	82.1	10	19	W76023	LM609 grafted anti
23	45	80.4	10	19	W76037	LM609 grafted anti
24	45	80.4	10	19	W76020	LM609 grafted anti
25	42	75.0	110	20	W84099	Vironection alpha-
26	42	75.0	117	20	W84093	Murine vitronectin
27	42	75.0	117	20	W84097	Humanised anti-alp
28	41	73.2	8	20	Y06371	Murine monoclonal
29	41	73.2	10	19	W76038	LM609 grafted anti
30	38	67.9	464	19	W72907	Mycobacterium tube
31	38	67.9	464	20	Y21924	Amino acid sequenc
32	37	66.1	119	19	Y86109	S. pneumoniae derl
33	36	64.3	117	16	R79157	Human IGE receptor
34	36	64.3	117	16	R79155	Human IGE receptor
35	36	64.3	117	18	W27357	Heavy chain variab
36	36	64.3	117	18	W27526	Heavy chain variab
37	36	64.3	117	18	W27354	Heavy chain variab
38	36	64.3	119	18	W01578	Lead binding Mab 8
39	36	64.3	239	20	W73874	Human antiFc epsil
40	36	64.3	242	20	W73876	Human antiFc epsil
41	35	62.5	243	20	Y34866	Chlamydia pneumoni
42	34	60.7	30	21	Y81870	Yeast IPPI protein
43	34	60.7	33	18	W45312	Glucagon-like pept
44	34	60.7	165	19	W38713	S. pneumoniae glut
45	34	60.7	407	19	W98453	H. pylori GHPO 639

ALIGNMENTS

RESULT 1

W76026
ID W76026 standard; Protein; 10 AA.
XX
AC W76026;
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
XX
OS Mus sp.
XX
PN W09833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49863.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00086;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 |||||
 Db 1 arhnygsfad 10

RESULT 2

ID W76027 standard; Protein; 10 AA.

AC W76027;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI: 1998-437472/37.

XX DR N-PSDB: V49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 92.9%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0041;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
 |||||
 Db 1 arhnygsfae 10

RESULT 3

ID W76024 standard; Protein; 10 AA.

XX W76024;

XX DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI: 1998-437472/37.

XX DR N-PSDB: V49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

arthrititis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 arhnygsfa 9

RESULT 4

W76025
ID W76025 standard; Protein; 10 AA.

AC W76025;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX

Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-H region; CDR; complementarity determining region.

XX Mus sp.

XX OS

XX PN W09833919-A2.

XX XX 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX XX WPI; 1998-437472/37.

XX DR N-PSDB; V49862.

XX XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 arhnygsfa 9

RESULT 5

W76028
ID W76028 standard; Protein; 10 AA.

XX W76028;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #10.

XX

Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-H region; CDR; complementarity determining region.

XX Mus sp.

XX OS

XX PN W09833919-A2.

XX XX 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX XX WPI; 1998-437472/37.

XX DR N-PSDB; V49865.

XX XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |

Db 1 arhnygsfa 9

RESULT 6

W76029 ID W76029 standard; Protein; 10 AA.

AC W76029;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX W09833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49866.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.009;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 arhnygsfa 9

RESULT 7

W76030 ID W76030 standard; Protein; 10 AA.

AC W76030;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #12.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

XX W09833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; V49867.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.009;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 arhnygsfa 9

RESULT 8

W76010 ID W76010 standard; Protein; 10 AA.

XX W76010;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49847.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 1 arhnygsfa 9

RESULT 9
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 KW
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.

PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49820.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 89.3%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 97 arhnygsfa 105

RESULT 10
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX
 AC W76003;
 XX
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 KW
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
DR N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 89.3%; Score 50; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSEA 9
Db |||||
97 arhnygsfa 105

RESULT 11
Y06381
ID Y06381 standard; Protein; 117 AA.

AC Y06381;

DT 06-SEP-1999 (first entry)

DE Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Mus musculus.

OS WO9929888-A1.

PN 17-JUN-1999.

PF 04-DEC-1998; 98WO-US25828.

PR 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

DR WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

PS Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX Sequence 117 AA;

Query Match 89.3%; Score 50; DB 20; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSEA 9
Db |||||
97 arhnygsfa 105

RESULT 12
Y06387
ID Y06387 standard; Protein; 117 AA.

AC Y06387;

DT 06-SEP-1999 (first entry)

DE Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

OS Homo sapiens.

OS Synthetic.

XX Location/Qualifiers

Key 1..2

Peptide /note= "vector-encoded residues"

Region 31..35

Region /note= "CDR1"

Region 50..66

Region /note= "CDR2"

Region 107..117

Region /note= "CDR3"

WO9929888-A1.

PN 17-JUN-1999.

PF 04-DEC-1998; 98WO-US25828.

PR 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

DR WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

PS Disclosure; Page 52; 55pp; English.

XX This sequence represents the heavy chain variable region of a

CC humanised LM609 antibody. LM609 is directed to human integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX
 XX Sequence 117 AA;

Query Match 89.3%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 97 arhnygsfa 105

RESULT 13
 Y06384
 ID Y06384 standard; Protein; 118 AA.
 XX
 AC Y06384;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	31..37
Region	/note= "CDR1"
Region	52..67
Region	/note= "CDR2"
Region	100..107
Region	/note= "CDR3"

WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 XX Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 51; 55pp; English.

CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX
 XX Sequence 118 AA;

Query Match 89.3%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

RESULT 14
 Y06385
 ID Y06385 standard; Protein; 118 AA.
 XX
 AC Y06385;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	31..37
Region	/note= "CDR1"
Region	52..67
Region	/note= "CDR2"
Region	100..107
Region	/note= "CDR3"

WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 XX Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 51; 55pp; English.

CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX Sequence 118 AA;

Query Match 89.3%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

RESULT 15
 Y06386
 ID Y06386 standard; Protein; 118 AA.
 XX
 AC Y06386;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 DE
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37 "CDR1"
 FT /note=
 FT Region 52..67 "CDR2"
 FT /note=
 FT Region 100..107 "CDR3"
 FT /note=
 XX W0929888-A1.
 PN
 XX
 XX 17-JUN-1999.
 PD
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX
 PS Disclosure; Page 51-52; 55pp; English.
 XX
 CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX Sequence 118 AA;

Query Match 89.3%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

Search completed: March 28, 2001, 06:59:48
 Job time: 1384 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:55 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSFAD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	64.3	94	3	US-09-147-550-14
2	36	64.3	94	3	US-09-147-550-45
3	36	64.3	94	3	US-09-147-550-48
4	36	64.3	94	3	US-09-147-550-77
5	36	64.3	94	3	US-09-147-550-84
6	36	64.3	94	3	US-09-147-550-90
7	36	64.3	94	3	US-09-147-550-101
8	36	64.3	119	3	US-08-767-128-6
9	34	60.7	286	2	US-08-809-267-3
10	34	60.7	286	4	PCT-US95-13662A-3
11	34	60.7	287	2	US-08-741-437-5
12	34	60.7	287	2	US-09-134-593-5
13	33	58.9	584	1	US-08-448-196A-7
14	32	57.1	15	1	US-08-618-464-7
15	32	57.1	15	3	US-09-107-615-7
16	32	57.1	25	2	US-08-480-190-44
17	32	57.1	25	2	US-08-488-379-44
18	32	57.1	25	4	PCT-US93-07545-44
19	32	57.1	36	1	US-08-053-131-84
20	32	57.1	36	1	US-08-645-641-84
21	32	57.1	36	1	US-07-853-408B-84
22	32	57.1	36	2	US-08-096-762-84
23	32	57.1	36	2	US-08-308-865-84
24	32	57.1	36	4	PCT-US92-10983-84
25	32	57.1	80	1	US-08-264-250A-1
26	32	57.1	89	1	US-08-025-038-30
27	32	57.1	89	1	US-08-039-137-17
28	32	57.1	90	2	US-08-485-133-23

29	32	57.1	94	3	US-09-147-550-12	Sequence 12, Appl
30	32	57.1	94	3	US-09-147-550-13	Sequence 13, Appl
31	32	57.1	94	3	US-09-147-550-15	Sequence 15, Appl
32	32	57.1	94	3	US-09-147-550-16	Sequence 16, Appl
33	32	57.1	94	3	US-09-147-550-17	Sequence 17, Appl
34	32	57.1	94	3	US-09-147-550-18	Sequence 18, Appl
35	32	57.1	94	3	US-09-147-550-19	Sequence 19, Appl
36	32	57.1	94	3	US-09-147-550-20	Sequence 20, Appl
37	32	57.1	94	3	US-09-147-550-21	Sequence 21, Appl
38	32	57.1	94	3	US-09-147-550-22	Sequence 22, Appl
39	32	57.1	94	3	US-09-147-550-24	Sequence 24, Appl
40	32	57.1	94	3	US-09-147-550-25	Sequence 25, Appl
41	32	57.1	94	3	US-09-147-550-26	Sequence 26, Appl
42	32	57.1	94	3	US-09-147-550-27	Sequence 27, Appl
43	32	57.1	94	3	US-09-147-550-28	Sequence 28, Appl
44	32	57.1	94	3	US-09-147-550-29	Sequence 29, Appl
45	32	57.1	94	3	US-09-147-550-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||
80 RHNYGVF 86

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match. 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match. 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match. 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match. 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT

ORGANISM: BOVINE
US-09-147-550-90

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHYGVSF 8
|||||

Db 80 RHYGVF 86

RESULT 7

US-09-147-550-101
Sequence 101, Application US/09147550
Patent No. 6090540
GENERAL INFORMATION:
APPLICANT: Aida Yoko
TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
CURRENT APPLICATION NUMBER: US/09/147,550
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: PCT/JP97/02485
EARLIER FILING DATE: 1997-07-17
EARLIER APPLICATION NUMBER: JP 8-190933
EARLIER FILING DATE: 1996-07-19
EARLIER APPLICATION NUMBER: JP 9-77979
EARLIER FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 101
LENGTH: 94
TYPE: PRT
ORGANISM: BOVINE
US-09-147-550-101

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHYGVSF 8
|||||

Db 80 RHYGVF 86

RESULT 8

US-08-767-128-6
Sequence 6, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079 West Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-6

Query Match 64.3%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 97 ARHHYGYA 105

RESULT 9

US-08-809-267-3
Sequence 3, Application US/08809267
Patent No. 5861296
GENERAL INFORMATION:
APPLICANT: LENNOX, Tricia L.
APPLICANT: SLATKO, Barton E.
APPLICANT: SEARS, Lauren E.
TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
TITLE OF INVENTION: LITORALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,267

;; FILING DATE: 12-MAR-1997
;; CLASSIFICATION: 433
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/13662
;; FILING DATE:
;; APPLICATION NUMBER: US 08/329,721
;; FILING DATE: 25-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILLIAMS, GREGORY D.
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-105-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 927-5054
;; TELEFAX: (508) 927-1705
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-809-267-3

Query Match 60.7%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 10
PCT-US95-13662A-3
;; Sequence 3, Application PC/TUS9513662A
;; GENERAL INFORMATION:
;; APPLICANT: LENNOX, Tricia L.
;; APPLICANT: SLATKO, Barton E.
;; APPLICANT: SEARS, Lauren E.
;; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
;; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
;; TITLE OF INVENTION: LITORALIS
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
;; STREET: 32 TOZER ROAD
;; CITY: BEVERLY
;; STATE: MASSACHUSETTS
;; COUNTRY: USA
;; ZIP: 01915
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/13662A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/329,721
;; FILING DATE: 25-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILLIAMS, GREGORY D.
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-105-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 927-5054
;; TELEFAX: (508) 927-1705
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; PCT-US95-13662A-3

Query Match 60.7%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 11
US-08-741-437-5
;; Sequence 5, Application US/08741437
;; Patent No. 5843665
;; GENERAL INFORMATION:
;; APPLICANT: Hawkins, Phillip R.
;; APPLICANT: Hillman, Jennifer L.
;; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/741,437
;; FILING DATE: Filed Herewith
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0148 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 855-0555
;; TELEFAX: (415) 845-4166
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 287 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 4199
;; US-08-741-437-5

Query Match 60.7%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 12

US-09-134-593-5
; Sequence 5, Application US/09134593
; Patent No. 5981232
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09134,593
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-09-134-593-5

Query Match 60.7%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 13
US-08-448-196A-7
; Sequence 7, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: RELATED PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BROAD JR., ROBERT L.
; REGISTRATION NUMBER: 18,757
; REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 205-544-0021
; TELEFAX: 205-544-0258
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-448-196A-7

Query Match 58.9%; Score 33; DB 1; Length 584;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAD 10
Db 81 RDNVYGEAD 89

RESULT 14
US-08-618-464-7
; Sequence 7, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INVOLVED IN IMMUNE PROTECTION AGAINST ARTHR
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: S1
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-08-618-464-7

Query Match 57.1%; Score 32; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 11 RHNYG 15

RESULT 15
US-09-107-615-7
Sequence 7, Application US/09107615
Patent No. 6153200
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
APPLICANT: ALBANI, SALVATORE
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
INDUCING IMMUNE PROTECTION AGAINST
TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400 -
CITY: La Jolla
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,615
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: S1
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-09-107-615-7

Query Match 57.1%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 11 RHNYG 15

Search completed: March 28, 2001, 07:01:55
Job time: 1334 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:23 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	70.9	446	2 T19625	hypothetical prote
2	39	70.9	723	2 F83173	outer membrane pro
3	38	69.1	275	2 G75130	translation initia
4	38	69.1	275	2 D71087	probable translati
5	37	67.3	347	2 S43771	phosphatidylcholin
6	36	65.5	82	2 I51106	Major Histocompati
7	36	65.5	89	2 S38688	MHC class II histo
8	36	65.5	89	2 S38683	MHC class II histo
9	36	65.5	89	2 S38684	MHC class II histo
10	36	65.5	210	1 B69265	conserved hypothet
11	36	65.5	225	2 I47095	MHC class II OVAR-
12	36	65.5	326	2 S47248	site-specific DNA-
13	35	63.6	287	1 PWBY	inorganic pyrophos
14	35	63.6	287	1 PWKL	inorganic pyrophos
15	35	63.6	507	2 H82580	glycerol-3-phospha
16	34	61.8	108	2 S26316	ig heavy chain v r
17	34	61.8	110	2 S26317	ig heavy chain v r
18	34	61.8	189	2 D75026	hypothetical prote
19	34	61.8	192	2 D71211	hypothetical prote
20	34	61.8	364	2 C64326	succinyl-CoA synth
21	34	61.8	464	2 B70828	hypothetical prote
22	34	61.8	484	2 G72395	alpha-L-arabinofur
23	33	60.0	80	2 I54469	MHC HLA-DR-beta-1
24	33	60.0	80	2 I68777	MHC HLA-DR-beta-1
25	33	60.0	81	2 I54550	HLA DRB1*1202 - hu
26	33	60.0	85	2 I59634	MHC class II DR-be
27	33	60.0	89	2 S38676	MHC class II histo
28	33	60.0	89	2 S38680	MHC class II histo
29	33	60.0	89	2 S57512	MHC class II histo

RESULT 1
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2: 85/1: 120/2: 183/3: 218/3: 255/3: 285/2: 331/3: 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
|||||
DB 51 RHNYGSHA 58

RESULT 2
F83173
outer membrane protein OprC PA3790 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
C:Accession: F83173
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: AB2950
A:Accession: F83173
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-723 <STO>
A:Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AA07177.1; GSPDB:GN
C:Genetics:
A:Experimental source: strain PA01
A:Gene: oprC; PA3790

ALIGNMENTS

30	33	60.0	123	2	C25239	MHC class II histo
31	33	60.0	127	2	G70105	conserved hypothet
32	33	60.0	167	2	T16454	hypothetical prote
33	33	60.0	200	2	D32526	class II histocomp
34	33	60.0	220	2	T46055	hypothetical prote
35	33	60.0	237	2	C27060	class II histocomp
36	33	60.0	266	2	I54287	gene HLA-DRB1 prot
37	33	60.0	266	2	A27618	class II histocomp
38	33	60.0	266	2	I54295	lymphocyte antigen
39	33	60.0	275	2	T04480	acyl-CoA oxidase h
40	33	60.0	279	2	T05421	hypothetical prote
41	33	60.0	302	2	T26540	hypothetical prote
42	33	60.0	383	2	S56179	secreted glycoprot
43	33	60.0	395	2	G75587	hypothetical prote
44	33	60.0	448	1	A60003	nucleocapsid prote
45	33	60.0	470	2	H71667	glutamate--cRNA 11

Query Match 70.9%; Score 39; DB 2; Length 723;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAE 10
 Db 407 HNYGAFGE 414
 |||||

RESULT 3
 G75130
 translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: G75130
 R:anonymous, Genoscope
 A:Submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A:Reference number: A75001
 A:Accession: G75130
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <RAW>
 A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545827
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: aif2A; PAB0568
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 69.1%; Score 38; DB 2; Length 275;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAE 10
 Db 23 HNYGAFLE 30
 |||||

RESULT 4
 D71087
 probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C:Accession: D71087
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137
 A:Accession: D71087
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-275 <RAW>
 A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:g3257375
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0961
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 69.1%; Score 38; DB 2; Length 275;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAE 10
 Db 23 HNYGAFLE 30
 |||||

RESULT 5

S43771
 phosphatidylcholine desaturase (EC 1.3.1.35) - Synechococcus sp. (strain PCC 7002)
 N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misiden
 C:Species: Synechococcus sp.
 A:Variety: PCC 7002
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S43771
 R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
 Plant Mol. Biol. 24, 643-650, 1994
 A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
 A:Reference number: S43770; MUID:94207189
 A:Accession: S43771
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <SAK>
 A:Cross-references: GB:DJ3779; NID:g488510; PIDN:BAA02922.1; PID:g488511
 C:Superfamily: omega-3 fatty acid desaturase
 C:Keywords: oxidoreductase

Query Match 67.3%; Score 37; DB 2; Length 347;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAE 10
 Db 334 AEHNYISFAQ 343
 |||||

RESULT 6
 I51106
 Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
 C:Species: Phasianus colchicus (ring-necked pheasant)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C:Accession: I51106
 R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
 A:Reference number: I51103; MUID:94245280
 A:Accession: I51106
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-82 <WIT>
 A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 82;
 Best Local Similarity 85.7%; Pred. No. 5.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||||

RESULT 7
 S38688
 MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushba
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38688
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
 A:Reference number: S38676
 A:Accession: S38688
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:227158
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81

RESULT 8

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38683
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced
 A:Reference number: S38676
 A:Accession: S38683
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27153
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81

RESULT 9

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38684
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced
 A:Reference number: S38676
 A:Accession: S38684
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27154
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81

RESULT 10

conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: B69265
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ..; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: B69265
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-210 <KLE>
 A:Cross-references: GB:AE001098; GB:AE000782; NID:q2689421; PIDN:AAB91117.1; PID:q265
 C:Superfamily: conserved hypothetical protein AF0119

Query Match 65.5%; Score 36; DB 1; Length 210;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAE 10
 Db 128 RHAYGSFVD 136

RESULT 11

MHC class II OVAR-DR-beta-3 - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
 C:Accession: I47095
 R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
 Anim. Genet. 24, 249-255, 1993
 A:Title: Isolation, characterization and evolution of ovine major histocompatibility
 A:Reference number: I47075; MUID:94057592
 A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-225 <FAB>
 A:Cross-references: GB:L04790; NID:g458880; PIDN:AAAL6562.1; PID:g458881
 C:Genetics:
 A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
 F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 36; DB 2; Length 225;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 68 RHNYGVF 74

RESULT 12

site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) phi37II - phage
 S47248
 C:Species: phage phi-37
 C:Date: 08-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-May-2000
 C:Accession: S47248; S50099
 R:Noyer-Weidner, M.; Walter, J.; Terschueren, P.A.; Chai, S.; Trautner, T.A.
 submitted to the EMBL Data Library, August 1994
 A:Description: M.phi37II: a new monospecific C5-DNA-methyltransferase with pronounced
 A:Reference number: S47248

A:Accession: S47248
 A:Molecule type: DNA
 A:Residues: 1-326 <NOY>

A:Cross-references: EMBL:X80202; NID:g535136; PIDN:CAA56493.1; PID:g535137
 R:Noyer-Weidner, M.; Walter, J.; Terschueren, P.A.; Chai, S.; Trautner, T.A.

Nucleic Acids Res. 22, 4066-4072, 1994

A:Title: M.phi37II: a new monospecific DNA (cytosine-C5) methyltransferase with pronoc
 A:Reference number: S50099; MUID:95023172

A:Accession: S50099

A:Molecule type: DNA

A:Residues: 1-90,120-130,177-237 <NOW>

A:Cross-references: EMBL:X80202

C:Genetics:

A:Gene: M.phi37II

C;Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII
C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 65.5%; Score 36; DB 2; Length 326;
Best Local Similarity 55.6%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

OY 2 RHYGSAE 10
||||:|
Db 52 RHNEGDVE 60

RESULT 13

PWKL

inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein YBR011c; protein YBR0202; pyrophosphate phosphohydrolase
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Nov-1980 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C;Accession: S45864; S07679; A01014; S29189
R;Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Bole
submitted to the Protein Sequence Database, August 1994

A;Reference number: S45862

A;Gene: IPP

C;Superfamily: inorganic pyrophosphatase

C;Keywords: hydrolase

F;79/151/Active site: Arg, Glu #status predicted

A;Residues: 1-287 <ENT>

A;Molecule type: DNA

A;Cross-references: EMBL:X13253; NID:g536205; PIDN:CAA84949.1; PID:g536206; GSPDB:GN0000

A;Experimental source: strain S288C

R;Kolaskowski Jr., L.F.; Schloesser, M.; Cooperman, B.S.

Nucleic Acids Res. 16, 10441-10452, 1988

A;Title: Cloning, molecular characterization and chromosome localization of the inorganic

A;Reference number: S07679; MUID:89083474

A;Accession: S07679

A;Molecule type: DNA

A;Residues: 1-266, 'L', 268-287 <KOL>

A;Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g4199

R;Cohen, S.A.; Sterner, R.; Keim, P.S.; Heinrikson, R.L.

J. Biol. Chem. 253, 889-897, 1978

A;Title: Covalent structural analysis of yeast inorganic pyrophosphatase.

A;Reference number: A92241; MUID:78087552

A;Accession: A01014

A;Molecule type: protein

A;Residues: 2-40, 'D', 42-71, 'N', 73-75-117, 'N', 119-123, 'Q', 125-136, 'E', 138-186, 'D', 188-224

A;Note: this is the final paper in a series

A;Note: no disulfide bonds are present

R;Razinikov, A.V.; Skiyankina, V.A.; Awaeva, S.M.

FEBS Lett. 308, 62-64, 1992

A;Title: Tyrosine-89 is important for enzymatic activity of *S. cerevisiae* inorganic pyro

A;Reference number: S29189; MUID:92354770

A;Accession: S29189

A;Molecule type: protein

A;Residues: 83-105, 'E', 107-112 <RAZ>

R;Bond, M.W.; Chiu, N.Y.; Cooperman, B.S.

Biochemistry 19, 94-102, 1980

A;Title: Identification of an arginine important for enzymatic activity within the coval

A;Reference number: A90443

A;Contents: annotation; active site

C;Genetics:

A;Gene: SGD:IPP1; PPA; MIPS:YBR011c

A;Cross-references: SGD:S000215; MIPS:YBR011c

A;Map position: 2R

C;Function:

A;Description: catalyzes hydrolysis of pyrophosphate to orthophosphate

A;Note: requires divalent metal cation

C;Superfamily: inorganic pyrophosphatase

C;Keywords: homodimer; hydrolase

F;2-287/Product: inorganic pyrophosphate #status experimental <MAT>

F;79/Binding site: pyrophosphate (Arg) #status experimental

Query Match

Best Local Similarity 63.6%; Score 35; DB 1; Length 287;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNYGSFAE 10
||||:|
Db 92 HNYGAFPQ 99

RESULT 14

PWKL

inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Kluyveromyces marxianus* var. *lactis*)
C;Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C;Accession: S07894
R;Stark, M.J.R.; Milner, J.S.

Yeast 5, 35-50, 1989

A;Title: Cloning and analysis of the *Kluyveromyces lactis* TRP1 gene: a chromosomal lo

A;Reference number: S07892; MUID:89189093

A;Accession: S07894

A;Molecule type: DNA

A;Residues: 1-287 <STA>

A;Cross-references: EMBL:X14230; NID:g2900; PIDN:CAA32446.1; PID:g2903

C;Genetics:

A;Gene: IPP

C;Superfamily: inorganic pyrophosphatase

C;Keywords: hydrolase

F;79/151/Active site: Arg, Glu #status predicted

Query Match 63.6%; Score 35; DB 1; Length 287;

Best Local Similarity 62.5%; Pred. No. 30;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HNYGSFAE 10
||||:|
Db 92 HNYGAFPQ 99

RESULT 15

H82580

glycerol-3-phosphate dehydrogenase XF2266 [imported] - *Xylella fastidiosa* (strain 9a5

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C;Accession: H82580

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82580

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-507 <SIM>

A;Cross-references: GB:AE004038; GB:AE003849; NID:g9107408; PIDN:AAF85065.1; GSPDB:GN

A;Experimental source: strain 9a5C

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sancelli, R.V.; Sawa

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF2266

C;Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)

Query Match

63.6%; Score 35; DB 2; Length 507;

Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches

1; Indels 0; Gaps 0;

QY 3 HNYGSPAE 10

||||: ||

Db 422 HNYGTCAE 429

Search completed: March 28, 2001, 07:04:24
Job time: 1062 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:02 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSFAE 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	69.1	275	1 IF2A_PYRAB	Q9V0E4 pyrococcus
2	38	69.1	275	1 IF2A_PYRHO	OS8655 pyrococcus
3	35	63.6	284	1 IPYR_PICPA	013505 pichia past
4	35	63.6	286	1 IPYR_KLULA	P13998 kluyveromyc
5	35	63.6	286	1 IPYR_YEAST	P08817 saccharomyc
6	34	61.8	364	1 SDCC_METJA	Q57663 methanococc
7	33	60.0	448	1 NCAP_CVHOC	P33469 human coron
8	33	60.0	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
9	33	60.0	473	1 SYE2_AQUAE	O67271 aquifex aeo
10	33	60.0	682	1 VG50_RPML5	Q05262 mycobacteri
11	33	60.0	1267	1 VL3_REOVL	P17378 reovirus (t
12	33	60.0	1267	1 VL3_REOVL	P17376 reovirus (t
13	32	58.2	65	1 CCSA_OENBE	P31565 oenothera b
14	32	58.2	65	1 CCSA_PEA	P31172 pisum sativ
15	32	58.2	196	1 WBBJ_ECOLI	P37750 escherichia
16	32	58.2	198	1 HB2J_HUMAN	P01911 homo sapien
17	32	58.2	220	1 SDHB_BACSU	O34635 bacillus su
18	32	58.2	262	1 VP2_BPCHP	P19193 bacterioph
19	32	58.2	266	1 HB2A_HUMAN	P01913 homo sapien
20	32	58.2	266	1 HB2B_HUMAN	P01912 homo sapien
21	32	58.2	266	1 HB2C_HUMAN	P01914 homo sapien
22	32	58.2	266	1 HB2D_CANFA	P18470 canis fami
23	32	58.2	266	1 HB2E_HUMAN	P13759 homo sapien
24	32	58.2	266	1 HB2F_HUMAN	P04229 homo sapien
25	32	58.2	266	1 HB2G_HUMAN	P13758 homo sapien
26	32	58.2	266	1 HB2H_HUMAN	P13760 homo sapien
27	32	58.2	266	1 HB2I_HUMAN	P20039 homo sapien
28	32	58.2	266	1 HB2J_HUMAN	P13761 homo sapien
29	32	58.2	310	1 APBA_AQUAE	O67619 aquifex aeo
30	32	58.2	313	1 CCSA_TOBAC	P12216 nicotiana t
31	32	58.2	321	1 CCSA_MAIZE	P46659 zea mays (m
32	32	58.2	321	1 CCSA_ORYSA	P12215 oryza sativ
33	32	58.2	328	1 CCSA_ARATH	P56770 arabidopsis

34 32 58.2 349 1 YJY9_YEAST P41903 saccharomyc
35 32 58.2 480 1 VP5_BRD P21230 broadhaven
36 32 58.2 528 1 PRI2_YEAST P20457 saccharomyc
37 32 58.2 581 1 MIK1_SCHPO P30290 schizosacch
38 32 58.2 629 1 KSYK_RAT Q64725 rattus norv
39 32 58.2 649 1 GPDH_SCHPO O14400 schizosacch
40 32 58.2 853 1 PHS1_DICDI Q00766 dictyosteli
41 32 58.2 872 1 UL47_HSVE4 P25073 equine herp
42 32 58.2 938 1 NM21_HUMAN Q05586 homo sapien
43 32 58.2 938 1 NM21_MOUSE P35438 mus musculu
44 32 58.2 938 1 NM21_RAT P35439 rattus norv
45 32 58.2 1095 1 PIPA_DROME P13217 drosophila

ALIGNMENTS

RESULT 1
IF2A_PYRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
CC -----
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CC -----
CC EMBL: AJ248285; CAB49760.1; -
DR INTERPRO: IPR003029; -
DR PFAM: PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;
Query Match 69.1%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFAE 10
DB 23 HNYGAFLE 30
RESULT 2
IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PH0961
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE; 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 R Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
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 CC -----
 DR EMBL; AF000004; BAA30058.1;
 DR INTERPRO; IPR003029;
 DR PFAM; PF00575; SI; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83 SI MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

 Query Match 69.1%; Score 38; DB 1; Length 275;
 Best Local Similarity 75.0%; Pred. NO. 2.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSPAE 10
 | | | | | | | |
 DB 23 HNYGAFLE 30

 RESULT 3
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC OL3505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosgro I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
 RT HIS3 genes";
 RL Yeast 14:861-867(1998).

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CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ001000; CA040453.1;
 DR HSP; P00817; IWGI.
 DR INTERPRO; IPR001596;
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolyase; Magnesium.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

 Query Match 63.6%; Score 35; DB 1; Length 284;
 Best Local Similarity 62.5%; Pred. NO. 8.9;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSAFE 10
 | | | | | | | |
 DB 91 HNYGAFQP 98

 RESULT 4
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC PI3998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).

 CC SIMILARITY TO E. COLI AND YEAST PPASES.
 CC MEDLINE; 90254161.
 CC Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 CC Cooperman B.S.;
 CC "Conservation of functional residues between yeast and E. coli
 CC inorganic pyrophosphatases.";
 CC Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X14230; CAA32446.1; -
 DR PIR; S07894; PWVKL.
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PRAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 DR Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 286;
 Best Local Similarity 62.5%; Pred. No. 8.9;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAE 10
 Db 91 HNYGAFPQ 98
 RESULT 5
 ID IPYR-YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Kelm P.S., Heinrikson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN=S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database."
 RL Electrophoresis 15:1466-1486(1994).
 [5]

RP SEQUENCE OF 239-249.
 RC STRAIN=ATCC 38531 / Y41;
 RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT *Saccharomyces cerevisiae*."
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 [6]
 RN RN
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 [7]
 RN RN
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution."
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 [8]
 RN RN
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 [9]
 RN RN
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 [10]
 RN RN
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 95096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of *Saccharomyces cerevisiae*
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 [11]
 RN RN
 RP SIMILARITY TO E. COLI AND K. LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X13253; CAA31629.1; -
 DR EMBL; Z35880; CAA84949.1; -
 DR PIR; S45864; PWBY.
 DR PDB; LPYP; 15-OCT-91.
 DR PDB; IYPP; 07-DEC-96.
 DR PDB; IWGI; 19-NOV-97.
 DR PDB; IWGJ; 19-NOV-97.
 DR PDB; 1HJG; 08-APR-98.

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DR PDB; 1HUK; 08-APR-98.
DR PDB; 117E; 23-DEC-98.
DR PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -.
DR SGD; S0000215; IPPI.
DR INTERPRO; IPR001596; -.
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 E -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT TURN 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 286;
Best Local Similarity 62.5%; Pred. No. 8.9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAE 10
Db 91 HNYGAPFQ 98

RESULT 6
SUCC_METJA STANDARD; PRT; 364 AA.
AC Q57663;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5) (SCS-BETA).
GN SUCC OR MJ0210.

Query Match 61.8%; Score 34; DB 1; Length 364;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAE 10
Db 215 RHNYEEFEE 223

RESULT 7
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR INTERPRO; IPR001218; -.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A. 2661 / ATCC 43067;
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: SUCCINATE + COA + ATP = SUCCINYL-COA + ADP +
CC ORTHOPHOSPHATE.
CC -!- SIMILARITY: TO OTHER BETA SUBUNITS OF SUCCINYL-COA SYNTHETASES.
CC -----
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CC -----
DR EMBL; U67477; AAB98195.1; -.
DR HSP; P07460; LSCU.
DR TIGR; MJ0210; -.
DR INTERPRO; IPR000303; -.
DR PFAM; PF00549; ligase-CoA; 1.
DR PROSITE; PS01217; SUCCINYL_COA_Lig_3; 1.
KW Ligase; Tricarboxylic acid cycle.
SQ SEQUENCE 364 AA; 40907 MW; 16937FC54694770C CRC64;

Query Match 61.8%; Score 34; DB 1; Length 364;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSPAE 10
Db 215 RHNYEEFEE 223

RESULT 7
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR INTERPRO; IPR001218; -.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

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Query Match 60.0%; Score 33; DB 1; Length 448;
 Best Local Similarity 85.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 ||| |||
 DB 103 RHNGSF 109

RESULT 8
 ID_SYE2_RICPR
 AC Q9ZCT8; STANDARD; PRT; 470 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
 DE (GLURS 2).
 GN GLUT2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RX MEDLINE; 99039499.
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O., Naeslund A.K.,
 RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Kurland C.G.;
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria."
 RL Nature 396:133-140(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ235272; CAAL5066.1; -
 CC HSP; P27000; IGLN.
 CC INTERPRO; IPR000924; -
 CC PFAM; PF00749; TRNA-synt_1c; 1.
 CC PRINTS; PR00987; TRNASYNTHGLU.
 CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 CC SIMILAR 10 20 "HIGH" REGION.
 CC FT SIMILAR 239 243 "KMSKS" REGION.
 CC FT BINDING 242 242 ATP (BY SIMILARITY).
 CC SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 60.0%; Score 33; DB 1; Length 470;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 ||| | |
 DB 31 ARHNGKF 38

RESULT 9
 ID_SYE_AQUAE

ID_SYE_AQUAE STANDARD; PRT; 473 AA.
 AC Q67271.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
 DE (GLURS).
 GN GLTX OR AQ_1221.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE; 98195666.
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus".
 RL Nature 392:353-358(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF000729; AAC07230.1; -
 CC INTERPRO; IPR000924; -
 CC PFAM; PF00749; TRNA-synt_1c; 1.
 CC PRINTS; PR00987; TRNASYNTHGLU.
 CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 CC SIMILAR 10 20 "HIGH" REGION.
 CC FT SIMILAR 242 246 "KMSKS" REGION.
 CC FT BINDING 245 245 ATP (BY SIMILARITY).
 CC SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 60.0%; Score 33; DB 1; Length 473;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 ||| | | |
 DB 31 ARHNGKF 38

RESULT 10
 ID_VG50_BPML5 STANDARD; PRT; 682 AA.
 AC Q05262;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
 DE (EC 1.17.4.2) (GP50).
 GN 50.
 OS Mycobacteriophage L5.
 OC Viruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93211282.
 RA Hatfull G.F., Sarkis G.J.;

RT "DNA sequence, structure and gene expression of mycobacteriophage L5.

RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -1- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
CC OXIDIZED THIOREDOXIN + H(2)O = RIBONUCLEOSIDE TRIPHOSPHATE +
CC REDUCED THIOREDOXIN.
CC -----
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CC -----
DR EMBL; Z18946; CAA79426.1; -;
DR PIR; S30995; S30995.
DR INTERPRO; IPR000788; -;
DR PFAM; PF00317; ribonucleo_red; 1.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
I: |||||
DB 311 AKEGYGSFA 319

RESULT 11
VL3_REOVL STANDARD; PRT; 1267 AA.
AC P17378;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE MINOR CORE PROTEIN LAMBDA 3.
GN L1.
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89163254.
RA Wiener J.R., Joklik W.K.;
RT "The sequences of the reovirus serotype 1, 2, and 3 L1 genome
RT segments and analysis of the mode of divergence of the reovirus
RT serotypes."
RL Virology 169:194-203(1989).
CC -1- MISCELLANEOUS: IT IS UNLIKELY THAT CORES CONTAIN MORE THAN 12
CC MOLECULES OF PROTEIN LAMBDA 3.
CC -1- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
DR PIR; A30121; MWXR31.
KW Core protein.
SQ SEQUENCE 1267 AA; 142269 MW; FC9FD43CEF527148 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
Best Local Similarity 55.6%; Pred. No. 1.le+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGSFAE 10
I: || ||:
DB 1043 RHSYSSFSK 1051

Db 1043 RHSYSSFSK 1051
||:| ||:
RESULT 12
VL3_REOVL STANDARD; PRT; 1267 AA.
AC P17376;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE MINOR CORE PROTEIN LAMBDA 3.
GN L1
OS Reovirus (type 1 / strain Lang).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89163254.
RA Wiener J.R., Joklik W.K.;
RT "The sequences of the reovirus serotype 1, 2, and 3 L1 genome
RT segments and analysis of the mode of divergence of the reovirus
RT serotypes."
RL Virology 169:194-203(1989).
CC -1- MISCELLANEOUS: IT IS UNLIKELY THAT CORES CONTAIN MORE THAN 12
CC MOLECULES OF PROTEIN LAMBDA 3.
CC -1- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
DR PIR; A30121; MWXR31.
KW Core protein.
SQ SEQUENCE 1267 AA; 142354 MW; 157EBFD4D664FCDB CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
Best Local Similarity 55.6%; Pred. No. 1.le+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGSFAE 10
I: || ||:
DB 1043 RHSYSSFSK 1051

RESULT 13
CCSA_OENBE STANDARD; PRT; 65 AA.
ID CCSA_OENBE
AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Oenothera bertiana (Bertero's evening primrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Myrtales; Onagraceae; Oenothera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93169690.
RA Nimzyk R., Schoendorf T., Hachtel W.;
RT "In-frame length mutations associated with short tandem repeats are
RT located in unassigned open reading frames of Oenothera chloroplast
RT DNA."
RL Curr. Genet. 23:265-270(1993).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL: X64617; CAA45900.1; -
DR EMBL: X64614; CAA45894.1; -
DR PIR: S1981; S1981.
DR PIR: S1998; S1998.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7441 MW; 343566DDA1492C0C CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 7.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 57 HSYGSF 62

RESULT 14
CCSA_PEA
ID CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Pisum sativum (Garden pea).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE: 91355950.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
RL in pea chloroplasts.";
PL Plant Mol. Biol. 17:541-545(1991).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CLL/NRFE/CCSA FAMILY.
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CC -----
DR EMBL: X59015; CAA41754.1; -
DR PIR: S17441; S17441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 7.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 57 HSYGSF 62

RESULT 15
WBBJ_ECOLI
ID WBBJ_ECOLI STANDARD; PRT; 196 AA.
AC P37750; P76375;

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DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PUTATIVE LIPOPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ
DE (EC 2.3.1.-).
GN WBBJ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE: 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosyntheses
RT region (rfb) of Escherichia coli K-12 W3110: Identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a.";
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=K12 / W31;
RX MEDLINE: 94292435.
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
RA Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
RT of its rfb gene cluster.";
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RC REVISIONS TO 168-176 AND 187-189.
RC STRAIN=K12 / W31;
RA Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
RC STRAIN=K12 / W31655;
RX MEDLINE: 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RC SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE: 97251358.
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
CC ON THE O ANTIGEN
CC -1- PATHWAY: LIPOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC -----
DR EMBL: U03041; AAC31635.1; -
DR EMBL: U09876; AAB88406.1; -
DR EMBL: AE000294; AAC75094.1; -

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DR EMBL; D90841; CAB21803.1; -;
DR EMBL; D90842; CAB21811.1; -;
DR ECOGENE; EG11984; WEBJ;
DR INTERPRO; IPR001451; -;
DR PFAM; PF00132; hexapep; 1;
DR PROSITE; PS00101; HEXAPEP-TRANSFERASES; FALSE_NEG.
KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1B1 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 196;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
||:||||
Db 105 HNHGSF 110

Search completed: March 28, 2001, 07:35:03
Job time: 140 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:05 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	81.8	839	10	O9LIE5
2	39	70.9	446	5	O62086 caenorhabdi
3	39	70.9	723	2	P72121 pseudomonas
4	38	69.1	89	7	O19495 gallus gall
5	37	67.3	347	2	Q55231 synechococc
6	36	65.5	39	7	P79474 cervus elap
7	36	65.5	39	7	P79477 cervus elap
8	36	65.5	39	7	P79478 cervus elap
9	36	65.5	39	7	P79479 cervus elap
10	36	65.5	74	6	O9TTM4 bos taurus
11	36	65.5	76	7	Q9TFC2 macaca mula
12	36	65.5	78	6	O97835 ovis aries
13	36	65.5	78	6	O97839 ovis aries
14	36	65.5	78	6	O97844 ovis aries
15	36	65.5	78	6	O97968 ovis aries
16	36	65.5	78	7	Q9MTW6 leopardus p
17	36	65.5	78	7	Q9MTW5 leopardus p
18	36	65.5	78	7	Q9MTW4 leopardus p
19	36	65.5	79	7	O19191 prionailuru

20	36	65.5	79	7	O19192	O19192 prionailuru
21	36	65.5	79	7	O19380	O19380 felis silve
22	36	65.5	79	7	O19381	O19381 felis silve
23	36	65.5	79	7	O19382	O19382 felis silve
24	36	65.5	79	7	O19396	O19396 felis silve
25	36	65.5	79	7	O19397	O19397 felis silve
26	36	65.5	79	7	O19405	O19405 felis silve
27	36	65.5	79	7	O19406	O19406 felis silve
28	36	65.5	79	7	O19407	O19407 felis silve
29	36	65.5	79	7	O19408	O19408 felis silve
30	36	65.5	79	7	O19435	O19435 felis silve
31	36	65.5	79	7	O9MX19	O9MX19 leopardus p
32	36	65.5	79	7	O9MX13	O9MX13 leopardus p
33	36	65.5	79	7	O9MX03	O9MX03 leopardus p
34	36	65.5	79	7	O9MX00	O9MX00 leopardus p
35	36	65.5	79	7	O9MW29	O9MW29 leopardus p
36	36	65.5	79	7	O9MW28	O9MW28 leopardus p
37	36	65.5	79	7	O9MW27	O9MW27 leopardus p
38	36	65.5	79	7	O9MWY9	O9MWY9 leopardus p
39	36	65.5	79	7	O9MWY8	O9MWY8 leopardus p
40	36	65.5	79	7	O9MWY6	O9MWY6 leopardus p
41	36	65.5	79	7	O9MWY5	O9MWY5 leopardus p
42	36	65.5	79	7	O9MWY4	O9MWY4 leopardus p
43	36	65.5	79	7	O9MWY3	O9MWY3 leopardus p
44	36	65.5	79	7	O9MWX6	O9MWX6 leopardus p
45	36	65.5	79	7	O9MWX5	O9MWX5 leopardus p

ALIGNMENTS

RESULT 1

Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC O9LIE5:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -;
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 81.8%; Score 45; DB 10; Length 839;
Best Local Similarity 70.0%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAE 10

:|||||:

Db 274 SRHNYGSFCD 283

RESULT 2

O62086

ID O62086 PRELIMINARY; PRT; 446 AA.
 AC 062086;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE C31H5.6 PROTEIN.
 GN C31H5.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlhans P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL; Z93778; CAB07846.1; -;
 DR INTERPRO; IPR000379; -;
 DR DR INTERPRO; IPR002925; -;
 DR PFAM; PF01738; DLH; 2.
 SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

 Query Match 70.9%; Score 39; DB 5; Length 446;
 Best Local Similarity 87.5%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNYGSFA 9
 Db 51 RHNYGSHA 58

 RESULT 3
 ID P72121 PRELIMINARY; PRT; 723 AA.
 AC P72121;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE OUTER MEMBRANE PROTEIN C PRECURSOR.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=96349120; PubMed=8760927;
 RA Yoneyama H., Nakae T.;
 RT "Protein C (OprC) of the outer membrane of Pseudomonas aeruginosa is a
 copper-regulated channel protein.";
 RL Microbiology 142:2137-2144(1996).
 DR EMBL; D28119; BAA05664.1; -;
 DR INTERPRO; IPR000531; -;
 DR INTRPRO; IPR001005; -;
 DR PFAM; PF00593; TonB_boxC; 1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 KW Signal.

FT SIGNAL 1 55 POTENTIAL.
 FT CHAIN 56 723 MATURE PROTEIN C.
 SQ SEQUENCE 723 AA; 79303 MW; E9FC33618E830A3E CRC64;

 Query Match 70.9%; Score 39; DB 2; Length 723;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 3 HNYGSFAE 10
 Db 407 HNYGAFGE 414

 RESULT 4
 ID O19495 PRELIMINARY; PRT; 89 AA.
 AC O19495;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15.15I-5; TISSUE=BURSA;
 RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
 RL Immunogenetics 47:350-354(1998).
 DR EMBL; U91532; AAC13613.1; -;
 DR INTERPRO; IPR000353; -;
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

 Query Match 69.1%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNYGSF 8
 Db 75 RHNYGDF 81

 RESULT 5
 ID Q55231 PRELIMINARY; PRT; 347 AA.
 AC Q55231;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE DELTA 12 DESATURASE.
 GN DESA.
 OS Synechococcus sp.
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1129;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC7002;
 RX MEDLINE=94207189; PubMed=8155883;
 RA Sakamoto T., Wada H., Nishida I., Ohmori M., Murata N.;
 RT "Identification of conserved domains in the delta 12 desaturases of
 cyanobacteria.";
 RL Plant Mol. Biol. 24:643-650(1994).
 RN [2]
 RP SEQUENCE FROM N.A.

RA Sakamoto T., Bryant D.A.;
 RT "Molecular characterization of the ammonium transporter gene of
 RL *Synechococcus* sp. PC7002.";
 DR EMBL; D13779; BAA02922.1; -;
 DR EMBL; U36388; AAF21445.1; -;
 DR INTERPRO: IPR000595; -;
 DR INTERPRO: IPR001225; -;
 DR PFAM: PF00487; FA_desaturase; 1.
 DR PROSITE: PS00888; CNMP_BINDING_1; UNKNOWN_1.
 DR PRODOM: PD001081; -; 1.
 SQ SEQUENCE 347 AA; 40655 MW; EC099B226A9B96D9 CRC64;

Query Match 67.3%; Score 37; DB 2; Length 347;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 Db 334 AEHNTISPAQ 343
 |||||

RESULT 6
 P79474
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -;
 KW MHC.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 25 RHNYGVF 31
 |||||

RESULT 7
 P79477
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63080; AAB37780.1; -;
 KW MHC.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 25 RHNYGVF 31
 |||||

RESULT 8
 P79478
 ID P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -;
 KW MHC.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 25 RHNYGVF 31
 |||||

RESULT 9
 P79479
 ID P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -;
 KW MHC.
 FT NON_TER 1
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 25 RHNYGVF 31

RESULT 10

Q9TTM4
 ID Q9TTM4 PRELIMINARY; PRT; 74 AA.
 AC Q9TTM4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MHC (BOLA) CLASS II DR-BETA CHAIN (FRAGMENT).
 GN BOLA-DRB3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE BLACK;
 RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
 RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033388; BAA85470.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1
 FT NON_TER 74
 SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 74;
 Best Local Similarity 85.7%; Pred. No. 7.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 68 RHNYGVF 74

RESULT 11

Q9TPC2
 ID Q9TPC2 PRELIMINARY; PRT; 76 AA.
 AC Q9TPC2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MHC CLASS II ANTIGEN (FRAGMENT).
 GN MAMU-DRB1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saueremann U., Khazand M., Nagy M., Peiberg C.;
 RT "Mhc-DQ-DRB-haplotype analysis in the rhesus macaque: evidence for a
 number of different haplotypes displaying a low allelic
 polymorphism."
 RL Tissue Antigens 0:0-0(1999).
 DR EMBL; AF175315; AAF07040.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 76

SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 76;
 Best Local Similarity 85.7%; Pred. No. 7.7;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 67 RHNYGVF 73

RESULT 12

O97835
 ID O97835 PRELIMINARY; PRT; 78 AA.
 AC O97835;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N20.2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7407; TISSUE=BLOOD;
 RA Aida Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017207; BAA36764.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 9677 MW; 653346CE7D1E1388 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 72 RHNYGVF 78

RESULT 13

O97839
 ID O97839 PRELIMINARY; PRT; 78 AA.
 AC O97839;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
 RA Aida Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017212; BAA36769.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1

FT NON_TER 78 78
SQ SEQUENCE 78 AA: 9430 MW; AF8A0B87E34B6832 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 72 RHNYGVF 78

RESULT 14

O97844 ID O97844 PRELIMINARY; PRT; 78 AA.

AC O97844;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUFFOLK BREED; TISSUE-BLOOD;
RA Alda Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017220; BAA36777.1; -.
DR INTERPRO: IPR000353; -.
DR PFAM: PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA: 9645 MW; 505346CE7D0860CF CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 72 RHNYGVF 78

RESULT 15

O97968 ID O97968 PRELIMINARY; PRT; 78 AA.

AC O97968;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N21.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA Alda Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017231; BAA36788.1; -.
DR EMBL; AB017204; BAA36761.1; -.
DR INTERPRO: IPR000353; -.

DR PFAM: PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA: 9436 MW; 72907E039EC167B2 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 72 RHNYGVF 78

Search completed: March 28, 2001, 07:53:06
Job time: 499 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:48 ; Search time 154.19 Seconds

(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	19 W76027	LM609 grafted anti
2	52	94.5	10	19 W76026	LM609 grafted anti
3	50	90.9	10	19 W76024	LM609 grafted anti
4	50	90.9	10	19 W76025	LM609 grafted anti
5	50	90.9	10	19 W76028	LM609 grafted anti
6	50	90.9	10	19 W76029	LM609 grafted anti
7	50	90.9	10	19 W76030	LM609 grafted anti
8	50	90.9	10	19 W76010	LM609 grafted anti
9	50	90.9	117	19 W76001	Vitaxin antibody h
10	50	90.9	117	19 W76003	LM609 antibody hea
11	50	90.9	117	20 Y06381	Murine monoclonal
12	50	90.9	117	20 Y06387	Humanised LM609 an

13	50	90.9	118	20 Y06384	Humanised LM609 an
14	50	90.9	118	20 Y06385	Humanised LM609 an
15	50	90.9	118	20 Y06386	Humanised LM609 an
16	50	90.9	118	20 Y06383	Murine monoclonal
17	50	90.9	130	20 Y06379	LM609 grafted anti
18	49	89.1	10	19 W76039	LM609 grafted anti
19	47	85.5	10	19 W76021	LM609 grafted anti
20	46	83.6	10	19 W76040	LM609 grafted anti
21	46	83.6	10	19 W76022	LM609 grafted anti
22	46	83.6	10	19 W76023	LM609 grafted anti
23	45	81.8	10	19 W76037	LM609 grafted anti
24	45	81.8	10	19 W76020	LM609 grafted anti
25	42	76.4	110	20 W84099	Vitronectin alpha-
26	42	76.4	117	20 W84093	Murine vitronectin
27	42	76.4	117	20 W84097	Humanised anti-aiP
28	41	74.5	8	20 Y06371	Murine monoclonal
29	41	74.5	10	19 W76038	LM609 grafted anti
30	37	67.3	119	19 Y86109	S. pneumoniae deri
31	36	65.5	117	16 R79157	Human IgE receptor
32	36	65.5	117	16 R79155	Human IgE receptor
33	36	65.5	117	18 W27357	Heavy chain variab
34	36	65.5	117	18 W27356	Heavy chain variab
35	36	65.5	117	18 W27354	Heavy chain variab
36	36	65.5	119	18 W01578	Lead binding MAb 8
37	36	65.5	239	20 W73874	Human antiFc epsll
38	36	65.5	242	20 W73876	Human antiFc epsll
39	35	63.6	30	21 Y81870	Yeast IPPI protein
40	34	61.8	464	19 W72907	Mycobacterium tube
41	34	61.8	464	20 Y21924	Amino acid sequenc
42	33	60.0	80	12 R13395	HLA-DRw12a antigen
43	33	60.0	80	12 R13397	HLA-DRw12b antigen
44	33	60.0	89	17 Y14338	Protein encoded by
45	33	60.0	89	17 Y14306	Protein encoded by

ALIGNMENTS

RESULT 1

ID W76027 standard; Protein; 10 AA.

AC W76027;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

DR WPI; 1998-437472/37.

DR N-PSDB; V49864.

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 | | | | | | | | | |
 Db 1 arhnygsfae 10

RESULT 2
 W76026
 ID W76026 standard; Protein; 10 AA.

AC W76026;
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #8.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.

XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-USO1826.
 XX
 PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.
 XX
 PA Glaser SM, Huse WD;
 XX
 PI WPI; 1998-437472/37.
 XX
 DR N-PSDB; V49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 94.5%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0035;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 | | | | | | | | | |
 Db 1 arhnygsfad 10

RESULT 3
 W76024
 ID W76024 standard; Protein; 10 AA.

XX W76024;
 AC
 XX
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #6.

DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.
 OS
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-USO1826.

XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX
 PA Glaser SM, Huse WD;
 XX
 PI WPI; 1998-437472/37.
 XX
 DR N-PSDB; V49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

RESULT 4

ID W76025 standard; Protein; 10 AA.

XX AC W76025;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

RESULT 5

ID W76028 standard; Protein; 10 AA.

XX AC W76028;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #10.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49865.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||

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Db      1 arhnygsfa 9

RESULT      6
W76029      6
ID      W76029 standard; Protein; 10 AA.
XX
AC      W76029;
XX
DT      02-NOV-1998 (first entry)
XX
DE      LM609 grafted antibody V-H region CDR3 protein fragment #11.
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
OS      Mus sp.
XX
PN      WO9833919-A2.
XX
PD      06-AUG-1998.
XX
PE      30-JAN-1998; 98WO-US01826.
XX
PR      30-JAN-1997; 97US-0791391.
XX
PA      (IXSY-) IXSYS INC.
XX
PI      Glaser SM, Huse WD;
XX
DR      WPI; 1998-437472/37.
XX
DR      N-PSDB; V49866.
XX
PT      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
PS      Claim 62; Page 41; 129pp; English.
XX
CC      W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC      LM609 heavy and light chain variable region. LM609 and the antibody
CC      vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC      inhibit binding of alphavbeta3 to a ligand and thus block
CC      integrin-mediated signal transduction. This is useful in the treatment,
CC      prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC      arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC      contain non-murine framework regions so are suitable for use in humans.
CC      Enhanced types of LM609 have affinity more than 90 times greater than
CC      that of parent the parent antibody.
XX
SQ      Sequence 10 AA;

Query Match      90.9%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSFA 9
Db      1 arhnygsfa 9

RESULT      8
W76010      8
ID      W76010 standard; Protein; 10 AA.
XX
AC      W76010;
XX
DT      02-NOV-1998 (first entry)
XX
DE      LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

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KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI: 1998-437472/37.

XX DR N-PSDB; V49847.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis.

XX PS Disclosure; Page 40; 129pp; English.

XX CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 arhnygsfa 9

RESULT 9

ID W76001 standard; Protein; 117 AA.

XX AC W76001;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN (IXSY-) IXSYS INC.

PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI: 1998-437472/37.

XX DR N-PSDB; V49820.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 1; Fig 1a; 129pp; English.

XX CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 97 arhnygsfa 105

RESULT 10

ID W76003 standard; Protein; 117 AA.

XX AC W76003;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody heavy chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

```

XX Glaser SM, Huse WD;
PI
DR WPI: 1998-437472/37.
DR N-PSDB; V49822.
XX
PT Humanised antibody. Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 43; Fig 2a; 129pp; English.
XX
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db ||||||
97 arhnygsfa 105

RESULT 11
Y06381
ID Y06381 standard; Protein; 117 AA.
AC Y06381;
XX
DT 06-SEP-1999 (first entry)
XX
DE Murine monoclonal antibody LM609 VH region.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Mus musculus.
XX
PN WO9929888-A1.
XX
PD 17-JUN-1999.
XX
PF 04-DEC-1998; 98WO-US25828.
XX
PR 05-DEC-1997; 97US-0986016.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
PS Disclosure; Page 52-53; 55pp; English.
XX
CC This sequence represents the heavy chain variable region of murine

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XX monoclonal antibody LM609. LM609 is directed to integrin
XX alpha-v beta-3. It selectively promotes apoptosis of vascular
XX cells that have been stimulated to undergo angiogenesis, making it
XX a tool for cancer diagnosis and therapy. The invention provides
XX humanised antibodies, especially humanised LM609. In such humanized
XX antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX grafted onto a human light chain, and a heavy chain CDR from a mouse
XX antibody is grafted onto a human antibody heavy chain to produce
XX libraries from which a humanised murine antibody having the desired
XX specificity is selected. By preserving the original CDR sequences
XX such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
XX humanisation strategy ensures epitope conservation.
XX
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 20; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db ||||||
97 arhnygsfa 105

RESULT 12
Y06387
ID Y06387 standard; Protein; 117 AA.
XX
AC Y06387;
XX
DT 06-SEP-1999 (first entry)
XX
DE Humanised LM609 antibody VH domain.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN Synthetic.
XX
PH
XX
FT Key Location/Qualifiers
FT Peptide 1..2
FT Region /note= "vector-encoded residues"
FT Region 31..35
FT Region /note= "CDR1"
FT Region 50..66
FT Region /note= "CDR2"
FT Region 107..117
FT Region /note= "CDR3"
XX
PN WO9929888-A1.
XX
PD 17-JUN-1999.
XX
PF 04-DEC-1998; 98WO-US25828.
XX
PR 05-DEC-1997; 97US-0986016.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
PS Disclosure; Page 52; 55pp; English.
XX
CC This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin

```

CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX
 SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 |||||
 Db 97 arnygsfa 105

RESULT 13
 Y06384
 ID Y06384 standard; Protein; 118 AA.
 AC Y06384;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	31..37
Region	/note= "CDR1"
Region	52..67
Region	/note= "CDR2"
Region	100..107
Region	/note= "CDR3"

WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 XX
 SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 |||||
 Db 98 arnygsfa 106

RESULT 14
 Y06385
 ID Y06385 standard; Protein; 118 AA.
 AC Y06385;
 XX

DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.

XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	31..37
Region	/note= "CDR1"
Region	52..67
Region	/note= "CDR2"
Region	100..107
Region	/note= "CDR3"

WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

RESULT 15
 Y06386
 ID Y06386 standard; Protein: 118 AA.
 XX AC Y06386;
 XX DT 06-SEP-1999 (first entry)
 XX DE Humanised LM609 antibody VH domain.
 XX DE
 XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"
 XX WO929888-A1.
 XX 17-JUN-1999.
 XX 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 XX Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 51-52; 55pp; English.
 CC This sequence represents the heavy chain variable region of a
 CC humanised antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

Search completed: March 28, 2001, 06:59:48
 Job time: 1384 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:55 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-74

Perfect score: 55

Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgnl_7/ptodata/1/iaa/5A-COMB.pep.*

2: /cgnl_7/ptodata/1/iaa/5B-COMB.pep.*

3: /cgnl_7/ptodata/1/iaa/6-COMB.pep.*

4: /cgnl_7/ptodata/1/iaa/PCTUS-COMB.pep.*

5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	65.5	94	3	US-09-147-550-14
2	36	65.5	94	3	US-09-147-550-45
3	36	65.5	94	3	US-09-147-550-48
4	36	65.5	94	3	US-09-147-550-77
5	36	65.5	94	3	US-09-147-550-84
6	36	65.5	94	3	US-09-147-550-90
7	36	65.5	94	3	US-09-147-550-101
8	36	65.5	119	3	US-08-767-128-6
9	35	63.6	286	2	US-08-809-267-3
10	35	63.6	286	4	PCT-US95-13662A-3
11	35	63.6	287	2	US-08-741-437-5
12	35	63.6	287	2	US-09-134-593-5
13	32	58.2	15	1	US-08-618-464-7
14	32	58.2	15	3	US-09-107-615-7
15	32	58.2	25	2	US-08-480-190-44
16	32	58.2	25	2	US-08-488-379-44
17	32	58.2	25	4	PCT-US93-07545-44
18	32	58.2	36	1	US-08-053-131-84
19	32	58.2	36	1	US-08-645-641-84
20	32	58.2	36	1	US-07-853-408B-84
21	32	58.2	36	2	US-08-096-762-84
22	32	58.2	36	2	US-08-308-865-84
23	32	58.2	36	4	PCT-US92-10983-84
24	32	58.2	80	1	US-08-264-250A-1
25	32	58.2	89	1	US-08-025-038-30
26	32	58.2	89	1	US-08-039-137-17
27	32	58.2	90	2	US-08-485-133-23
28	32	58.2	94	3	US-09-147-550-12

29	32	58.2	94	3	US-09-147-550-13	Sequence 13, Appl
30	32	58.2	94	3	US-09-147-550-15	Sequence 15, Appl
31	32	58.2	94	3	US-09-147-550-16	Sequence 16, Appl
32	32	58.2	94	3	US-09-147-550-17	Sequence 17, Appl
33	32	58.2	94	3	US-09-147-550-18	Sequence 18, Appl
34	32	58.2	94	3	US-09-147-550-19	Sequence 19, Appl
35	32	58.2	94	3	US-09-147-550-20	Sequence 20, Appl
36	32	58.2	94	3	US-09-147-550-21	Sequence 21, Appl
37	32	58.2	94	3	US-09-147-550-22	Sequence 22, Appl
38	32	58.2	94	3	US-09-147-550-24	Sequence 24, Appl
39	32	58.2	94	3	US-09-147-550-25	Sequence 25, Appl
40	32	58.2	94	3	US-09-147-550-26	Sequence 26, Appl
41	32	58.2	94	3	US-09-147-550-27	Sequence 27, Appl
42	32	58.2	94	3	US-09-147-550-28	Sequence 28, Appl
43	32	58.2	94	3	US-09-147-550-29	Sequence 29, Appl
44	32	58.2	94	3	US-09-147-550-30	Sequence 30, Appl
45	32	58.2	94	3	US-09-147-550-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14

; Sequence 14, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; TYPE: PRT

; ORGANISM: BOVINE

; US-09-147-550-14

Query Match 65.5%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 9.6;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

DB 80 RHNYGVF 86

RESULT 2

US-09-147-550-45

; Sequence 45, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 3
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 4
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 6
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER FILING DATE: 1996-07-19
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT

ORGANISM: BOVINE
US-09-147-550-90

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Alda, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 8

US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079 West Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: - FastSeq Version 1.5
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-6

Query Match 65.5%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
DB 97 ARHNYGYA 105

RESULT 9

US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,267

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; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 433
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662
; FILING DATE:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-809-267-3

Query Match 63.6%; Score 35; DB 2; Length 286;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
Db 91 HNYGAFFQ 98

RESULT 10
PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
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; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US95-13662A-3

Query Match 63.6%; Score 35; DB 4; Length 286;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
Db 91 HNYGAFFQ 98

RESULT 11
US-08-741-437-5
; Sequence 5, Application US/08741437
; Patent No. 5843665
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741.437
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
; US-08-741-437-5

Query Match 63.6%; Score 35; DB 2; Length 287;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
Db 92 HNYGAFFQ 99

RESULT 12
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US-09-134-593-5
; Sequence 5, Application US/09134593
; Patent No. 5981232
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,593
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-09-134-593-5

Query Match 63.68; Score 35; DB 2; Length 287;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSEAE 10
|||||:
Db 92 HNYGAFPQ 99

RESULT 13
US-08-618-464-7
; Sequence 7, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INDUCING
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US

ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: S1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-08-618-464-7

Query Match 58.2%; Score 32; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
|||||
Db 11 RHNYG 15

RESULT 14
US-09-107-615-7
; Sequence 7, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIS
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: S1
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-09-107-615-7

Query Match 58.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 11 RHNYG 15

RESULT 15
US-08-480-190-44
Sequence 44, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-44

Query Match 58.2%; Score 32; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 15 RHNYG 19

Search completed: March 28, 2001, 07:01:55
Job time: 1334 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:24 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-76

Perfect score: 55

Sequence: 1 ARHNYGSFAM 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	446	2 T19625	hypothetical prote
2	37	67.3	430	2 C81402	probable integral
3	36	65.5	82	2 I51106	Major Histocompat
4	36	65.5	89	2 S38688	MHC class II histo
5	36	65.5	89	2 S38683	MHC class II histo
6	36	65.5	89	2 S38684	MHC class II histo
7	36	65.5	225	2 I47095	MHC class II OVAR-
8	35	63.6	347	2 S43771	phosphatidylcholin
9	35	63.6	383	2 S56179	secreted glycoprot
10	35	63.6	473	2 D70405	glutamate--tRNA, li
11	34	61.8	108	2 S26316	Ig heavy chain V r
12	34	61.8	110	2 S26317	Ig heavy chain V r
13	34	61.8	210	1 B69265	conserved hypothet
14	34	61.8	220	2 T46055	hypothetical prote
15	34	61.8	275	2 G75130	translation initia
16	34	61.8	275	2 D71087	probable translati
17	34	61.8	287	1 PWB5	inorganic pyrophos
18	34	61.8	287	1 PWBKL	inorganic pyrophos
19	34	61.8	321	1 S58614	cytochrome c-type
20	34	61.8	321	1 JQ0288	protein-tyrosine k
21	34	61.8	628	1 A56707	gene 50 protein -
22	34	61.8	682	2 S30995	outer membrane pro
23	34	61.8	723	2 F83173	MHC HLA-DR-beta-1
24	33	60.0	80	2 I54469	MHC HLA-DR-beta-1
25	33	60.0	80	2 I68777	MHC HLA-DR-beta-1
26	33	60.0	81	2 I54550	HLA DRB1*1202 - hu
27	33	60.0	85	2 I59634	MHC class II DR-be
28	33	60.0	89	2 S38676	MHC class II histo
29	33	60.0	89	2 S38680	MHC class II histo

30	33	60.0	89	2 S57512	MHC class II histo
31	33	60.0	123	2 C25239	MHC class II histo
32	33	60.0	167	2 T16454	hypothetical prote
33	33	60.0	200	2 D32526	class II histocomp
34	33	60.0	237	2 C27060	class II histocomp
35	33	60.0	266	2 I54287	gene HLA-DRB1 prot
36	33	60.0	266	2 A27618	class II histocomp
37	33	60.0	266	2 I54295	lymphocyte antigen
38	33	60.0	279	2 T03421	hypothetical prote
39	33	60.0	405	2 D75441	Fcma-related prote
40	33	60.0	448	1 A60003	nucleocapsid prote
41	33	60.0	470	2 H71667	glutamate--tRNA li
42	33	60.0	548	2 T25424	hypothetical prote
43	33	60.0	582	1 S51945	ferredoxin--nitrit
44	33	60.0	583	1 S20495	ferredoxin--nitrit
45	33	60.0	594	1 S16603	ferredoxin--nitrit

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19625

R:Kershaw, J.

Submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

RESULT 2

C81402

probable integral membrane protein Cj0555 [Imported] - Campylobacter jejuni (strain N

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000

C:Accession: C81402

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chlil

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals

A:Reference number: AB1250; MUID:20150912

A:Accession: C81402

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-430 <PAR>

A:Cross-references: GB:AL139075; GB:AL111168; MID:g6967817; PIDN:CAB75191.1; PID:g696

A:Experimental source: serotype O2, strain NCIC 11168

C:Genetics:

A:Gene: Cj0555

Query Match 67.3%; Score 37; DB 2; Length 430;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAM 10
 Db 22 RHNYGIFAM 30
 ||| | |||

RESULT 3
 IS1106
 Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
 C:Species: Phasianus colchicus (ring-necked pheasant)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C:Accession: IS1106
 R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
 A:Reference number: IS1103; MUID:94245280
 A:Accession: IS1106
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <FIG>
 A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 82;
 Best Local Similarity 85.7%; Pred. No. 4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||| |

RESULT 4
 S38688
 MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38688
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
 A:Reference number: S38676
 A:Accession: S38688
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:227158
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||| |

RESULT 5
 S38683
 MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38683
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
 A:Reference number: S38676
 A:Accession: S38683

A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:227153
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||| |

RESULT 6
 S38684
 MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38684
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
 A:Reference number: S38676
 A:Accession: S38684
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:227154
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||| |

RESULT 7
 I47095
 MHC class II OVAR-DR-beta-3 - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
 C:Accession: I47095
 R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
 Anim. Genet. 24, 249-255, 1993
 A:Title: Isolation, characterization and evolution of ovine major histocompatibility
 A:Reference number: I47075; MUID:94057592
 A:Accession: I47095
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-225 <FAB>
 A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
 C:Genetics:
 A:Gene: OVAR-DRB3
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
 F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 36; DB 2; Length 225;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 68 RHNYGVF 74
 |||| |

RESULT 8
 S43771

phosphatidylcholine desaturase (EC 1.3.1.35) - *Synechococcus* sp. (strain PCC 7002)
 N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misidentified]
 C:Species: *Synechococcus* sp.

A:Variety: PCC 7002
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S43771

R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
 Plant Mol. Biol. 24, 643-650, 1994

A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacteria
 A:Reference number: S43770; MUID:94207189

A:Accession: S43771

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-347 <SAK>

A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:g488511

C:Superfamily: omega-3 fatty acid desaturase

C:Keywords: oxidoreductase

Query Match 63.6%; Score 35; DB 2; Length 347;
 Best Local Similarity 77.8%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 334 ARHNWISFA 342

RESULT 9

S56179 secreted glycoprotein EP4, 47K, precursor - carrot (fragment)

C:Species: *Daucus carota* (carrot)

C:Date: 27-Oct-1995 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C:Accession: S56179; S56180

R:vant Engelen, F.A.; de Jong, A.J.; Meijer, E.A.; Kuil, C.W.; Meyboom, J.K.; Dirkse, W.G.

Plant Mol. Biol. 27, 901-910, 1995

A:Title: Purification, immunological characterization and cDNA cloning of a 47 kDa glycoprotein

A:Reference number: S56179; MUID:95284347

A:Accession: S56179

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-383 <VAN>

A:Cross-references: EMBL:L36956; NID:g886222; PIDN:AAA98926.1; PID:g886223

A:Accession: S56180

A:Molecule type: protein

A:Residues: 121-133; 272-276; 281-284 <VAM>

C:Superfamily: myrosinase-associated protein MyAP

C:Keywords: glycoprotein

F:1-15/Domain: signal sequence (fragment) #status predicted <SIG>

F:16-383/Product: secreted glycoprotein EP4, 47K #status predicted <MAT>

Query Match 63.6%; Score 35; DB 2; Length 383;
 Best Local Similarity 55.6%; Pred. No. 32;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYSFAM 10

Db 305 RYNYGFSL 313

RESULT 10

D70405

glutamate--tRNA ligase (EC 6.1.1.17) - *Aquifex aeolicus*

C:Species: *Aquifex aeolicus*

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000

C:Accession: D70405

R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A:Reference number: A70300; MUID:98196666

A:Accession: D70405

A:Accession: D70405

A:Accession: D70405

A:Accession: D70405

A:Accession: D70405

A:Accession: D70405

A:Accession: D70405

A:Accession: D70405

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-473 <AQF>

A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00

A:Experimental source: strain VF5

C:Genetics:

A:Gene: gltX

C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

F:4-276/Domain: glutamine--tRNA ligase homology <EGL>

Query Match 63.6%; Score 35; DB 2; Length 473;

Best Local Similarity 60.0%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAM 10

Db 31 ARHNGGFVL 40

RESULT 11

S26316

Ig heavy chain V region - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26316

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a proteol

A:Reference number: S26309; MUID:91341421

A:Accession: S26316

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <STA>

A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 108;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 84 ARNGNYIA 92

RESULT 12

S26317

Ig heavy chain V region - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26317

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a proteol

A:Reference number: S26309; MUID:91341421

A:Accession: S26317

A:Molecule type: mRNA

A:Residues: 1-110 <STA>

A:Cross-references: EMBL:X59186

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 110;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 || |||||
 Db 86 ARGNYGNYA 94

RESULT 13

B69265

conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: B69265
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 :; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343
 A:Accession: B69265
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-210 <KLE>
 A:Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PIDN:AAB91117.1; PID:g265053
 C:Superfamily: conserved hypothetical protein AF0119

Query Match 61.8%; Score 34; DB 1; Length 210;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 || |||||
 Db 128 RHAYGSF 134

RESULT 14

T46055

hypothetical protein T16K5.240 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T46055
 R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23015
 A:Accession: T46055
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <RIE>
 A:Cross-references: EMBL:AL132965
 A:Experimental source: cultivar Columbia; BAC clone T16K5
 C:Genetics:
 A:Map position: 3
 A:Introns: 64/3; 113/1; 136/3; 208/3
 A:Note: T16K5.240

Query Match 61.8%; Score 34; DB 2; Length 220;
 Best Local Similarity 62.5%; Pred. No. 29;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
 |||||
 Db 46 HNYGDFRL 53

RESULT 15

G75130

translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: G75130
 R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
 A:Reference number: A75001
 A:Accession: G75130
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <KAW>
 A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: aif2a; PAB0568
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 61.8%; Score 34; DB 2; Length 275;
 Best Local Similarity 83.3%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||
 Db 23 HNYGAF 28

Search completed: March 28, 2001, 07:04:24
 Job time: 1062 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:03 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-76

Perfect score: 55

Sequence: 1 ARHNYGSFAM 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	63.6	473	1 SVE_AQUAE	O67271 aquifex aeo
2	34	61.8	275	1 IF2A_PYRAB	Q9V0E4 pyrococcus
3	34	61.8	275	1 IF2A_PYRHO	OS8655 pyrococcus
4	34	61.8	284	1 IPYR_PICPA	O13505 pichia past
5	34	61.8	286	1 IPYR_KLJLA	P13998 kluyveromyc
6	34	61.8	286	1 IPYR_YEAST	P00817 saccharomyc
7	34	61.8	321	1 CCSA_MAIZE	P46559 zea mays (m
8	34	61.8	321	1 CCSA_ORYSA	P12215 oryza sativ
9	34	61.8	629	1 KSYK_RAT	Q64725 rattus norv
10	34	61.8	682	1 VG50_BPML5	Q05262 mycobacteri
11	33	60.0	448	1 NCAP_CVHOC	P33469 human coron
12	33	60.0	470	1 SVE2_RICPR	Q92ct8 rickettsia
13	33	60.0	583	1 NIR_BETVE	P38500 betula verr
14	33	60.0	594	1 NIR_SPIOL	P05314 spinacia ol
15	32	58.2	65	1 CCSA_OERBE	P31565 oenothera b
16	32	58.2	65	1 CCSA_PEA	P31172 pisum sativ
17	32	58.2	196	1 WBJJ_ECOLI	P37750 escherichia
18	32	58.2	197	1 Y61A_METJA	P81310 methanococc
19	32	58.2	198	1 HB2G_HUMAN	P01911 homo sapien
20	32	58.2	266	1 HB2A_HUMAN	P01913 homo sapien
21	32	58.2	266	1 HB2B_HUMAN	P01912 homo sapien
22	32	58.2	266	1 HB2C_HUMAN	P01914 homo sapien
23	32	58.2	266	1 HB2D_CANFA	P18470 canis famil
24	32	58.2	266	1 HB2D_HUMAN	P13759 homo sapien
25	32	58.2	266	1 HB2E_HUMAN	P04229 homo sapien
26	32	58.2	266	1 HB2F_HUMAN	P13758 homo sapien
27	32	58.2	266	1 HB2H_HUMAN	P13758 homo sapien
28	32	58.2	266	1 HB2I_HUMAN	P20039 homo sapien
29	32	58.2	266	1 HB2J_HUMAN	P13761 homo sapien
30	32	58.2	313	1 CCSA_TORAC	P12216 nicotiana t
31	32	58.2	328	1 CCSA_ARATH	P56770 arabidopsis
32	32	58.2	349	1 YJY9_YEAST	P41903 saccharomyc
33	32	58.2	469	1 YJ8_CAEEL	P34631 caenorhabdi

ALIGNMENTS

RESULT 1

ID	SYE_AQUAE	STANDARD;	PRT;	473 AA.
AC	O67271;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)			
DE	(GLURS).			
GN	GLTX OR AQ_1221.			
OS	Aquifex aeolicus.			
OC	Bacteria; Aquificales; Aquificaceae; Aquifex.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=VF5;			
RX	MEDLINE; 98196666.			
RA	Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,			
RA	Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,			
RA	Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;			
RT	"The complete genome of the hyperthermophilic bacterium Aquifex			
RT	aeolicus."			
RL	Nature 392:353-358(1998).			
CC	-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA (GLU) = AMP +			
CC	PYROPHOSPHATE + L-GLUTAMYL-TRNA (GLU).			
CC	-!- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; AF000729; AAC07230.1; -			
DR	INTERPRO; IPR000924; -			
DR	INTERPRO; IPR001412; -			
DR	PFAM; PF00749; TRNA-synt_lc; 1.			
DR	PRINTS; PR00987; TRNASYNTHGLU.			
DR	PROSITE; PS00178; AA-TRNA_LIGASE_I; 1.			
KW	Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.			
FT	SIMILAR 10 20 "HIGH" REGION.			
FT	SIMILAR 242 246 "KMSKS" REGION.			
FT	BINDING 245 245 ATP (BY SIMILARITY).			
SQ	SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;			

Query Match 63.6%; Score 35; DB 1; Length 473;

Best Local Similarity 60.0%; Pred. No. 13;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10

|||||

DB 31 ARHNGGEVL 40

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RESULT 2
ID IF2A_PVRAB STANDARD; PRT; 275 AA.
AC Q3V0E4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PAB0568
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT 'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution.';
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
EMBL: AJ248285; CAB49760.1;
DR INTERPRO: IPR003029;
DR PFAM: PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

```

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Query Match 61.8%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 3 HNYGSF 8
Db 23 HNYGAF 28

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RESULT 3
ID IF2A_PVRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE: 98344137.
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

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RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
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CC
EMBL: AP000004; BAA30058.1;
DR INTERPRO: IPR003029;
DR PFAM: PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

```

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Query Match 61.8%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 3 HNYGSF 8
Db 23 HNYGAF 28

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RESULT 4
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE: 99034033.
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COPACATOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC
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DR EMBL; AJ001000; CAA04453.1; -
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0
 FT ACT_SITE 56 56 BY SIMILARITY.
 FT BINDING 78 78 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SO SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNYGSF 8
 DB 91 HNYGAF 96

RESULT 5
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E. COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
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 CC -----
 DR EMBL; X14230; CAA32446.1; -
 DR PIR; S07894; PWKL.
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.

FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNYGSF 8
 DB 91 HNYGAF 96

RESULT 6
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288C;
 RX MEDLINE; 78087552.
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RX STRAIN=S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 RT database";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]
 RP SEQUENCE OF 239-249.
 RX STRAIN=ATCC 38531 / Y41;
 RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT Saccharomyces cerevisiae";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase";
 RL Biochemistry 19:94-102(1980).
 RN [7]

RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunyan E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Valstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytia T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RN SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; X13253; CAA31629.1; -;
DR EMBL; Z35880; CAA84949.1; -;
DR PIR; S45864; PMBY.
DR PDB; 1PYP; 15-OCT-91.
DR PDB; 1YPP; 07-DEC-96.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1HUI; 08-APR-98.
DR PDB; 1HUK; 08-APR-98.
DR PDB; 117E; 23-DEC-98.
DR PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -;
DR SGD; S0000215; IPPI.
DR INTERPRO; IPR001596; -;
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).

FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Dy 91 HNYGAF 96

RESULT 7

CCSA_MAIZE STANDARD; PRT; 321 AA.
AC P46659;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Zea mays (Maize).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95395841.
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing.";
RL J. Mol. Biol. 251:614-628(1995).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.

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 CC -----
 DR EMBL; X86563; CAA60348.1; -
 DR MAIZEDB; 118255; -
 DR INTERPRO; IPR002541; -
 DR PFAM; PF01578; CytC.asn; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 321 AA; 36693 MW; AF981BA461A5D1B CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 321;
 Best Local Similarity 62.5%; Pred. No. 14;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 3 HNYGSFAM 10
 I:||||:
 Db 311 HSYGSFTL 318

 RESULT 8
 ID CCSA_ORYSA STANDARD; PRT; 321 AA.
 AC P12215;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
 GN CCSA.
 OS Oryza sativa (Rice).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sugura M.;
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP COMPLETE GENOME.
 RX MEDLINE; 89364698.
 RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
 RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
 RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugura M.;
 RT "The complete sequence of the rice (*Oryza sativa*) chloroplast
 RT intermolecular recombination between distinct tRNA genes accounts for
 RT a major plastid DNA inversion during the evolution of the cereals.";
 RL Mol. Gen. Genet. 217:185-194(1989).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLL/NRFE/CCSA FAMILY.
 CC -----
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 CC -----
 DR EMBL; X15901; CAA33952.1; -
 DR PIR; JQ0288; JQ0288.
 DR INTERPRO; IPR002541; -
 DR PFAM; PF01578; CytC.asn; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 321 AA; 36702 MW; D959FE24A619B650 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 321;
 Best Local Similarity 62.5%; Pred. No. 14;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 3 HNYGSFAM 10
 I:||||:
 Db 312 HSYGSFTL 319

 RESULT 9
 ID KSYK_RAT STANDARD; PRT; 629 AA.
 AC Q64725;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
 GN SYK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95279402.
 RA Rowley R.B., Bolen J.B., Fargnoli J.;
 RT "Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
 RT splicing.";
 RL J. Biol. Chem. 270:12659-12664(1995).
 CC -1- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
 CC LYMPHOCYTE ACTIVATION.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: SYKA AND SYKB (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SYK/ZAP-70 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; U21684; AAA75167.1; -
 DR EMBL; U21683; AAA75166.1; -
 DR HSP; P43405; 1CSY.
 DR INTERPRO; IPR000719; -
 DR INTERPRO; IPR000980; -
 DR INTERPRO; IPR001245; -
 DR PFAM; PF00017; SH2; 2.
 DR PFAM; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 2.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Alternative splicing.
 FT DOMAIN 14 106
 FT SH2.
 FT DOMAIN 167 258
 FT SH2.
 FT DOMAIN 365 625
 FT NP_BIND 371 379
 FT BINDING 396 396
 FT ACT_SITE 488 488
 FT MOD_RES 519 519
 FT VARSPPLIC 277 539
 FT SEQUENCE 629 AA; 71528 MW; 81169A643EC6A6FE CRC64;

Query Match 61.8%; Score 34; DB 1; Length 629;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
| | | | |
DB 195 ARDNGSFAL 204

RESULT 10
VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -!- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
OXIDIZED THIOREDOXIN + H(2)O = RIBONUCLEOSIDE TRIPHOSPHATE +
REDUCED THIOREDOXIN.
CC -----
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CC -----
DR EMBL; Z18946; CAA79426.1; -
DR PIR; S30995; S30995
DR INTERPRO; IPR000788; -
DR PFAM; PF00317; ribonucleo_red; 1.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 682;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
| | | | |
DB 311 AKEGYGSFAV 320

RESULT 11
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
DE N.
GN Human coronavirus (strain OC43).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; #9243809.

RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR INTERPRO; IPR001218; -
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
DB 103 RHNRGSF 109

RESULT 12
SYE2_RICPR STANDARD; PRT; 470 AA.
ID SYE2_RICPR
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS, 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -
DR HSP; P27000; IGLN.
DR INTERPRO; IPR000924; -
DR PFAM; PF00749; trna-synt_ic; 1.
DR PRINTS; PRO0987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 60.0%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 33;

Matches: 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
| | | | |

Db 31 ARHNGKF 38

RESULT 13

NIR_BETVE STANDARD; PRT; 583 AA.
AC P38500;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FERREDOXIN--NITRITE REDUCTASE PRECURSOR (EC 1.7.7.1).
GN NIR.
OS Betula verrucosa (White birch) (Betula pendula).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fagales; Betulaceae; Betula.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=LEAF;
RX MEDLINE; 92167960.
RA Eriemann A., Brinkmann K., Hachtel W.;
RT "Sequence of a cDNA encoding nitrite reductase from the tree Betula
pendula and identification of conserved protein regions.";
RL Mol. Gen. Genet. 231:411-416(1992).
CC -1- CATALYTIC ACTIVITY: AMMONIA + H(2)O + OH(-) + 3 OXIDIZED
FERREDOXIN = NITRITE + 3 REDUCED FERREDOXIN.
CC -1- COFACTOR: THIS ENZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S
IRON-SULFUR CENTER AS PROSTHETIC GROUPS.
CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).

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CC EMBL; X60093; CAA42690.1; -;
CC INTERPRO; IPR000660; -;
CC PFAM; PF01077; NIR_SIR; 1.
CC PRINTS; PR00397; SIROHAEM.
CC PROSITE; PS00365; NIR_SIR; 1.
CC Oxidoreductase; Chloroplast; Transit peptide; Nitrate assimilation;
KW Heme; Iron-sulfur; 4Fe-4S.
FT TRANSIT 1 22
FT CHAIN 23 583
FT METAL 461 461
FT METAL 467 467
FT METAL 502 502
FT METAL 506 506
FT METAL 506 506
SQ SEQUENCE 583 AA; 65229 MW; 482111EF7E66991F CRC64;

Query Match 60.0%; Score 33; DB 1; Length 583;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAM 10

Db 120 KHVGGRFMM 128

RESULT 14

NIR_SPIOL STANDARD; PRT; 594 AA.
AC P05314;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FERREDOXIN--NITRITE REDUCTASE PRECURSOR (EC 1.7.7.1).
GN NIR.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC Caryophyllales; Chenopodiaceae; Spinacia.
[1]
RN SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RX MEDLINE; 88232431.
RA Back E., Burkhardt W., Moyer M., Privalle L., Rothstein S.;
RT "Isolation of cDNA clones coding for spinach nitrite reductase:
complete sequence and nitrate induction.";
RL Mol. Gen. Genet. 212:20-26(1988).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. DARK GREEN BLOOMSDALE; TISSUE=LEAF;
RX MEDLINE; 91329742.
RA Back E., Dunne W., Schneiderbauer A., de Framond A., Rastogi R.,
RA Rothstein S.J.;
RT "Isolation of the spinach nitrite reductase gene promoter which
confers nitrate inducibility on GUS gene expression in transgenic
tobacco.";
RL Plant Mol. Biol. 17:9-18(1991).
CC -1- CATALYTIC ACTIVITY: AMMONIA + H(2)O + OH(-) + 3 OXIDIZED
FERREDOXIN = NITRITE + 3 REDUCED FERREDOXIN.
CC -1- COFACTOR: THIS ENZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S
IRON-SULFUR CENTER AS PROSTHETIC GROUPS.
CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
CC -1- SUBUNIT: MONOMER.
CC -1- INDUCTION: BY NITRATE.
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).

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CC EMBL; X07568; CAA30453.1; -;
CC EMBL; X17031; CAA34893.1; -;
CC PIR; S16603; S16603.
CC INTERPRO; IPR000660; -;
CC PFAM; PF01077; NIR_SIR; 1.
CC PRINTS; PR00397; SIROHAEM.
CC PROSITE; PS00365; NIR_SIR; 1.
CC Oxidoreductase; Chloroplast; Transit peptide; Nitrate assimilation;
KW Heme; Iron-sulfur; 4Fe-4S.
FT TRANSIT 1 32
FT CHAIN 33 594
FT METAL 473 473
FT METAL 479 479
FT METAL 514 514
FT METAL 518 518
FT METAL 518 518
FT VARIANT 221 221
FT SEQUENCE 594 AA; 66394 MW; 2B3DCAAC16DE06A3 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 594;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGSEFAM 10
 Db 132 KHYGREMM 140

RESULT 15

CCSA_OENBE STANDARD; PRT; 65 AA.
 ID CCSA_OENBE PRT; 65 AA.
 AC P31565;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
 GN CCSA.
 OS Oenothera bertiana (Bertero's evening primrose).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Myrtales; Onagraceae; Oenothera.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93169690.
 RA Nimzyk R., Schoendorf T., Hachtel W.;
 RT "In-frame length mutations associated with short tandem repeats are
 RT located in unassigned open reading frames of Oenothera chloroplast
 RT DNA".
 RL Curr. Genet. 23:265-270(1993).
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
 CC -----
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 CC -----
 CC EMBL; X64617; CAA45900.1; -.
 CC EMBL; X64614; CAA45894.1; -.
 DR PIR; S19981; S19981.
 DR PIR; S19988; S19988.
 KW Cytochrome c-type biogenesis; Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 65 AA; 7441 MW; 343E66DDA1492C0C CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
 Best Local Similarity 83.3%; Pred. No. 6.3;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RHYGSF 8
 Db 57 HSYGSF 62

Search completed: March 28, 2001, 07:35:04
 Job time: 141 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:06 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	78.2	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	39	70.9	446	5 O62086	O62086 caenorhabdi
3	38	69.1	89	7 O19495	O19495 gallus gall
4	36.5	66.4	89	7 O30217	O30217 homo sapien
5	36	65.5	39	7 P79474	P79474 cervus elap
6	36	65.5	39	7 P79477	P79477 cervus elap
7	36	65.5	39	7 P79478	P79478 cervus elap
8	36	65.5	39	7 P79479	P79479 cervus elap
9	36	65.5	74	6 Q9TWM4	Q9TWM4 bos taurus
10	36	65.5	76	7 Q9TFC2	Q9TFC2 macaca mula
11	36	65.5	78	6 Q97835	Q97835 ovis aries
12	36	65.5	78	6 Q97839	Q97839 ovis aries
13	36	65.5	78	6 Q97844	Q97844 ovis aries
14	36	65.5	78	6 Q97968	Q97968 ovis aries
15	36	65.5	78	7 Q9MWT6	Q9MWT6 leopardus p
16	36	65.5	78	7 Q9MWT5	Q9MWT5 leopardus p
17	36	65.5	78	7 Q9MWT4	Q9MWT4 leopardus p
18	36	65.5	79	7 O19191	O19191 prionalluru
19	36	65.5	79	7 O19192	O19192 prionalluru

20	36	65.5	79	7 O19380	O19380 felis silve
21	36	65.5	79	7 O19381	O19381 felis silve
22	36	65.5	79	7 O19382	O19382 felis silve
23	36	65.5	79	7 O19396	O19396 felis silve
24	36	65.5	79	7 O19397	O19397 felis silve
25	36	65.5	79	7 O19405	O19405 felis silve
26	36	65.5	79	7 O19406	O19406 felis silve
27	36	65.5	79	7 O19407	O19407 felis silve
28	36	65.5	79	7 O19408	O19408 felis silve
29	36	65.5	79	7 O19435	O19435 felis silve
30	36	65.5	79	7 Q9MX19	Q9MX19 leopardus p
31	36	65.5	79	7 Q9MX13	Q9MX13 leopardus p
32	36	65.5	79	7 Q9MX03	Q9MX03 leopardus p
33	36	65.5	79	7 Q9MX00	Q9MX00 leopardus p
34	36	65.5	79	7 Q9MW29	Q9MW29 leopardus p
35	36	65.5	79	7 Q9MW28	Q9MW28 leopardus p
36	36	65.5	79	7 Q9MW27	Q9MW27 leopardus p
37	36	65.5	79	7 Q9MWY9	Q9MWY9 leopardus p
38	36	65.5	79	7 Q9MWY8	Q9MWY8 leopardus p
39	36	65.5	79	7 Q9MWY6	Q9MWY6 leopardus p
40	36	65.5	79	7 Q9MWY5	Q9MWY5 leopardus p
41	36	65.5	79	7 Q9MWY4	Q9MWY4 leopardus p
42	36	65.5	79	7 Q9MWY3	Q9MWY3 leopardus p
43	36	65.5	79	7 Q9MWX6	Q9MWX6 leopardus p
44	36	65.5	79	7 Q9MWX5	Q9MWX5 leopardus p
45	36	65.5	79	7 Q9MWX4	Q9MWX4 leopardus p

ALIGNMENTS

```

RESULT 1
Q9LIE5 ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl.,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AF001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

```

Query Match 78.2%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

Db 274 SRHNYGSF 281

RESULT 2
O62086

ID O62086 PRELIMINARY; PRT; 446 AA.
 AC O62086;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE C31H5.6 PROTEIN.
 GN C31H5.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Saldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: Z93778; CAB07846.1; -
 DR INTERPRO: IPR000379; -
 DR DR INTERPRO: IPR002925; -
 DR PFAM: PF01738; DLH; 2.
 SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 70.9%; Score 39; DB 5; Length 446;
 Best Local Similarity 87.5%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
 |||||
 DB 51 RHNYGSHA 58

RESULT 3
 ID O19495 PRELIMINARY; PRT; 89 AA.
 AC O19495;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15.151-5; TISSUE=Bursa;
 RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
 RL Immunogenetics 47:350-354(1998).
 DR EMBL: U91532; AAC15813.1; -
 DR INTERPRO: IPR000353; -
 DR PFAM: PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AE1379 CRC64;

Query Match 69.1%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 3.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 75 RHNYGDF 81

RESULT 4
 ID Q30217 PRELIMINARY; PRT; 89 AA.
 AC Q30217;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE DB9 PROTEIN (FRAGMENT).
 GN DB9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95279172; PubMed=7759314;
 RA Arvidsson A.K., Svensson A.C., Widmark E., Andersson G., Rask L.,
 RA Larhammar D.;
 RT "Characterization of three separated exons in the HLA class II DR
 RT region of the human major histocompatibility complex.";
 RL Hum. Immunol. 42:254-264(1995).
 DR EMBL: S78510; AAD14284.1; -
 FT NON_TER 1 1
 SQ SEQUENCE 89 AA; 10489 MW; 10027003DC27E99E CRC64;

Query Match 66.4%; Score 35.5; DB 7; Length 89;
 Best Local Similarity 66.7%; Pred. No. 7;
 Matches 8; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 2 RHNYG---SFAM 10
 |||||
 DB 75 RHNYGVFESFSM 86

RESULT 5
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U63077; AAB37777.1; -
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.7;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 6
P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 7
P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 8

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P79479 PRELIMINARY; PRT; 39 AA.
ID P79479;
AC P79479;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 9
Q9TTM4 PRELIMINARY; PRT; 74 AA.
ID Q9TTM4;
AC Q9TTM4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MHC (BOLA) CLASS II DR-BETA CHAIN (FRAGMENT).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPANESE BLACK;
RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033388; BAA85470.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 74;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 68 RHNYGVF 74

RESULT 10
Q9TPC2 PRELIMINARY; PRT; 76 AA.
ID Q9TPC2;
AC Q9TPC2;

```

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE MHC CLASS II ANTIGEN (FRAGMENT).
 GN MAMU-DRB1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sauerbmann U., Khazand M., Nagy M., Peiberg C.;
 RT "MHC-DQ-DRB-haplotype analysis in the rhesus macaque: evidence for a
 number of different haplotypes displaying a low allelic
 polymorphism."; 0:0-0(1999).
 RL Tissue Antigens 0:0-0(1999).
 DR EMBL; AF175315; AAF07040.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 76 76
 SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 76;
 Best Local Similarity 85.7%; Pred. No. 7.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 67 RHNYGVF 73

RESULT 11

ID 097835 PRELIMINARY; PRT; 78 AA.
 AC 097835;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N20.2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7407; TISSUE=BLOOD;
 RA Alda Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017207; BAA36764.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9677 MW; 653346CE7D1E1388 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 72 RHNYGVF 78

RESULT 12

ID 097839 PRELIMINARY; PRT; 78 AA.
 AC 097839;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED AND CORRIDAILE BREED; TISSUE=BLOOD;
 RA Alda Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017212; BAA36769.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9430 MW; AF8A0B87E34B6832 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 72 RHNYGVF 78

RESULT 13

ID 097844 PRELIMINARY; PRT; 78 AA.
 AC 097844;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N8.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
 RA Alda Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017220; BAA36777.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9645 MW; 505346CE7D0860CF CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 72 RHNYGVF 78

Search completed: March 28, 2001, 07:53:06
Job time: 499 sec

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RESULT 14
O97968
ID O97968 PRELIMINARY: PRT; 78 AA.
AC O97968;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N21.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017231; BAA36788.1; -.
DR EMBL; AB017204; BAA36761.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9436 MW; 72907E039EC167B2 CRC64;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 15
O9MWT6
ID O9MWT6 PRELIMINARY: PRT; 78 AA.
AC O9MWT6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
GN LEPA-DRB.
OS Leopardus pardalis (ocelot).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX NCBI_TaxID=32538;
RN [1]
RP SEQUENCE FROM N.A.
RA Yunxi N., Eizirik E., Johnson W.E., O'Brien S.J.;
RT "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT pardalis) and Margay (Leopardus wiedii).";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057894; AAF70946.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9559 MW; 77863043708EC5B8 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 71 RHNYGVF 77

```

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	55	100.0	10	19	W76028	LM609 grafted anti	
2	50	90.9	10	19	W76024	LM609 grafted anti	
3	50	90.9	10	19	W76025	LM609 grafted anti	
4	50	90.9	10	19	W76026	LM609 grafted anti	
5	50	90.9	10	19	W76027	LM609 grafted anti	
6	50	90.9	10	19	W76029	LM609 grafted anti	
7	50	90.9	10	19	W76030	LM609 grafted anti	
8	50	90.9	10	19	W76010	LM609 grafted anti	
9	50	90.9	117	19	W76001	Vitaxin antibody h	
10	50	90.9	117	19	W76003	LM609 antibody hea	
11	50	90.9	117	20	Y06381	Murine monoclonal	
12	50	90.9	117	20	Y06387	Humanised LM609 an	

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00088;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFAM 10
 |||||
 Db 1 arhnygsfam 10

RESULT 2
 W76024
 ID W76024 standard; Protein; 10 AA.
 XX
 AC W76024;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.
 XX
 XX WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX

PA (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX
 XX WPI: 1998-437472/37.
 DR
 DR N-PSDB; V49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
 |||||
 Db 1 arhnygsfa 9

RESULT 3
 W76025
 ID W76025 standard; Protein; 10 AA.
 XX
 AC W76025;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.
 XX
 XX WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX
 XX WPI: 1998-437472/37.
 DR
 DR N-PSDB; V49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 arhnygsfa 9

RESULT 4

ID W76026 standard; Protein; 10 AA.

XX AC W76026;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #8.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 arhnygsfa 9

RESULT 5

ID W76027 standard; Protein; 10 AA.

XX AC W76027;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||

```

Db      1 arhnygsfa 9

RESULT      6
W76029
ID      W76029 standard; Protein; 10 AA.
AC      W76029;
DT      02-NOV-1998 (first entry)
XX      LM609 grafted antibody V-H region CDR3 protein fragment #11.
DE      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
XX      complementarity determining region.
XX      Mus sp.
OS      WO9833919-A2.
PN      06-AUG-1998.
XX      30-JAN-1998; 98WO-US01826.
XX      30-JAN-1997; 97US-0791391.
XX      (IXSY-) IXSYS INC.
XX      Glaser SM, Huse WD;
PI      WPI; 1998-437472/37.
XX      N-PSDB; V49866.
XX      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX      Claim 62; Page 41; 129pp; English.
XX      W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC      LM609 heavy and light chain variable region. LM609 and the antibody
CC      vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC      inhibit binding of alphavbeta3 to a ligand and thus block
CC      integrin-mediated signal transduction. This is useful in the treatment,
CC      prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC      arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC      contain non-murine framework regions so are suitable for use in humans.
CC      Enhanced types of LM609 have affinity more than 90 times greater than
CC      that of parent the parent antibody.
XX      Sequence 10 AA:
SQ      Query Match      90.9%; Score 50; DB 19; Length 10;
          Best Local Similarity 100.0%; Pred. No. 0.0064;
          Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARHNYGSFA 9
Db      1 arhnygsfa 9

RESULT      8
W76010
ID      W76010 standard; Protein; 10 AA.
XX      W76010;
AC      W76010;
XX      02-NOV-1998 (first entry)
DT      LM609 grafted antibody V-H region CDR3 protein fragment #1.
DE      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX      KW

```

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region.
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 OS
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49847.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence. 10 AA;

 Query Match 90.9%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

 RESULT 9
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX

PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49820.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

 Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

 RESULT 10
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX
 AC W76003;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 DR N-PSDB; V49822.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 43; Fig 2a; 129pp; English.
 PS This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db ||||||||
 97 arhnygsfa 105

RESULT 11
 Y06381
 ID Y06381 standard; Protein; 117 AA.
 AC Y06381;
 XX
 DT 06-SEP-1999 (first entry)
 XX Murine monoclonal antibody LM609 VH region.
 DE Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX Mus musculus.
 OS
 XX WO9929888-A1.
 PN 17-JUN-1999.
 PD 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 PR (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 DR Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 52-53; 55pp; English.
 PS This sequence represents the heavy chain variable region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db ||||||||
 97 arhnygsfa 105

RESULT 12
 Y06387
 ID Y06387 standard; Protein; 117 AA.
 AC Y06387;
 XX
 DT 06-SEP-1999 (first entry)
 XX Humanised LM609 antibody VH domain.
 DE Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX WO9929888-A1.
 PN 17-JUN-1999.
 PD 04-DEC-1998; 98WO-US25828.
 XX 05-DEC-1997; 97US-0986016.
 PR (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Rader C;
 XX WPI; 1999-394979/33.
 DR Production of humanized mouse monoclonal antibodies
 XX Disclosure; Page 52; 55pp; English.
 PS This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX
 XX Sequence 117 AA;

Query Match 90.9%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 97 arhnygsfa 105

RESULT 13

Y06384
 ID Y06384 standard; Protein: 118 AA.

XX AC Y06384;

DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	31..37
Region	/note= "CDR1"
Region	52..67
Region	/note= "CDR2"
Region	100..107
Region	/note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 98 arhnygsfa 106

RESULT 14

Y06385
 ID Y06385 standard; Protein: 118 AA.

XX AC Y06385;

DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	31..37
Region	/note= "CDR1"
Region	52..67
Region	/note= "CDR2"
Region	100..107
Region	/note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | |
Db 98 arhnygsfa 106

RESULT 15
Y06386
ID Y06386 standard; Protein; 118 AA.
XX
AC Y06386;
XX
DT 06-SEP-1999 (first entry)
XX
DE -Humanised LM609 antibody VH domain.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..2
FT /note= "vector-encoded residues"
FT Region 31..37
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..107
FT /note= "CDR3"

XX WO929888-A1.
PN XX
XX 17-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US25828.
XX
XX 05-DEC-1997; 97US-0986016.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C;
XX
XX WPI; 1999-394979/33.
XX
XX Production of humanized mouse monoclonal antibodies
PT
PS Disclosure; Page 51-52; 55pp; English.
XX

CC This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha^v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;

Query Match 90.9%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | |
Db 98 arhnygsfa 106

Search completed: March 28, 2001, 06:59:48
Job time: 1384 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:55 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNGSPAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep: *
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep: *
3: /cgnl_7/ptodata/1/iaa/6_COMB.pep: *
4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep: *
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	74.5	119	3	US-08-767-128-6
2	36	65.5	94	3	US-09-147-550-14
3	36	65.5	94	3	US-09-147-550-45
4	36	65.5	94	3	US-09-147-550-48
5	36	65.5	94	3	US-09-147-550-77
6	36	65.5	94	3	US-09-147-550-84
7	36	65.5	94	3	US-09-147-550-90
8	36	65.5	94	3	US-09-147-550-101
9	34	61.8	286	2	US-08-809-267-3
10	34	61.8	286	4	PCT-US95-13662A-3
11	34	61.8	287	2	US-08-741-437-5
12	34	61.8	287	2	US-09-134-593-5
13	32	58.2	15	1	US-08-618-464-7
14	32	58.2	15	3	US-09-107-615-7
15	32	58.2	25	2	US-08-480-190-44
16	32	58.2	25	2	US-08-488-379-44
17	32	58.2	25	4	PCT-US93-07545-44
18	32	58.2	36	1	US-08-053-131-84
19	32	58.2	36	1	US-08-645-641-84
20	32	58.2	36	1	US-07-853-408B-84
21	32	58.2	36	2	US-08-096-762-84
22	32	58.2	36	2	US-08-308-865-84
23	32	58.2	36	4	PCT-US92-10983-84
24	32	58.2	80	1	US-08-264-250A-1
25	32	58.2	89	1	US-08-025-038-30
26	32	58.2	89	1	US-08-039-137-17
27	32	58.2	90	2	US-08-485-133-23
28	32	58.2	94	3	US-09-147-550-12

29 32 58.2 94 3 US-09-147-550-13 Sequence 13, Appl
30 32 58.2 94 3 US-09-147-550-15 Sequence 15, Appl
31 32 58.2 94 3 US-09-147-550-16 Sequence 16, Appl
32 32 58.2 94 3 US-09-147-550-17 Sequence 17, Appl
33 32 58.2 94 3 US-09-147-550-18 Sequence 18, Appl
34 32 58.2 94 3 US-09-147-550-19 Sequence 19, Appl
35 32 58.2 94 3 US-09-147-550-20 Sequence 20, Appl
36 32 58.2 94 3 US-09-147-550-21 Sequence 21, Appl
37 32 58.2 94 3 US-09-147-550-22 Sequence 22, Appl
38 32 58.2 94 3 US-09-147-550-24 Sequence 24, Appl
39 32 58.2 94 3 US-09-147-550-25 Sequence 25, Appl
40 32 58.2 94 3 US-09-147-550-26 Sequence 26, Appl
41 32 58.2 94 3 US-09-147-550-27 Sequence 27, Appl
42 32 58.2 94 3 US-09-147-550-28 Sequence 28, Appl
43 32 58.2 94 3 US-09-147-550-29 Sequence 29, Appl
44 32 58.2 94 3 US-09-147-550-30 Sequence 30, Appl
45 32 58.2 94 3 US-09-147-550-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 74.5%; Score 41; DB 3; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
|||:|:|
Db 97 ARHNYGYAM 106

RESULT 2
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGF 8
|||||
Db 80 RHNYSGVF 86

RESULT 3
US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGF 8
|||||
Db 80 RHNYSGVF 86

RESULT 4
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGF 8
|||||
Db 80 RHNYSGVF 86

RESULT 5
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77

;
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 6

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84

; LENGTH: 94
; TYPE: PRT

; ORGANISM: BOVINE
US-09-147-550-84

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90

; LENGTH: 94
; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-90

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101

; LENGTH: 94
; TYPE: PRT

; ORGANISM: BOVINE
US-09-147-550-101

Query Match 65.5%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 9

US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296

; GENERAL INFORMATION:

; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NEW ENGLAND BIOLABS, INC.

; STREET: 32 TOZER ROAD

; CITY: BEVERLY

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 01915

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/809,267

;; FILING DATE: 12-MAR-1997
;; CLASSIFICATION: 433
;; PRIOR APPLICATION DATA: PCT/US95/13662
;; APPLICATION NUMBER: PCT/US95/13662
;; FILING DATE:
;; APPLICATION NUMBER: US 08/329,721
;; FILING DATE: 25-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILLIAMS, GREGORY D.
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-105-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 927-5054
;; TELEFAX: (508) 927-1705
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-809-267-3

Query Match 61.8%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 10
PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: PCT/US95/13662A
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/329,721
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; PCT-US95-13662A-3

Query Match 61.8%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 11
US-08-741-437-5
; Sequence 5, Application US/08741437
; Patent No. 5843665
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741.437
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
; US-08-741-437-5

Query Match 61.8%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 12

US-09-134-593-5
; Sequence 5, Application US/09134593
; Patent No. 5981232
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,593
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 853-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-09-134-593-5

Query Match 61.8%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 13
US-08-618-464-7
; Sequence 7, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INDUCING
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US

ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: S1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-08-618-464-7

Query Match 58.2%; Score 32; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 11 RHNYG 15

RESULT 14
US-09-107-615-7
; Sequence 7, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: S1
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-09-107-615-7

Query Match 58.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNyg 6
Db 11 RHNyg 15

RESULT 15
US-08-480-190-44
Sequence 44, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-44

Query Match 58.2%; Score 32; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNyg 6
Db 15 RHNyg 19

Search completed: March 28, 2001, 07:01:55
Job time: 1334 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:24 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNYGSFAG 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-66.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	69.6	446	2	T19625
2	38	67.9	697	3	T41445
3	36	64.3	82	2	I51106
4	36	64.3	89	2	S38688
5	36	64.3	89	2	S38683
6	36	64.3	89	2	S38684
7	36	64.3	225	2	I47095
8	35	62.5	320	2	T09288
9	35	62.5	347	2	S43771
10	35	62.5	405	1	Q08E35
11	34	60.7	108	2	S26316
12	34	60.7	110	2	S26317
13	34	60.7	110	2	T02485
14	34	60.7	138	2	P81900
15	34	60.7	210	1	B69265
16	34	60.7	275	2	G75130
17	34	60.7	275	2	D71087
18	34	60.7	287	1	PWBV
19	34	60.7	287	1	PWKL
20	34	60.7	384	1	SYEC5M
21	34	60.7	384	2	H64187
22	34	60.7	385	2	E82319
23	34	60.7	386	2	S51436
24	34	60.7	396	2	H83576
25	34	60.7	400	2	D69657
26	34	60.7	403	2	F70899
27	34	60.7	403	2	E82810
28	34	60.7	468	2	H82321
29	34	60.7	502	2	T08776

30	34	60.7	609	2	S45930	probable amino aci
31	34	60.7	723	2	F83173	outer membrane pro
32	34	60.7	856	2	T13159	ELB-55kDa-associat
33	34	60.7	939	2	S28394	probable serine/th
34	33	58.9	80	2	I54469	MHC HLA-DR-beta-1
35	33	58.9	80	2	I68777	MHC HLA-DR-beta-1
36	33	58.9	81	2	I54550	HLA DRB1*1202 - hu
37	33	58.9	85	2	I59634	MHC class II DR-be
38	33	58.9	89	2	S38676	MHC class II histo
39	33	58.9	89	2	S38680	MHC class II histo
40	33	58.9	89	2	S57512	MHC class II histo
41	33	58.9	123	2	C25239	MHC class II histo
42	33	58.9	167	2	T16454	hypothetical prote
43	33	58.9	200	2	D32526	class II histocomp
44	33	58.9	220	2	T46055	hypothetical prote
45	33	58.9	228	2	T35418	probable transcrip

ALIGNMENTS

RESULT 1

T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
C:Experimental source: clone C31H5
C:Genetics:
A:Map position: 1
A:Gene: CESP:C31H5.6
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 69.6%; Score 39; DB 2; Length 446;

Best Local Similarity 87.5%; Pred. No. 10;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

RESULT 2

T41445
hypothetical protein SPCC594.01 - fission yeast (Schizosaccharomyces pombe) (fragment
C:Species: Schizosaccharomyces pombe
C:Date: 27-Nov-1999 #sequence_revision 27-Nov-1999 #text_change 27-Nov-1999
C:Accession: T41445
R:Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21994
A:Accession: T41445
A:Status: preliminary
A:Residues: 1-697 <RIE>
A:Cross-references: EMBL:AL031523; PIDN:CAA20660.1; GSPDB:GN00068; SPDB:SPCC594.01

Query Match 67.9%; Score 38; DB 3; Length 697;

Best Local Similarity 77.8%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAG 10

Db 11 RHNYGSHA 58

Db 155 RHRYWSFAG 163

RESULT 3

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
 C:Species: Phasianus colchicus (ring-necked pheasant)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C:Accession: I51106
 R:Witzell, H.; von Schantz, T.; Zorob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant (Phasianus colchicus)
 A:Reference number: I51103; MUID:94245280
 A:Accession: I51106
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <WIT>
 A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 7.4;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 4

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 23-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38688
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the sequence
 A:Reference number: S38676
 A:Accession: S38688
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27158
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 8.1;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 5

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38683
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the sequence
 A:Reference number: S38676
 A:Accession: S38683
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27153
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 8.1;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8,

|||||

Db 75 RHNYGVF 81

RESULT 6

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: S38684
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the sequence
 A:Reference number: S38676
 A:Accession: S38684
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27154
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 8.1;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 7

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
 C:Accession: I47095
 R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
 Anim. Genet. 24, 249-255, 1993
 A:Title: Isolation, characterization and evolution of ovine major histocompatibility complex class II genes
 A:Reference number: I47075; MUID:94057592
 A:Accession: I47095
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-225 <FAB>
 A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
 C:Genetics:

QY 2 RHNYGSF 8

|||||

Db 68 RHNYGVF 74

RESULT 8

T09288

late embryonic abundant protein EMB7 - white spruce
 C:Species: Picea glauca (white spruce)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T09288
 R:Dong, J.Z.; Dunstan, D.I.
 submitted to the EMBL Data Library, June 1996

A:Description: Cloning and characterization of 6 novel plant embryogenesis-associated genes
A:Reference number: Z16629
A:Accession: T09288
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-320 <DON>
A:Cross-references: EMBL:L47117; NID:g1350542; PID:g1350543
C:Genetics:
A:Gene: EMB7

Query Match 62.5%; Score 35; DB 2; Length 320;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
||| ||
DB 217 HNYGIAG 224

RESULT 9
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - *Synechococcus* sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misidentified]
C:Species: *Synechococcus* sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacteria
A:Reference number: S43770; MUID:94207189
A:Accession: S43771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:g488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 62.5%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
||| |||
DB 334 AEHNYISFA 342

RESULT 10
Q0BE35
BBR35 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C:Accession: G43043; A03777; S33030
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17.166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713
A:Accession: G43043
A:Molecule type: DNA
A:Residues: 1-405 <BAN>
A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24825.1; PID:g1334889
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667
A:Contents: annotation; protein coding region
C:Superfamily: cytomegalovirus UL100 protein

Query Match 62.5%; Score 35; DB 1; Length 405;

Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAG 10
||| ||
DB 267 RHNFGPYCG 275

RESULT 11
S26316
Ig heavy chain V region - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26316
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421
A:Accession: S26316
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <STA>
A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:g1334035
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 34; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|| ||| ||
DB 84 ARGNYGNYA 92

RESULT 12
S26317
Ig heavy chain V region - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26317
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421
A:Accession: S26317
A:Molecule type: mRNA
A:Residues: 1-110 <STA>
A:Cross-references: EMBL:X59186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 34; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|| ||| ||
DB 86 ARGNYGNYA 94

RESULT 13
T02485
hypothetical protein P23F1.8 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 20-Jun-2000
C:Accession: T02485
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, August 1998

A;Description: Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence.

A;Reference number: Z14675

A;Accession: T02485

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-110 <RQU>

A;Cross-references: EMBL:AC004680; NID:g3420043; PID:g3420051

A;Experimental source: cultivar Columbia

C;Genetics:

A;Map position: 2

A;Note: F23F1.8

C;Superfamily: Arabidopsis thaliana hypothetical protein F23F1.8

Query Match 60.7%; Score 34; DB 2; Length 110;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 NYGSFAG 10

Db 50 NYGSFQG 56

RESULT 14

F81900

hypothetical protein NMA1316 [imported] - Neisseria meningitidis (group A strain Z2491)

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000

C;Accession: F81900

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: AB1775; MUID:20222556

A;Accession: F81900

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-138 <PAR>

A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84568.1; PID:g737999

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA1316

Query Match 60.7%; Score 34; DB 2; Length 138;

Best Local Similarity 60.0%; Pred. No. 29;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ARHNYGSFAG 10

Db 93 AIHNFEGMAG 102

RESULT 15

B69265

conserved hypothetical protein AF0122 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C;Accession: B69265

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A;Reference number: A69250; MUID:98049343

A;Accession: B69265

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-210 <KLE>

A;Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PIDN:AAB91117.1; PID:g265053

C;Superfamily: conserved hypothetical protein AF0119

Query Match 60.7%; Score 34; DB 1; Length 210;

Best Local Similarity 85.7%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8

Db 128 RHAYGSF 134

Search completed: March 28, 2001, 07:04:26

Job time: 1064 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:04 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-78

Perfect score: 56

Sequence: 1 ARHNYGSPAG 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	64.3	218	1 Y4VH_RHISN	Q53216 rhizobium s
2	35	62.5	405	1 VGLM_EBV	P03215 epstein-bar
3	34	60.7	275	1 IF2A_PYRAB	Q9V084 pyrococcus
4	34	60.7	275	1 IF2A_PYRAB	O58655 pyrococcus
5	34	60.7	284	1 IPYR_PICPA	O13505 pichia past
6	34	60.7	286	1 IPYR_KLULA	P13998 kluyveromyc
7	34	60.7	286	1 IPYR_YEAST	P00817 saccharomyc
8	34	60.7	384	1 METK_ECOLI	P04384 escherichia
9	34	60.7	384	1 METK_HAEIN	P43762 haemophilus
10	34	60.7	386	1 PEXD_YEAST	P80667 saccharomyc
11	34	60.7	400	1 METK_BACSU	P54419 bacillus su
12	34	60.7	403	1 METK_MYCTU	P77899 mycobacteri
13	34	60.7	609	1 BAP2_YEAST	P38084 saccharomyc
14	34	60.7	939	1 ST20_YEAST	Q03497 saccharomyc
15	33	58.9	257	1 HB2P_RABIT	P20756 oryctolagus
16	33	58.9	347	1 MREB_ECOLI	P13519 escherichia
17	33	58.9	396	1 METK_TREPA	O83772 treponema p
18	33	58.9	448	1 NCAP_CVHOC	P33469 human coron
19	33	58.9	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
20	33	58.9	473	1 SYE_AQUAE	O67271 aquifex aeo
21	33	58.9	682	1 VG50_BPML5	Q05262 mycobacteri
22	33	58.9	722	1 BPB1_YEAST	P53297 saccharomyc
23	33	58.9	1859	1 RPBI_CAEEL	P16356 caenorhabdi
24	32	57.1	65	1 CCSA_OENBE	P31585 oenothera b
25	32	57.1	65	1 CCSA_PEA	P31172 pisum sativ
26	32	57.1	196	1 WBRJ_ECOLI	P37750 escherichia
27	32	57.1	198	1 HB2G_HUMAN	P01911 homo sapien
28	32	57.1	266	1 HB2A_HUMAN	P01913 homo sapien
29	32	57.1	266	1 HB2B_HUMAN	P01912 homo sapien
30	32	57.1	266	1 HB2C_HUMAN	P01914 homo sapien
31	32	57.1	266	1 HB2D_CANFA	P18470 canis famli
32	32	57.1	266	1 HB2D_HUMAN	P13759 homo sapien
33	32	57.1	266	1 HB2E_HUMAN	P04229 homo sapien

34 32 57.1 266 1 HB2F_HUMAN P13758 homo sapien
35 32 57.1 266 1 HB2H_HUMAN P13760 homo sapien
36 32 57.1 266 1 HB2I_HUMAN P20039 homo sapien
37 32 57.1 266 1 HB2J_HUMAN P13761 homo sapien
38 32 57.1 313 1 CCSA_TOBAC P12216 nicotiana t
39 32 57.1 321 1 CCSA_MAIZE P46659 zea mays (m
40 32 57.1 321 1 CCSA_ORYSA P12215 oryza sativ
41 32 57.1 328 1 CCSA_ATHAT P56770 arabidopsis
42 32 57.1 349 1 YJY9_YEAST P41903 saccharomyc
43 32 57.1 383 1 METK_MYCGE P47293 mycoplasma
44 32 57.1 383 1 METK_MYCPN P78003 mycoplasma
45 32 57.1 397 1 METK_STAAU P50307 staphylococ

ALIGNMENTS

RESULT 1
Y4VH_RHISN
ID Y4VH_RHISN STANDARD; PRT; 218 AA.
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 24.6 KDA PROTEIN Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97305956.
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96389014.
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
NGR234 using dye terminators and a thermostable 'sequenase': a
beginning";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: NONE OBVIOUS.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z68203; CAA92423.1; .
DR EMBL; AE000101; AAB91896.1; .
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 218;
Best Local Similarity 60.0%; Pred No. 7, 7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSPAG 10
|||I:::
Db 68 ARDNHGSYSG 77

RESULT 2
VGLM_EBV
ID VGLM_EBV STANDARD; PRT; 405 AA.

P03215;
 21-JUL-1986 (Rel. 01, Created)
 21-JUL-1986 (Rel. 01, Last sequence update)
 01-APR-1993 (Rel. 25, Last annotation update)
 GLYCOPROTEIN M.
 GN BREF3.
 OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gamaherpesvirinae; Lymphocryptovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84270567.
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tuffnell P.S., Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1994).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.
 CC -----
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 CC -----
 CC EMBL: V01555; CAA24825.1; -;
 DR PIR: A03777; Q0BE35.
 DR PIR: S33030; S33030.
 DR INTERPRO: IPR000785; -;
 DR PFAM: PF01528; Herpes_glycop; 1.
 DR PRINTS: PR00333; HSVINTEGRMP.
 DR Transmembrane; Glycoprotein; Late protein.
 FT TRANSMEM 18 38 POTENTIAL.
 FT TRANSMEM 77 97 POTENTIAL.
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 150 170 POTENTIAL.
 FT TRANSMEM 208 228 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 268 288 POTENTIAL.
 FT TRANSMEM 300 320 POTENTIAL.
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 367 377 SER/THR-RICH.
 SQ SEQUENCE 405 AA; 45792 MW; 25A8A46B6CDC0AE1 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 405;
 Best Local Similarity 55.6%; Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAG 10
 |||:|:|
 Db 267 RHNFYFCG 275

RESULT 3
 IF2A_PYRAB
 ID IF2A_PYRAB - STANDARD; PRT; 275 AA.
 AC Q9V0E4;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PAB0568.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR6AY;
 RA Heilig R.;

*Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
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 CC -----
 CC EMBL: AJ248285; CAB49760.1; -;
 DR INTERPRO: IPR003029; -;
 DR PFAM: PF00575; SI; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83 SI MOTIF.
 SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 60.7%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 ||||:|
 Db 23 HNYGAF 28

RESULT 4
 IF2A_PYRHO
 ID IF2A_PYRHO STANDARD; PRT; 275 AA.
 AC O38655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE; 98344137.
 RA Kwarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
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 CC -----

DR EMBL; AP000004; BAA30058.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 83 S1 MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

DB 23 HNYGAF 28

RESULT 5
 IPYR_PICPA STANDARD; PRT; 284 AA.
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC Q13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP STRAIN-NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----

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DR EMBL; AJ001000; CAA04453.1; -
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 24;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

DB 91 HNYGAF 96

RESULT 6
 IPYR_KLULA STANDARD; PRT; 286 AA.
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.K., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E.COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----

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DR EMBL; X14230; CAA32446.1; -
 DR PIR; S07894; PWVKL.
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4BD916A2F CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 24;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

DB 91 HNYGAF 96

RESULT 7
 IPYR_YEAST STANDARD; PRT; 286 AA.
 ID IPYR_YEAST STANDARD; PRT; 286 AA.

AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PBASE).
 GN IPPI OR PPA1 OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Kelm P.S., Heinrikson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN=S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database.";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]
 RP SEQUENCE OF 239-249.
 RC STRAIN=ATCC 38531 / Y41;
 RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT *Saccharomyces cerevisiae*.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohn W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.

RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyttia T.,
 RA Kapyta J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The K78K and D117E active-site variants of *Saccharomyces cerevisiae*
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E. COLI AND K. LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Viininen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X13253; CAA31629.1;
 DR EMBL; Z35880; CAA84949.1;
 DR PIR; S45864; PMBY.
 DR PDB; 1XPY; 15-OCT-91.
 DR PDB; 1YPP; 07-DEC-96.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1HUI; 08-APR-98.
 DR PDB; 1HUK; 08-APR-98.
 DR PDB; 117E; 23-DEC-98.
 DR PDB; 8PRK; 23-DEC-98.
 DR SWISS-2DPAGE; P00817; YEAST.
 DR YEPD; 7305;
 DR SGD; S0000215; IPPI.
 DR INTERPRO: IPR001596;
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 DR KW Hydrolyase; Magnesium; 3D-structure.
 FT INIT_MET 0
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
 FT CONFLICT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 71 71 D -> N (IN REF. 3).
 FT CONFLICT 74 74 MISSING (IN REF. 3).
 FT CONFLICT 123 123 E -> Q (IN REF. 3).
 FT CONFLICT 136 136 Q -> E (IN REF. 3).
 FT CONFLICT 186 186 N -> D (IN REF. 3).
 FT CONFLICT 224 224 D -> N (IN REF. 3).
 FT CONFLICT 266 266 L -> P (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 16 20
 FT STRAND 25 25
 FT STRAND 28 30
 FT TURN 38 41
 FT TURN 45 45
 FT STRAND 55 55
 FT STRAND 79 79
 FT TURN 97 98
 FT TURN 111 112
 FT TURN 121 123

FT TURN 131 132
 FT STRAND 135 135
 FT STRAND 138 146
 FT STRAND 151 158
 FT TURN 160 161
 FT TURN 165 167
 FT TURN 172 175
 FT TURN 176 177
 FT TURN 179 180
 FT TURN 182 197
 FT STRAND 203 203
 FT STRAND 205 207
 FT STRAND 210 210
 FT STRAND 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 24;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 ||||:|
 Db 91 HNYGAF 96

RESULT 8
 METK_ECOLI
 ID METK_ECOLI STANDARD; PRT; 384 AA.
 AC P04384; P30869;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 GN METK OR METX.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85054924.
 RA Markham G.D., Deparasis J., Gatmaitan J.;
 RT "The sequence of metK, the structural gene for S-adenosylmethionine
 RT synthetase in Escherichia coli.";
 RL J. Biol. Chem. 259:14505-14507(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE; 94049123.
 RA Satishchandran C., Taylor J.C., Markham G.D.;
 RT "Isozymes of S-adenosylmethionine synthetase are encoded by tandemly
 RT duplicated genes in Escherichia coli.";
 RL Mol. Microbiol. 9:835-846(1993).
 RN [4]
 RP SEQUENCE OF 1-63 FROM N.A.
 RX MEDLINE; 90330576.

RA Moore R.C., Boyle S.M.;
 RT "Nucleotide sequence and analysis of the speA gene encoding
 RT biosynthetic arginine decarboxylase in Escherichia coli.";
 RL J. Bacteriol. 172:4631-4640(1990).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE; 96132894.
 RA Takusagawa F., Kamitori S., Misaki S., Markham G.D.;
 RT "Crystal structure of S-adenosylmethionine synthetase.";
 RL J. Biol. Chem. 271:136-147(1996).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE; 96180683.
 RA Takusagawa F., Kamitori S., Markham G.D.;
 RT "Structure and function of S-adenosylmethionine synthetase: crystal
 RT structures of S-adenosylmethionine synthetase with ADP, BRADP, and
 RT PPI at 2.8-A resolution.";
 RL Biochemistry 35:2586-2596(1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 RX MEDLINE; 96304769.
 RA Fu Z., Hu Y., Markham G.D., Takusagawa F.;
 RT "Flexible loop in the structure of S-adenosylmethionine synthetase
 RT crystallized in the tetragonal modification.";
 RL J. Biomol. Struct. Dyn. 13:727-739(1996).
 CC -|- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -|- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
 CC -|- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -|- SUBUNIT: HOMOTETRAMER.
 CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -|- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC -|- CAUTION: WAS ORIGINALLY (REF.3) THOUGHT TO DIFFER FROM METX THAT
 CC WAS ASSIGNED TO BE A SECOND ADOMET SYNTHETASE BEFORE BEING SHOWN
 CC TO BE IDENTICAL TO METK.
 CC -----
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 CC -----
 CC EMBL; K02129; AAA24164.1;
 CC EMBL; U28377; AAA69109.1;
 CC EMBL; AE000377; AAC75979.1;
 CC EMBL; M98266; AAB05197.1;
 CC EMBL; M31770; AAA24645.1;
 CC PIR; A00590; SYECSM.
 CC PDB; 1MXA; 11-JUL-96.
 CC PDB; 1MXB; 11-JUL-96.
 CC PDB; 1MXC; 11-JUL-96.
 CC PDB; 1FUG; 01-AUG-96.
 CC PDB; 1XRA; 08-MAR-96.
 CC PDB; 1XPB; 08-MAR-96.
 CC PDB; 1XRC; 08-MAR-96.
 CC SWISS-2DPAGE; P04384; COLI.
 CC EC02DBASE; C044.6; 6TH EDITION.
 CC ECOGENE; EGI0589; METK.
 CC INTERPRO; IPR002133;
 CC PFAM; PF00438; S-Adomet_synt; 1.
 CC PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
 CC PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
 CC Transferrase; One-carbon metabolism; ATP-binding; 3D-structure.
 CC NP_BIND 116 121
 CC ATG (POTENTIAL).
 CC CONFLICT 50 61
 CC MVLGGGEITSA -> IGFSWRRHHHQP (IN REF.
 CC 1 AND 4).
 CC MFGIATNETDV -> DVSATQLMKPTC (IN REF. 1).
 CC CONFLICT 123 133
 CC PWL -> RV (IN REF. 1 AND 3).
 CC CONFLICT 159 161
 CC Q -> S (IN REF. 1).
 CC CONFLICT 172 172
 CC Y -> T (IN REF. 1).
 CC CONFLICT 252 252

FT CONFLICT 305 305 V -> L (IN REF. 1).
FT CONFLICT 337 337 MISSING (IN REF. 1).
FT CONFLICT 339 339 Y -> I (IN REF. 1).
FT CONFLICT 375 376 OL -> HV (IN REF. 3).
FT CONFLICT 378 378 R -> P (IN REF. 3).
SQ SEQUENCE 384 AA; 41951 MW; 97FA8CF17B542941 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 384;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;

QY 1 ARHNYGSFAG 10
||| |::|
Db 256 ARHGGGAFSG 265

RESULT 9
METK_HAEIN STANDARD; PRT; 384 AA..
AC P43762;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
GN METK OR H11172
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE; 95350630.
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kienle A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.

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CC -----
CC EMBL: U32797; AAC22825.1;
CC HSSP: P04384; 1FUG.
CC TIGR: H11172;
CC INTERPRO: IPR002133;
CC PFAM: PF00438; S-Adomet_synt; 1.
CC PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
CC PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
CC Transferase: One-carbon metabolism; ATP-binding.
FT NP_BIND 116 121 ATP (POTENTIAL).
SQ SEQUENCE 384 AA; 41973 MW; 3E4F873092C331B7 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 384;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;

QY 1 ARHNYGSFAG 10
||| |::|
Db 256 ARHGGGAFSG 265

RESULT 10
PEXD_YEAST STANDARD; PRT; 386 AA..
ID P80667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).
GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97011156.
RA Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
RA Tabak H.F., Distel B.;
RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
RT protein Pex13p functions as a docking site for Pex5p, a mobile
RT receptor for the import PTS1-containing proteins.";
RL J. Cell Biol. 135:97-109(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favellio A., Fullon L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=S288C;
RX MEDLINE; 97011157.
RA Erdmann R., Blobel G.;
RT "Identification of Pex13p a peroxisomal membrane receptor for the
RT PTS1 recognition factor.";
RL J. Cell Biol. 135:111-121(1996).
CC -1- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
CC WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
CC (PAS10/PEX5).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC -----
CC EMBL: S82971; ABA46885.1;
CC EMBL: U37420; AAA79308.1;
CC EMBL: U17246; AAB67453.1;
CC EMBL: U14913; AAB67448.1;
CC HSSP: Q06187; LAWV.
CC SGD: S0004181; PEX13.
CC INTERPRO: IPR001452;
CC PFAM: PF00018; SH3; 1.

DR PRINTS; PRO0452; SH3DOMAIN.
 DR PROSITE; PS00002; SH3; 1.
 KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
 FT DOMAIN 1 263 LUMENAL (POTENTIAL).
 FT TRANSMEM 264 280 POTENTIAL.
 FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 306 372 SH3.
 SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 386;
 Best Local Similarity 75.0%; Pred. No. 33;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
 :|||||
 Db 117 NNYGSFYG 124

RESULT 11
 METK_BACSU STANDARD; PRT; 400 AA.
 AC P54419; Q34566;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 GN METK OR METE.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / PV79;
 RX MEDLINE; 96345628.
 RA Yocum R., Perkins J.B., Howitt C.L., Pero J.;
 RT "Cloning and characterization of the metE gene encoding S-
 RT adenosylmethionine synthetase from Bacillus subtilis.";
 RL J. Bacteriol. 178:4604-4610(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98048467.
 RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
 RT "Sequencing and functional annotation of the Bacillus subtilis genes
 RT in the 200 kb rnb-dnaB region";
 RL Microbiology 143:3431-3441(1997).
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC
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 CC
 CC EMBL; U52812; AB17066.1; -
 DR EMBL; AF008220; AAC00242.1; -
 DR EMBL; Z99119; CAB15033.1; -
 DR HSP; P04384; 1XRC.
 DR SUBTILIST; BG11840; METK.
 DR INTERPRO; IPR002133; -
 DR PFAM; PF00438; S-AdoMet_synth; 1.
 DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
 DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.

KW Transferase; One-carbon metabolism; ATP-binding.
 FT NP_BIND 129 134 ATP (POTENTIAL).
 FT CONFLICT 26 26 S -> Y (IN REF. 1).
 FT CONFLICT 111 111 Q -> P (IN REF. 1).
 FT CONFLICT 140 140 A -> V (IN REF. 1).
 SQ SEQUENCE 400 AA; 44042 MW; EF3D97DCD375714A CRC64;

Query Match 60.7%; Score 34; DB 1; Length 400;
 Best Local Similarity 60.0%; Pred. No. 34;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSEAG 10
 :|||:|:|
 Db 270 ARHGGGAFSG 279

RESULT 12
 METK_MYCTU STANDARD; PRT; 403 AA.
 AC P77899;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 GN METK OR RV1392 OR MTCY21B4.09.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE; 98295987.
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC
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 CC
 CC EMBL; Z80108; CAB02194.1; -
 DR HSP; P04384; 1XRC.
 DR TUBERCULIST; RV1392; -
 DR INTERPRO; IPR002133; -
 DR PFAM; PF00438; S-AdoMet_synth; 1.
 DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
 DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
 KW Transferase; One-carbon metabolism; ATP-binding.
 FT NP_BIND 131 136 ATP (BY SIMILARITY).
 SQ SEQUENCE 403 AA; 43046 MW; 2E18BE05D8267972 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 403;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFAG 10
||| 1:1:1
DB 276 ARHGGAFSG 285

RESULT 13
BAP2_YEAST STANDARD; PRT; 609 AA.
AC P38084;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE LEU/VAL/ILE AMINO-ACID PERMEASE (BRANCHED-CHAIN AMINO-ACID PERMEASE
2).
GN BAP2 OR YBR068C OR YBR0629.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Domdey H., Gassenhuber H., Obermaier B., Piravandi E.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 604-609 FROM N.A.
RC STRAIN=S288C;
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE; 96096693.
RA Grauslund M., Didion T., Kielland-Brandt M.C., Andersen H.A.;
RT "BAP2, a gene encoding a permease for branched-chain amino acids in
Saccharomyces cerevisiae.";
RL Blochim. Biophys. Acta 1269:275-280(1995).
CC -1- FUNCTION: AMINO ACID PERMEASE FOR LEUCINE, VALINE AND ISOLEUCINE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.

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CC EMBL; 235937; CAA85012.1; -;
CC PIR; S45930; S45930.
CC SGD; S0000272; BAP2.
CC INTERPRO: IPR002027; -;
CC PFAM; PF00324; aa_permeases; 1.
CC PROSITE; PS00218; AMINO-ACID-PERMEASE_1; 1.
CC Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 211 231 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 329 349 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.
FT TRANSMEM 428 448 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 501 521 POTENTIAL.
FT TRANSMEM 537 557 POTENTIAL.
SQ SEQUENCE - 609 AA; 67670 MW; 02249C5F744E16E5 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 609;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
||| 1:1:1
DB 273 HNPGEFAG 280

RESULT 14
ST20_YEAST STANDARD; PRT; 939 AA.
AC Q03497;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).
GN STE20 OR YHL007C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93099855.
RA Leberer E., Dignard D., Hargus D., Thomas D.Y., Whiteway M.;
RT "The protein kinase homologue Ste20p is required to link the yeast
RT pheromone response G-protein beta gamma subunits to downstream
RT signalling components.";
RL EMBO J. 11:4815-4824(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93133807.
RA Ramer S.W., Davis R.W.;
RT "A dominant truncation allele identifies a gene, STE20, that encodes
RT a putative protein kinase necessary for mating in Saccharomyces
RT cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:452-456(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE; 94378003.
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
CC -1- FUNCTION: REQUIRED TO LINK THE PHEROMONE RESPONSE G-PROTEIN BETA
CC GAMMA SUBUNITS TO DOWNSTREAM SIGNALING COMPONENTS. IT IS THOUGHT
CC THAT IT CAN PHOSPHORYLATE STE5, NEEDED FOR MATING IN HAPLOID
CC CELLS, INDUCTION OF A MATING-SPECIFIC GENE FUS1, INDUCTION OF
CC MATING-SPECIFIC MORPHOLOGIES, AND PHEROMONE-INDUCED PROLIFERATION
CC ARREST. PHOSPHORYLATES STE11.
CC -1- PATHWAY: RESPONSE TO PHEROMONE-INDUCED SIGNAL.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- PTM: AUTOPHOSPHORYLATED ON SERINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.

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CC EMBL; M94719; AAA35111.1; -;

DR EMBL; L04655; AAA35038.1; -
 DR EMBL; L04655; AAA35039.1; -
 DR EMBL; U11581; AAB69747.1; -
 DR PIR; S28394; S28394.
 DR PIR; S46821; S46821.
 DR HSSP; Q63450; LA06.
 DR SGD; S0000999; STE20.
 DR INTERPRO; IPR000095; -
 DR INTERPRO; IPR000719; -
 DR INTERPRO; IPR002290; -
 DR PFAM; PF00786; PBD; 1.
 DR PFAM; PF00069; pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Pheromone response; phosphorylation.
 FT DOMAIN 95 375
 FT NP_BIND 620 871
 FT BINDING 626 834
 FT ACT_SITE 739 739
 FT CONFLICT 19 19
 FT CONFLICT 134 134
 FT CONFLICT 271 271
 SQ SEQUENCE 939 AA; 102362 MW; 69C1C12F5B87733C CRC64;

Query Match 60.7%; Score 34; DB 1; Length 939;
 Best Local Similarity 75.0%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNYGSFAG 10
 |||||
 Db 440 HNYGSRTG 447

RESULT 15
 HB2P_RABIT
 ID HB2P_RABIT STANDARD; PRT; 257 AA.
 AC P20756;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE RLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP BETA CHAIN PRECURSOR (D10
 DE HAPLOTYPE)
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88159085.
 RA Sittisombut N., Mordacq J., Knight K.L.;
 RT "Rabbit MHC. II. Sequence analysis of the R-DP alpha- and
 beta-genes";
 RL J. Immunol. 140:3237-3243(1988).
 CC -----
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 CC -----
 DR EMBL; M21468; AAA31393.1; -
 DR EMBL; M21465; AAA31393.1; JOINED.
 DR EMBL; M21466; AAA31393.1; JOINED.
 DR EMBL; M21467; AAA31393.1; JOINED.
 DR PIR; A32283; A32283.
 DR HSSP; P13760; 2SEB.
 DR INTERPRO; IPR000353; -
 DR INTERPRO; IPR000495; -

DR INTERPRO; IPR003006; -
 DR PFAM; PF00969; MHC_II_beta; 1.
 DR PFAM; PF00047; ig; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 257
 FT DOMAIN 30 120
 FT DOMAIN 121 214
 FT DOMAIN 215 224
 FT TRANSMEM 225 245
 FT DOMAIN 246 257
 FT DISULFID 45 105
 FT DISULFID 143 199
 FT CARBOHYD 49 49
 SQ SEQUENCE 257 AA; 29090 MW; 60955374F2BD466C CRC64;

Query Match 58.9%; Score 33; DB 1; Length 257;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAG 10
 |||||
 Db 106 RHNYELFQG 114

Search completed: March 28, 2001, 07:35:04
 Job time: 141 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:06 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNYGSFAG 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	76.8	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	40	71.4	83	7 Q9TNX4	Q9tnx4 equus caball
3	39	69.6	446	5 O62086	O62086 caenorhabdi
4	38	67.9	89	7 O19495	O19495 gallus gall
5	38	67.9	618	10 Q9LWD5	Q9lwd5 oryza sativ
6	38	67.9	697	3 O74504	O74504 schizosacch
7	36	64.3	39	7 P79474	P79474 cervus elap
8	36	64.3	39	7 P79477	P79477 cervus elap
9	36	64.3	39	7 P79478	P79478 cervus elap
10	36	64.3	39	7 P79479	P79479 cervus elap
11	36	64.3	74	6 Q9TTM4	Q9ttm4 bos taurus
12	36	64.3	76	7 Q9TPC2	Q9tpc2 macaca mula
13	36	64.3	78	6 O97835	O97835 ovis aries
14	36	64.3	78	6 O97839	O97839 ovis aries
15	36	64.3	78	6 O97844	O97844 ovis aries
16	36	64.3	78	6 O97968	O97968 ovis aries
17	36	64.3	78	7 Q9MWT6	Q9mwt6 leopardus p
18	36	64.3	78	7 Q9MWT5	Q9mwt5 leopardus p
19	36	64.3	78	7 Q9MWT4	Q9mwt4 leopardus p

20	36	64.3	79	7	019191	019191 prionalluru
21	36	64.3	79	7	019192	019192 prionalluru
22	36	64.3	79	7	019380	019380 felis silve
23	36	64.3	79	7	019381	019381 felis silve
24	36	64.3	79	7	019382	019382 felis silve
25	36	64.3	79	7	019396	019396 felis silve
26	36	64.3	79	7	019397	019397 felis silve
27	36	64.3	79	7	019405	019405 felis silve
28	36	64.3	79	7	019406	019406 felis silve
29	36	64.3	79	7	019407	019407 felis silve
30	36	64.3	79	7	019408	019408 felis silve
31	36	64.3	79	7	019435	019435 felis silve
32	36	64.3	79	7	09MX19	09mx19 leopardus p
33	36	64.3	79	7	09MX13	09mx13 leopardus p
34	36	64.3	79	7	09MX03	09mx03 leopardus p
35	36	64.3	79	7	09MX00	09mx00 leopardus p
36	36	64.3	79	7	09MW29	09mw29 leopardus p
37	36	64.3	79	7	09MW28	09mw28 leopardus p
38	36	64.3	79	7	09MW27	09mw27 leopardus p
39	36	64.3	79	7	09MWY9	09mwy9 leopardus p
40	36	64.3	79	7	09MWY8	09mwy8 leopardus p
41	36	64.3	79	7	09MWY6	09mwy6 leopardus p
42	36	64.3	79	7	09MWY5	09mwy5 leopardus p
43	36	64.3	79	7	09MWY4	09mwy4 leopardus p
44	36	64.3	79	7	09MWY3	09mwy3 leopardus p
45	36	64.3	79	7	09MWX6	09mw6 leopardus p

ALIGNMENTS

RESULT 1

Q9LIE5
ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsi
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 76.8%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 6.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

Db 274 SRHNYGSF 281

RESULT 2

Q9TNX4

ID Q9TNX4 PRELIMINARY; PRT; 83 AA.
 AC Q9TNX4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE MHC CLASS II ANTIGEN (FRAGMENT).
 GN EQPR-DRB.
 OS Equus caballus przewalskii (Przewalski's horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9798;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hedrick P.W., Parker K.M., Miller E., Miller P.;
 RT "Major Histocompatibility Complex Variation in the Endangered
 RT Przewalski's Horse";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF084189; AAD52035.1; -
 DR INTERPRO; IPR000353; -
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 83
 SQ SEQUENCE 83 AA; 9573 MW; 54A51538DA54B0B5 CRC64;

 Query Match 71.4%; Score 40; DB 7; Length 83;
 Best Local Similarity 77.8%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 RHNYGSPAG 10
 Db | | | | | | |
 72 RHNYGVEDG 80

 RESULT 3
 O62086 PRELIMINARY; PRT; 446 AA.
 ID O62086;
 AC O62086;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE C31H5.6 PROTEIN.
 GN C31H5.6
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; Z93778; CAB07846.1; -
 DR INTERPRO; IPR000379; -
 DR INTERPRO; IPR002925; -
 DR PFAM; PF01738; DLH; 2
 SQ SEQUENCE, 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 69.6%; Score 39; DB 5; Length 446;
 Best Local Similarity 87.5%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNYGSFA 9
 Db | | | | | | |
 51 RHNYGSHA 58

 RESULT 4
 O19495 PRELIMINARY; PRT; 89 AA.
 ID O19495;
 AC O19495;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15.151-5; TISSUE=BURSA;
 RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
 RL Immunogenetics 47:350-354(1998).
 DR EMBL; U91532; AAC15813.1; -
 DR INTERPRO; IPR000353; -
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

 Query Match 67.9%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 5.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNYGSP 8
 Db | | | | | | |
 75 RHNYGDF 81

 RESULT 5
 Q9LWD5 PRELIMINARY; PRT; 618 AA.
 ID Q9LWD5;
 AC Q9LWD5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE EST C7288(EL328) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: pO483F08";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP002094; BAA96209.1; -
 SQ SEQUENCE 618 AA; 66394 MW; A616FECC0B8966D1 CRC64;

 Query Match 67.9%; Score 38; DB 10; Length 618;
 Best Local Similarity 70.0%; Pred. No. 42;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10

Db 227 ARNYGSFSG 236

|||||

RESULT 6

O74504

ID O74504 PRELIMINARY; PRT; 697 AA.

AC O74504

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE HYPOTHETICAL 77.8 KDA PROTEIN (FRAGMENT).

GN SFCC594.01.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;

OC Schizosaccharomycetaceae; Schizosaccharomyces.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972H-;

RA Rieger M., Lyne M., Rajandream M.A., Barrell B.G.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL031523; CA20660.1; -

KW Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 697 AA; 77841 MW; AC4561DD5E925132 CRC64;

Query Match

Best Local Similarity 67.9%; Score 38; DB 3; Length 697;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAG 10

|||||

Db 155 RHRYWSFAG 163

RESULT 7

P79474

ID P79474 PRELIMINARY; PRT; 39 AA.

AC P79474

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;

OC Cervidae; Cervinae; Cervus.

OX NCBI_TaxID=9860;

RN [1]

RP SEQUENCE FROM N.A.

RA Swarbrick P.A., Crawford A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63077; AAB3777.1; -

KW MHC.

FT NON_TER 1

39

SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match

Best Local Similarity 64.3%; Score 36; DB 7; Length 39;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 25 RHNYGVF 31

RESULT 10

P79479

ID P79479 PRELIMINARY; PRT; 39 AA.

AC P79479

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;

OC Cervidae; Cervinae; Cervus.

OX NCBI_TaxID=9860;

RN [1]

RP SEQUENCE FROM N.A.

RA Swarbrick P.A., Crawford A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63081; AAB37781.1; -

KW MHC.

FT NON_TER 1

39

SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

RESULT 8

P79477

ID P79477 PRELIMINARY; PRT; 39 AA.

AC P79477

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;

OC Cervidae; Cervinae; Cervus.

OX NCBI_TaxID=9860;

RN [1]

RP SEQUENCE FROM N.A.

RA Swarbrick P.A., Crawford A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63080; AAB37780.1; -

KW MHC.

FT NON_TER 1

39

SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match

Best Local Similarity 64.3%; Score 36; DB 7; Length 39;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 25 RHNYGVF 31

RESULT 9

P79478

ID P79478 PRELIMINARY; PRT; 39 AA.

AC P79478

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;

OC Cervidae; Cervinae; Cervus.

OX NCBI_TaxID=9860;

RN [1]

RP SEQUENCE FROM N.A.

RA Swarbrick P.A., Crawford A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63081; AAB37781.1; -

KW MHC.

FT NON_TER 1

39

SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match

Best Local Similarity 64.3%; Score 36; DB 7; Length 39;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 25 RHNYGVF 31

RESULT 10

P79479

ID P79479 PRELIMINARY; PRT; 39 AA.

AC P79479

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;

OC Cervidae; Cervinae; Cervus.

OX NCBI_TaxID=9860;

RN [1]

RP SEQUENCE FROM N.A.

RA Swarbrick P.A., Crawford A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63077; AAB3777.1; -

KW MHC.

FT NON_TER 1

39

SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

```

DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swadlow P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 11
Q9TTM4
ID Q9TTM4 PRELIMINARY; PRT; 74 AA.
AC Q9TTM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MHC(BOLA) CLASS II DR-BETA CHAIN (FRAGMENT).
GN BOLA-DRB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-JAPANESE BLACK;
RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
RT Identification of BOLA-DRB3 exon 2 of Japanese black cattle.
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033388; BAA85470.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 64.3%; Score 36; DB 6; Length 74;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 68 RHNYGVF 74

RESULT 12
Q9TPC2
ID Q9TPC2 PRELIMINARY; PRT; 76 AA.
AC Q9TPC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN MAMU-DRB1.
OS Macaca mulatta (Rhesus macaque).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Sauerbmann U., Khazand M., Nagy M., Peilberg C.;
RT "Mhc-DQ-DRB-haplotype analysis in the rhesus macaque: evidence for a
RT number of different haplotypes displaying a low allelic
RT polymorphism."; 0:0-0(1999).
RL Tissue Antigens 0:0-0(1999).
DR EMBL; AF175315; AAF07040.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 76 76
SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A94D0 CRC64;

Query Match 64.3%; Score 36; DB 7; Length 76;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 67 RHNYGVF 73

RESULT 13
O97835
ID O97835 PRELIMINARY; PRT; 78 AA.
AC O97835;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*W20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9677 MW; 653346CE7D1E1388 CRC64;

Query Match 64.3%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 14
O97839
ID O97839 PRELIMINARY; PRT; 78 AA.
AC O97839;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

```

DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
 RA Aida Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017212; BAA36769.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1
 FT NON_TER 78
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 9430 MW; AF8A0B87E34B6832 CRC64;

Query Match 64.3%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 15
 O97844
 ID O97844 PRELIMINARY; PRT: 78 AA.
 AC O97844;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N8.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
 RA Aida Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017220; BAA36777.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1
 FT NON_TER 78
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 9645 MW; 505346CE7D0860CF CRC64;

Query Match 64.3%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

Search completed: March 28, 2001, 07:53:06
 Job time: 499 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:48 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-78

Perfect score: 56

Sequence: 1 ARHNYGSFAG 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36.*

1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT.*
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20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	19	W76029
2	50	89.3	10	19	W76024
3	50	89.3	10	19	W76025
4	50	89.3	10	19	W76026
5	50	89.3	10	19	W76027
6	50	89.3	10	19	W76028
7	50	89.3	10	19	W76030
8	50	89.3	10	19	W76010
9	50	89.3	117	19	W76001
10	50	89.3	117	19	W76003
11	50	89.3	117	20	Y06381
12	50	89.3	117	20	Y06387
					Humanised LM609 an

13	50	89.3	118	20	Y06384	Humanised LM609 an
14	50	89.3	118	20	Y06385	Humanised LM609 an
15	50	89.3	118	20	Y06386	Humanised LM609 an
16	50	89.3	118	20	Y06383	Humanised LM609 an
17	50	89.3	130	20	Y06379	Murine monoclonal
18	47	83.9	10	19	W76021	LM609 grafted anti
19	46	82.1	10	19	W76039	LM609 grafted anti
20	46	82.1	10	19	W76040	LM609 grafted anti
21	46	82.1	10	19	W76022	LM609 grafted anti
22	46	82.1	10	19	W76023	LM609 grafted anti
23	45	80.4	10	19	W76037	LM609 grafted anti
24	45	80.4	10	19	W76020	LM609 grafted anti
25	42	75.0	110	20	W84099	Vitronectin alpha-
26	42	75.0	117	20	W84093	Murine vitronectin
27	42	75.0	117	20	W84097	Humanised anti-aiP
28	41	73.2	8	20	Y06371	Murine monoclonal
29	41	73.2	10	19	W76038	LM609 grafted anti
30	37	66.1	119	19	Y86109	S. pneumoniae derl
31	36	64.3	117	16	R79157	Human IgE receptor
32	36	64.3	117	16	R79155	Human IgE receptor
33	36	64.3	117	18	W27357	Heavy chain variab
34	36	64.3	117	18	W27526	Heavy chain variab
35	36	64.3	117	18	W27354	Heavy chain variab
36	36	64.3	119	18	W01578	Lead binding Mab 8
37	36	64.3	239	20	W73874	Human antiFc eps11
38	36	64.3	242	20	W73876	Human antiFc eps11
39	34	60.7	30	21	Y81870	Yeast IPPI protein
40	34	60.7	138	21	Y75465	Neisseria meningit
41	34	60.7	138	21	Y75466	Neisseria meningit
42	34	60.7	332	21	Y67216	ORF 15 encoded S-a
43	34	60.7	384	20	Y33263	E. coli S-adenosyl
44	34	60.7	384	20	Y33267	Plasmid pHS1 metK
45	34	60.7	384	20	Y33269	Plasmid pHS1 metK

ALIGNMENTS

RESULT 1

W76029
ID W76029 standard; Protein: 10 AA.

XX W76029;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSV-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49866.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSEAG 10
| | | | | | | | | |
Db 1 arhnygsfag 10

RESULT 2
W76024
ID W76024 standard; Protein; 10 AA.
XX
AC W76024;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49861.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 arhnygsfa 9

RESULT 3
W76025
ID W76025 standard; Protein; 10 AA.
XX
AC W76025;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49862.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db |||||

1 arhnygsfa 9

RESULT 4

ID W76026 standard; Protein; 10 AA.

XX AC W76026;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #8.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db |||||

1 arhnygsfa 9

RESULT 5

ID W76027 standard; Protein; 10 AA.

XX AC W76027;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db |||||

```

Db      1 arhnygsfa 9

RESULT 6
W76028
ID W76028 standard; Protein; 10 AA.
XX
AC W76028;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-0501826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49865.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 arhnygsfa 9

RESULT 7%
W76030
ID W76030 standard; Protein; 10 AA.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

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AC W76030;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49867.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 arhnygsfa 9

RESULT 8
W76010
ID W76010 standard; Protein; 10 AA.
XX
AC W76010;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

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KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO98333919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
DR WPI: 1998-437472/37.
DR N-PSDB; V49847.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Disclosure; Page 40; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 1 arhnygsfa 9

RESULT 9
W76001
ID W76001 standard; Protein; 117 AA.
XX
AC W76001;
XX
XX 02-NOV-1998 (first entry)
XX
XX Vitaxin antibody heavy chain variable region protein fragment.
DE
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO98333919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.

PN WO98333919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
DR WPI: 1998-437472/37.
DR N-PSDB; V49820.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 1; Fig 1a; 129pp; English.
XX
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 117 AA;

Query Match 89.3%; Score 50; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 97 arhnygsfa 105

RESULT 10
W76003
ID W76003 standard; Protein; 117 AA.
XX
AC W76003;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 antibody heavy chain variable region protein fragment.
DE
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO98333919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;
 PI WPI: 1998-437472/37.
 DR N-PSDB; V49822.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 43; Fig 2a; 129pp; English.
 XX
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 89.3%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

RESULT 11
 Y06381
 ID Y06381 standard; Protein; 117 AA.
 AC Y06381;
 XX
 XX 06-SEP-1999 (first entry)
 DT
 DE Murine monoclonal antibody LM609 VH region.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Mus musculus.
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 PS Disclosure; Page 52-53; 55pp; English.
 XX
 CC This sequence represents the heavy chain variable region of murine

CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 117 AA;

Query Match 89.3%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||

RESULT 12
 Y06387
 ID Y06387 standard; Protein; 117 AA.
 AC Y06387;
 XX
 XX 06-SEP-1999 (first entry)
 DT
 DE Humanised LM609 antibody VH domain.
 XX
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..66
 FT /note= "CDR2"
 FT Region 107..117
 FT /note= "CDR3"
 XX
 XX WO9929888-A1.
 PN
 XX 17-JUN-1999.
 PD
 XX 04-DEC-1998; 98WO-US25828.
 PF
 XX 05-DEC-1997; 97US-0986016.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Barbas CF, Rader C;
 PI
 XX WPI; 1999-394979/33.
 DR
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX Disclosure; Page 52; 55pp; English.
 PS
 XX This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin

alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides humanised antibodies, especially humanised LM609. In such humanized antibodies, a light chain CDR from a mouse antibody such as LM609 is grafted onto a human light chain, and a heavy chain CDR from a mouse antibody is grafted onto a human antibody heavy chain to produce libraries from which a humanised murine antibody having the desired specificity is selected. By preserving the original CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the humanisation strategy ensures epitope conservation.

Sequence 117 AA;

Query Match 89.3%; Score 50; DB 20; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 97 arhnygsfa 105

RESULT 13

Y06384

ID Y06384 standard; Protein: 118 AA.

AC Y06384;

DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..2
FT /note= "vector-encoded residues"
FT Region 31..37
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..107
FT /note= "CDR3"

XX W09929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a humanised LM609 antibody. LM609 is directed to human integrin alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it

cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides humanised antibodies, especially humanised LM609. In such humanized antibodies, a light chain CDR from a mouse antibody such as LM609 is grafted onto a human light chain, and a heavy chain CDR from a mouse antibody is grafted onto a human antibody heavy chain to produce libraries from which a humanised murine antibody having the desired specificity is selected. By preserving the original CDR sequences such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the humanisation strategy ensures epitope conservation.

Sequence 118 AA;

Query Match 89.3%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 98 arhnygsfa 106

RESULT 14

Y06385

ID Y06385 standard; Protein: 118 AA.

AC Y06385;

DT 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VH domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..2
FT /note= "vector-encoded residues"
FT Region 31..37
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..107
FT /note= "CDR3"

XX W09929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 51; 55pp; English.

XX This sequence represents the heavy chain variable region of a humanised LM609 antibody. LM609 is directed to human integrin alpha-v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 118 AA;

Query Match 89.3%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | |
Db 98 arhnygsfa 106

RESULT 15
Y06386
ID Y06386 standard; Protein; 118 AA.
XX AC Y06386;
XX DT 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.
XX KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
FT Peptide 1.2
FT Region /note= "vector-encoded residues"
FT Region 31..37
FT Region /note= "CDR1"
FT Region 52..67
FT Region /note= "CDR2"
FT Region 100..107
FT Region /note= "CDR3"
XX WO929888-A1.
XX PN
XX PD 17-JUN-1999.
XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Barbas CF, Rader C;
XX DR WPI; 1999-394979/33.
XX PT Production of humanized mouse monoclonal antibodies
XX PS Disclosure; Page 51-52; 55pp; English.
XX CC This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 118 AA;

Query Match 89.3%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | |
Db 98 arhnygsfa 106

Search completed: March 28, 2001, 06:59:48
Job time: 1384 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:55 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-78

Perfect score: 56

Sequence: 1 ARHNYGSFAG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgnl_7/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgnl_7/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgnl_7/ptodata/1/1aa/6-COMB.pep.*
- 4: /cgnl_7/ptodata/1/1aa/PCTUS-COMB.pep.*
- 5: /cgnl_7/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	64.3	94	3	US-09-147-550-14
2	36	64.3	94	3	US-09-147-550-45
3	36	64.3	94	3	US-09-147-550-48
4	36	64.3	94	3	US-09-147-550-77
5	36	64.3	94	3	US-09-147-550-84
6	36	64.3	94	3	US-09-147-550-90
7	36	64.3	94	3	US-09-147-550-101
8	36	64.3	119	3	US-08-767-128-6
9	34	60.7	286	2	US-08-809-267-3
10	34	60.7	286	4	PCT-US95-13662A-3
11	34	60.7	287	2	US-08-741-437-5
12	34	60.7	287	2	US-09-134-593-5
13	34	60.7	332	3	US-09-320-878-16
14	34	60.7	402	2	US-08-403-852D-19
15	34	60.7	402	3	US-08-510-646B-20
16	34	60.7	694	3	US-08-559-397A-31
17	32	57.1	15	1	US-08-618-464-7
18	32	57.1	15	3	US-09-107-615-7
19	32	57.1	25	2	US-08-480-190-44
20	32	57.1	25	2	US-08-488-379-44
21	32	57.1	25	4	PCT-US93-07545-44
22	32	57.1	36	1	US-08-053-131-84
23	32	57.1	36	1	US-08-645-641-84
24	32	57.1	36	1	US-07-853-408B-84
25	32	57.1	36	2	US-08-096-762-84
26	32	57.1	36	2	US-08-308-865-84
27	32	57.1	36	4	PCT-US92-10983-84
28	32	57.1	80	1	US-08-264-250A-1

29	32	57.1	89	1	US-08-025-038-30	Sequence 30, Appl
30	32	57.1	89	1	US-08-039-137-17	Sequence 17, Appl
31	32	57.1	90	2	US-08-485-133-23	Sequence 23, Appl
32	32	57.1	94	3	US-09-147-550-12	Sequence 12, Appl
33	32	57.1	94	3	US-09-147-550-13	Sequence 13, Appl
34	32	57.1	94	3	US-09-147-550-15	Sequence 15, Appl
35	32	57.1	94	3	US-09-147-550-16	Sequence 16, Appl
36	32	57.1	94	3	US-09-147-550-17	Sequence 17, Appl
37	32	57.1	94	3	US-09-147-550-18	Sequence 18, Appl
38	32	57.1	94	3	US-09-147-550-19	Sequence 19, Appl
39	32	57.1	94	3	US-09-147-550-20	Sequence 20, Appl
40	32	57.1	94	3	US-09-147-550-21	Sequence 21, Appl
41	32	57.1	94	3	US-09-147-550-22	Sequence 22, Appl
42	32	57.1	94	3	US-09-147-550-24	Sequence 24, Appl
43	32	57.1	94	3	US-09-147-550-25	Sequence 25, Appl
44	32	57.1	94	3	US-09-147-550-26	Sequence 26, Appl
45	32	57.1	94	3	US-09-147-550-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

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; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

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Query Match 64.3%; Score 36; DB 3; Length .94;
Best Local Similarity 85.7%; Pred. NO. 14;
Matches 6; Conservative 0; Mismatches 1; Indels

Qy	2	RHNYGSF	8
Db	80	RHNYGVF	86

RESULT 3
US-09-147-550-48
: Sequence 48, Application US/09147550

; Sequence 46; Application 05/0914/350
 ; Patent No. 6090540
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 ; CURRENT APPLICATION NUMBER: US/09/147,550
 ; CURRENT FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: PCT/JP97/02485
 ; EARLIER FILING DATE: 1997-07-17
 ; EARLIER APPLICATION NUMBER: JP 8-190933
 ; EARLIER FILING DATE: 1996-07-19
 ; EARLIER APPLICATION NUMBER: JP 9-77979
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6: Conservative 0: Mismatches 1: Indels

Qy 2 RHYGSF 8
Dy 80 RHYGVF 86

RESULT 4
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No 6090540

/ sequence 777, application 05/09147,550
 / Patent No. 6090540
 / GENERAL INFORMATION:
 / APPLICANT: Aida, Yoko
 / TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 / FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 / CURRENT APPLICATION NUMBER: US/09/147,550
 / CURRENT FILING DATE: 1999-04-23
 / EARLIER APPLICATION NUMBER: PCT/JP97/02485
 / EARLIER FILING DATE: 1997-07-17
 / EARLIER APPLICATION NUMBER: JP 8-190933
 / EARLIER FILING DATE: 1996-07-19
 / EARLIER APPLICATION NUMBER: JP 9-77979
 / EARLIER FILING DATE: 1997-03-28
 / NUMBER OF SEQ ID NOS: 115
 / SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

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Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels

QY	2	RHNYGSF	8
D6	80	RHNYGVF	86

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550

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; sequence 84, Application 05709147/350
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; SS-09-147-550-84

```

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6: Conservative 0; Mismatches 1; Indels

QY	2	RHNYGSF	8
Db	80	RHNYGVF	86

RESULT 6
US-09-147-550-90
: Sequence 90. Application US/09147550

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; Sequence 90, Application US/0914/350
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT

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; ORGANISM: BOVINE
US-09-147-550-90

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 64.3%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 64.3%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHHYGYVA 105

RESULT 9
US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,267

; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 433
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662
; FILING DATE:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-809-267-3

Query Match 60.7%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 10
PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids

; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US95-13662A-3

Query Match 60.7%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 11
US-08-741-437-5
; Sequence 5, Application US/08741437
; Patent No. 5843665
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-08-741-437-5

Query Match 60.7%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 12

US-09-134-593-5
; Sequence 5, Application US/09134593
; Patent No. 5981232
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,593
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-09-134-593-5

Query Match 60.78; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 13
US-09-320-878-16
; Sequence 16, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06

; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-16

Query Match 60.78; Score 34; DB 3; Length 332;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10
Db 203 ARHGGGAFSG 212

RESULT 14
US-08-403-852D-19
; Sequence 19, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852D
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-852D-19

Query Match 60.7%; Score 34; DB 2; Length 402;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ARHNYGSFAG 10
Db 273 ARHGGGAFSG 282

RESULT 15

US-08-510-646B-20
Sequence 20, Application US/08510646B
Patent No. 6077699

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995

CLASSIFICATION:

435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO:

20:

SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-510-646B-20

Query Match 60.7%; Score 34; DB 3; Length 402;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ARHNYGSFAG 10
Db 273 ARHGGGAFSG 282

Search completed: March 28, 2001, 07:01:55
Job time: 1334 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:26 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-80

Perfect score: 54

Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	446	2 T19625	hypothetical prote
2	36	66.7	82	2 I51106	Major Histocompati
3	36	66.7	89	2 S38688	MHC class II histo
4	36	66.7	89	2 S38683	MHC class II histo
5	36	66.7	89	2 S38684	MHC class II histo
6	36	66.7	225	2 I47095	MHC class II OVAR-
7	35	64.8	347	2 S43771	phosphatidylcholin
8	34	63.0	108	2 S26316	Ig heavy chain v r
9	34	63.0	110	2 S26317	Ig heavy chain v r
10	34	63.0	113	2 S26468	Ig heavy chain v r
11	34	63.0	210	1 B9265	conserved hypothet
12	34	63.0	275	2 G75130	translation initiat
13	34	63.0	275	2 D71087	probable translati
14	34	63.0	287	1 PNBV	inorganic pyrophos
15	34	63.0	287	1 PWKL	inorganic pyrophos
16	34	63.0	638	2 T44763	conserved hypothet
17	34	63.0	723	2 F83173	outer membrane pro
18	33	61.1	65	2 S17411	hypothetical prote
19	33	61.1	80	2 I54469	MHC HLA-DR-beta-1
20	33	61.1	80	2 I68777	MHC HLA-DR-beta-1
21	33	61.1	81	2 I54550	HLA DRB1*1202 - hu
22	33	61.1	85	2 I59634	MHC class II DR-be
23	33	61.1	89	2 S38676	MHC class II histo
24	33	61.1	89	2 S38680	MHC class II histo
25	33	61.1	89	2 S7512	MHC class II histo
26	33	61.1	123	2 C25239	MHC class II histo
27	33	61.1	167	2 T16454	hypothetical prote
28	33	61.1	200	2 D32526	class II histocomp
29	33	61.1	220	2 T46055	hypothetical prote

class II histocomp
gene HLA-DRB1 prot
class II histocomp
lymphocyte antigen
hypothetical prote
hypothetical prote
secreted glycoprot
nucleosapsid prote
glutamate--CRNA II
glutamate--tRNA II
gene 50 protein -
aconitate hydratase
DNA-directed RNA p
Ig heavy chain v r
hypothetical prote
MHC class II histo

30 33 61.1 237 2 C27060
31 33 61.1 266 2 I54287
32 33 61.1 266 2 A27618
33 33 61.1 266 2 I54295
34 33 61.1 279 2 T05421
35 33 61.1 360 2 S48566
36 33 61.1 383 2 S56179
37 33 61.1 448 1 A60003
38 33 61.1 470 2 H71667
39 33 61.1 473 2 D70405
40 33 61.1 682 2 S30995
41 33 61.1 789 2 S46631
42 33 61.1 1386 1 RNLCV2
43 32 59.3 9 2 S38850
44 32 59.3 31 2 S00685
45 32 59.3 51 2 D25239

ALIGNMENTS

RESULT 1
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Map position: 1
A:Gene: CESP:C31H5.6
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match 79.6%; Score 43; DB 2; Length 446;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAA 10
|||||
DB 51 RHNYGSFAA 59

RESULT 2
I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 3

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 4

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 5

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 6

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 68 RHNYGVF 74

RESULT 7

S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synechococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misiden
C:Species: Synechococcus sp.
A:Variety: PCC 7002
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189
A:Accession: S43771
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:g488511
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 64.8%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||
Db 334 AEHNYISFA 342

RESULT 8

S26316

Ig heavy chain v region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26316
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26316
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <STA>
 A:CROSS-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PTD:gl334035
 C:Superfamily: Immunoglobulin v region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F;2-85/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 84 ARGNYGNYA 92

RESULT 9
 S26317
 Ig heavy chain v region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:CROSS-references: EMBL:X59186
 C:Superfamily: Immunoglobulin v region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F;4-87/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 110;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 Db 86 ARGNYGNYA 94

RESULT 10
 S26468
 Ig heavy chain v region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26468
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26468
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <KAV>
 A:CROSS-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PTD:g51945
 C:Superfamily: Immunoglobulin v region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 113;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
 Db 93 ARHPYGNYYA 102

RESULT 11
 B69265
 conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: B69265
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 Godek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kalne, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343
 A:Accession: B69265
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-210 <KLE>
 A:CROSS-references: GB:AE000782; NID:g2689421; PIDN:AB91117.1; PID:g265
 C:Superfamily: conserved hypothetical protein AF0119

Query Match 63.0%; Score 34; DB 1; Length 210;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 Db 128 RHAYGSF 134

RESULT 12
 G75130
 translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus aby
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: G75130
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
 A:Reference number: A75001
 A:Accession: G75130
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <KAW>
 A:CROSS-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: aif2a; PAB0568
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.0%; Score 34; DB 2; Length 275;
 Best Local Similarity 83.3%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 Db 23 HNYGAF 28

RESULT 13
 D71087

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:04 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	34	63.0	275	1F2A_PYRAB	Q9V0E4 pyrococcus
2	34	63.0	275	1F2A_PYRHO	O58655 pyrococcus
3	34	63.0	284	1PYR_PICPA	Q13505 pichia past
4	34	63.0	286	1PYR_KLULA	P13998 kluyveromyc
5	34	63.0	286	1PYR_YEAST	P00817 saccharomyc
6	33	61.1	65	1CCSA_PEA	P31172 pisum sativ
7	33	61.1	328	1CCSA_ARATH	P56770 arabidopsis
8	33	61.1	448	1NCAP_CVHOX	P33469 human corin
9	33	61.1	470	1SYE2_RICPR	Q9ZCT8 rickettsia
10	33	61.1	473	1SYE_AQUAE	O67271 aquifex aeo
11	33	61.1	682	1VG50_BPML5	Q05262 mycobacteri
12	33	61.1	789	1ACOX_YEAST	P39533 saccharomyc
13	33	61.1	1386	1RPOD_MARPO	P06274 marchantia
14	32	59.3	65	1CCSA_OENBE	P31565 oenothera b
15	32	59.3	98	1VG7_BPPH2	P13848 bacterioph
16	32	59.3	98	1VG7_BPP2A	P07533 bacterioph
17	32	59.3	196	1WBJJ_ECOLI	P37750 escherichia
18	32	59.3	198	1HB2G_HUMAN	P01911 homo sapien
19	32	59.3	266	1HB2A_HUMAN	P01913 homo sapien
20	32	59.3	266	1HB2B_HUMAN	P01912 homo sapien
21	32	59.3	266	1HB2C_HUMAN	P01914 homo sapien
22	32	59.3	266	1HB2D_CANFA	P18470 canis fami
23	32	59.3	266	1HB2D_HUMAN	P13759 homo sapien
24	32	59.3	266	1HB2E_HUMAN	P04229 homo sapien
25	32	59.3	266	1HB2F_HUMAN	P13758 homo sapien
26	32	59.3	266	1HB2H_HUMAN	P13760 homo sapien
27	32	59.3	266	1HB2I_HUMAN	P20039 homo sapien
28	32	59.3	266	1HB2J_HUMAN	P13761 homo sapien
29	32	59.3	313	1CCSA_TORAC	P12216 nicotiana t
30	32	59.3	321	1CCSA_MAIZE	P46659 zea mays (m
31	32	59.3	321	1CCSA_ORISA	P12215 oryza sativ
32	32	59.3	349	1XYJ9_YEAST	P41903 saccharomyc
33	32	59.3	528	1PRI2_YEAST	P20457 saccharomyc

34	32	59.3	560	1THS1_HALVO	Q30561 halobacteri
35	32	59.3	629	1KSYK_RAT	Q64725 rattus norv
36	32	59.3	649	1GPDH_SCHPO	O14400 schizosacch
37	32	59.3	809	1UBPL_YEAST	P25037 saccharomyc
38	32	59.3	1074	1PLD1_HUMAN	Q13393 homo sapien
39	32	59.3	1075	1PLD1_RAT	P70496 rattus norv
40	32	59.3	1267	1VL3_REOVD	P17378 reovirus (t
41	32	59.3	1267	1VL3_REOVL	P17376 reovirus (t
42	31	57.4	201	1PRCG_HUMAN	P49721 homo sapien
43	31	57.4	201	1PRCG_MOUSE	Q9R1P3 mus musculu
44	31	57.4	201	1PRCG_RAT	P40307 rattus norv
45	31	57.4	330	1PROX_ECOLI	P14177 escherichia

ALIGNMENTS

RESULT 1
IF2A_PYRAB
ID IF2A_PYRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ORSAY;
RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome structure and evolution."
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.

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CC EMBL; AJ248285; CAB49760.1; -
CC INTERPRO; IPR003029; -
CC PFAM; PF00575; SI; 1.
CC Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 23 HNYGAF 28

RESULT 2
IF2A_PYRHO
ID IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)

```
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PH0961.
OS Pyrococcus horikoshii.
CC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3.
RX MEDLINE; 98344137.
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -1- SIMILARITY: CONTAINS 1 'SL MOTIF' DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF000004; BAA30058.1; -
DR INTERPRO; IPR003029; -
DR PFAM; PF00575; SL; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83
FT SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;
SQ
Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HNYGSF 8
DB 23 HNYGAF 28
|||||
-----
RESULT 3
IPYR_PICPA
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC 013505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE; 99034033.
RA Coshno I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
-----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF000004; BAA30058.1; -
DR INTERPRO; IPR003029; -
DR PFAM; PF00575; SL; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83
FT SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;
SQ
Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HNYGSF 8
DB 23 HNYGAF 28
|||||
-----
RESULT 3
IPYR_PICPA
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC 013505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE; 99034033.
RA Coshno I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
-----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001000; CAA04453.1; -
DR HSPG; P00817; IWGI.
DR INTERPRO; IPR001596; -
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolyase; Magnesium.
FT INIT_MET 0 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
FT SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;
SQ
Query Match 63.0%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HNYGSF 8
DB 91 HNYGAF 96
|||||
-----
RESULT 4
IPYR_KLULA
ID IPYR_KLULA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1 OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E. COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ001000; CAA04453.1; -
DR HSPG; P00817; IWGI.
DR INTERPRO; IPR001596; -
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolyase; Magnesium.
FT INIT_MET 0 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
FT SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;
SQ
Query Match 63.0%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HNYGSF 8
DB 91 HNYGAF 96
|||||
-----
RESULT 4
IPYR_KLULA
ID IPYR_KLULA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1 OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E. COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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 CC -----
 DR EMBL: X14230; CAA32446.1; -;
 DR PIR: S07894; PWVKL.
 DR HSSP: P00817; IWGI.
 DR INTERPRO: IPR001596; -;
 DR PFAM: PF00719; Pyrophosphatase; 1.
 DR PROSITE: PS00387; PPASE; 1.
 DR Hydrolase: Magnesium.
 KW INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

 Query Match 63.0%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 3 HNYGSP 8
 Db 91 HNYGAF 96

 RESULT 5
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE: 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE.
 RX MEDLINE: 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN=S288C;
 RX MEDLINE: 95203288.
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.K., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database."
 RL Electrophoresis 15:1466-1486(1994).
 [5]

RP SEQUENCE OF 239-249.
 RC STRAIN=ATCC 38531 / Y41;
 RX MEDLINE: 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT *Saccharomyces cerevisiae*."
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 [6]
 RP ACTIVE SITE.
 RX MEDLINE: 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase."
 RL Biochemistry 19:94-102(1980).
 [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution."
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE: 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis."
 RL Structure 4:1491-1508(1996).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE: 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of *Saccharomyces cerevisiae*
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications."
 RL J. Mol. Biol. 284:1565-1580(1998).
 [11]
 RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
 RX MEDLINE: 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*
 RT inorganic pyrophosphatases."
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -|- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -|- SUBUNIT: HOMODIMER.
 CC -|- CELLULAR LOCATION: CYTOPLASMIC.
 CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X13253; CAA31629.1; -;
 DR EMBL: Z35880; CAA84949.1; -;
 DR PIR: S45864; PWBY.
 DR PDB: 1PYP; 15-OCT-91.
 DR PDB: 1YPP; 07-DEC-96.
 DR PDB: 1WGI; 19-NOV-97.
 DR PDB: 1WJ; 19-NOV-97.
 DR PDB: 1HUJ; 08-APR-98.


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DR PDB; 1HUK; 08-APR-98.
DR PDB; 117E; 23-DEC-98.
DR PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -.
DR SGD; S0000215; IPPI.
DR INTERPRO; IPR001596; -.
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT. INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 53 53
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT TURN 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT STRAND 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60CB82 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96
|||||

RESULT 6
CCSA_PEA
ID CCSA_PEA STANDARD; PRT; 65 AA.
AC F31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.

Pisum sativum (Garden pea).
Chloroplast.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE; 9135950;
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
in pea chloroplasts.";
RL Plant Mol. Biol. 17:541-545(1991).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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-----
DR EMBL; X59015; CAA41754.1; -.
DR PIR; S17441; S17441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 61.1%; Score 33; DB 1; Length 65;
Best Local Similarity 62.5%; Pred. No. 4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAA 10
Db 57 HSYGSFTS 64
|||||

RESULT 7
CCSA_ARATH
ID CCSA_ARATH STANDARD; PRT; 328 AA.
AC P56770;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC EMBL: AP000423; BAA84436.1; -.
DR INTERPRO: IPR002541; -.
DR PFAM: PF01578; CytC_asm.1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 61.1%; Score 33; DB 1; Length 328;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAA 10
Db 1:|||||
320 HSYGSFTS 327

RESULT 8
NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR: A60003; A60003.
DR INTERPRO: IPR001218; -.
DR PFAM: PF00937; Corona_nucleocs.1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db |||||
103 RHNRGSF 109

RESULT 9
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
-----
RT mitochondria.";
RL Nature 396:133-140(1998).
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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-----
CC EMBL: AJ235272; CAA15066.1; -.
DR HSP: P27000; IGLN.
DR INTERPRO: IPR000924; -.
DR INTERPRO: IPR001412; -.
DR PFAM: PF00749; tRNA-synt_1c; 1.
DR PRINTS: PR00987; TRNASYNTHGLU.
DR PROSITE: PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 61.1%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db |||||
31 ARHNGKF 38

RESULT 10
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O6271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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CC -----
CC EMBL: AE000729; AAC07230.1; -
CC INTERPRO: IPR000924; -
CC INTERPRO: IPR001412; -
CC PFAM: PF00749; tRNA-synt_lc; 1.
CC PRINTS: PR00987; TRNASYNTHGLU.
CC PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminocacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "KWSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 61.1%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
DB 31 ARHNGGPF 38

RESULT 11
VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
DE {EC 1.17.4.2} (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RX MEDLINE: 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5: a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -1- CATALYTIC ACTIVITY: 2-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
CC OXIDIZED THIOREDOXIN + H(2)O -> RIBONUCLEOSIDE TRIPHOSPHATE +
CC REDUCED THIOREDOXIN.
CC -----
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CC -----
CC EMBL: Z18946; CAA79426.1; -
CC PIR: S30995; S30995.
CC INTERPRO: IPR000788; -
CC PFAM: PF00317; ribonucleo_red; 1.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

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Query Match 61.1%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
DB 31 ARHNGGSGFA 319

RESULT 12

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ACOX_YEAST STANDARD; PRT; 789 AA.
ID ACOX_YEAST
AC P39533;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE ACONITASE IN PRP21-UBP12 INTERGENIC REGION (EC 4.2.1.3).
GN YJL200C OR J0327.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE: 95274326.
RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
X identifies 24 open reading frames including NUC1, PRP21 (SP91),
CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1
and two homologues to chromosome III genes.";
RL Yeast 10:1235-1249(1994).
CC -1- CATALYTIC ACTIVITY: CITRATE -> CIS-ACONITATE + H(2)O.
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC -----
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CC -----
CC EMBL: X77688; CAA54757.1; -
CC EMBL: Z49475; CAA89495.1; -
CC PIR: S46631; S46631.
CC HSSP: P16276; 6ACN.
CC SGD: S0003736; YJL200C.
CC INTERPRO: IPR000573; -
CC INTERPRO: IPR001030; -
CC PFAM: PF00694; Aconitase_C; 1.
CC PFAM: PF00330; aconitase; 1.
CC PRINTS: PR00415; ACONITASE.
CC PROSITE: PS00450; ACONITASE_1; 1.
CC PROSITE: PS01244; ACONITASE_2; 1.
KW Hypothetical protein; Lyase, Tricarboxylic acid cycle; Iron-sulfur;
KW 4Fe-4S.
FT METAL 385 385 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 448 448 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 451 451 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 789 AA; 86583 MW; FABA4FE482D3F993 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 789;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
DB 663 AEHNYGEGSA 672

RESULT 13
RPOD_MARPO STANDARD; PRT; 1386 AA.
ID RPOD_MARPO
AC P06274;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE BETA" CHAIN (EC 2.7.7.6).
GN RPOC2.
OS Marchantia polymorpha (Liverwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Marchantiophyta; Marchantiales;

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RC MarChantiaceae; Marchantia.
RP [1]
RA SEQUENCE FROM N.A.
RL Ohyama K.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
[2]
RP COMPLETE GENOME.
RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
RA Umesono K., Shikl Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
RA Ozeki H.;
RT "Chloroplast gene organization deduced from complete sequence of
RT liverwort Marchantia polymorpha chloroplast DNA.";
RL Nature 322:572-574(1986)
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC RNA(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -----
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CC -----
DR EMBL; X04465; CAA28063.1; -.
DR PIR; A00698; RNIVC2.
DR PIR; S01575; S01575.
DR MENDEL; 4115; MARPO:rpoc2.1.
DR INTERPRO: IPR007022; -.
DR PFAM; PF00623; RNA_pol_A; 1.
DR Transference; Transcription; DNA-directed RNA polymerase; Chloroplast.
KW SEQUENCE 1386 AA; 160155 MW; 18BE458FC1A5C3F9 CRC64;
SQ
Query Match 61.1%; Score 33; DB 1; Length 1386;
Best Local Similarity 75.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 HNYGSFAA 10
DB 86 HNYGSLHA 93
RESULT 14
ID CCSA_OENBE STANDARD; PRT; 65 AA.
AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Oenothera bertiana (Bertero's evening primrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Myrtales; Onagraceae; Oenothera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93169690.
RA Nimzyk R., Schoendorf T., Hachtel W.;
RT "In-frame length mutations associated with short tandem repeats are
RT located in unassigned open reading frames of Oenothera chloroplast
RT DNA.";
RL Curr. Genet. 23:265-270(1993).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.

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CC -----
DR EMBL; X64617; CAA45900.1; -.
DR EMBL; X64614; CAA45894.1; -.
DR PIR; S19981; S19981.
DR PIR; S19988; S19988.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7441 MW; 343E66DDA1492C0C CRC64;
Query Match 59.3%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 6.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HNYGSF 8
DB 57 HSYGSF 62
RESULT 15
ID VG7_BPPH2 STANDARD; PRT; 98 AA.
AC P13848;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN 7.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87106857.
RA Vicek C., Paces V.;
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
RT completes the 19,285-bp sequence of phi 29 genome. Comparison with
RT the homologous sequence of phage PZA.";
RL Gene 46:215-225(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87016351.
RA Innis C.A., Garvey K.J., Ito J.;
RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
RT spacer between the major early and late genes.";
RL Nucleic Acids Res. 14:7129-7129(1986).
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CC -----
DR EMBL; M14782; AAA32279.1; -.
DR EMBL; X04386; CAA27974.1; -.
DR PIR; A28923; WMBPF9.
KW Late protein.
SQ SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;
Query Match 59.3%; Score 32; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 9.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 2 RHNYGSFAA 10
| | | | | :
Db 33 RVNYGSFVS 41

Search completed: March 28, 2001, 07:35:05
Job time: 142 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:06 ; Search time 443.95 Seconds
(Without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGFPA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	79.6	446	5 O62086	O62086 caenorhabdi
2	43	79.6	839	10 Q9LIE5	Q9LIE5 arabidopsis
3	38	70.4	89	7 O19495	O19495 gallus gall
4	36	66.7	39	7 P79474	P79474 cervus elap
5	36	66.7	39	7 P79477	P79477 cervus elap
6	36	66.7	39	7 P79478	P79478 cervus elap
7	36	66.7	39	7 P79479	P79479 cervus elap
8	36	66.7	74	6 Q9TWT4	Q9TWT4 bos taurus
9	36	66.7	76	7 Q9TWC2	Q9TWC2 macaca mula
10	36	66.7	78	6 Q97835	Q97835 ovis aries
11	36	66.7	78	6 Q97839	Q97839 ovis aries
12	36	66.7	78	6 Q97844	Q97844 ovis aries
13	36	66.7	78	6 Q97968	Q97968 ovis aries
14	36	66.7	78	7 Q9MWT6	Q9MWT6 leopardus p
15	36	66.7	78	7 Q9MWT5	Q9MWT5 leopardus p
16	36	66.7	78	7 Q9MWT4	Q9MWT4 leopardus p
17	36	66.7	79	7 Q91911	Q91911 prionalluru
18	36	66.7	79	7 Q91912	Q91912 prionalluru
19	36	66.7	79	7 Q91980	Q91980 felis silve

20	36	66.7	79	7	O19381	O19381 felis silve
21	36	66.7	79	7	O19382	O19382 felis silve
22	36	66.7	79	7	O19396	O19396 felis silve
23	36	66.7	79	7	O19397	O19397 felis silve
24	36	66.7	79	7	O19405	O19405 felis silve
25	36	66.7	79	7	O19406	O19406 felis silve
26	36	66.7	79	7	O19407	O19407 felis silve
27	36	66.7	79	7	O19408	O19408 felis silve
28	36	66.7	79	7	O19435	O19435 felis silve
29	36	66.7	79	7	Q9MX19	Q9MX19 leopardus p
30	36	66.7	79	7	Q9MX13	Q9MX13 leopardus p
31	36	66.7	79	7	Q9MX03	Q9MX03 leopardus p
32	36	66.7	79	7	Q9MX00	Q9MX00 leopardus p
33	36	66.7	79	7	Q9MWZ9	Q9MWZ9 leopardus p
34	36	66.7	79	7	Q9MWZ8	Q9MWZ8 leopardus p
35	36	66.7	79	7	Q9MWZ7	Q9MWZ7 leopardus p
36	36	66.7	79	7	Q9MWY9	Q9MWY9 leopardus p
37	36	66.7	79	7	Q9MWY8	Q9MWY8 leopardus p
38	36	66.7	79	7	Q9MWY6	Q9MWY6 leopardus p
39	36	66.7	79	7	Q9MWY5	Q9MWY5 leopardus p
40	36	66.7	79	7	Q9MWY4	Q9MWY4 leopardus p
41	36	66.7	79	7	Q9MWY3	Q9MWY3 leopardus p
42	36	66.7	79	7	Q9MWX6	Q9MWX6 leopardus p
43	36	66.7	79	7	Q9MWX5	Q9MWX5 leopardus p
44	36	66.7	79	7	Q9MWX4	Q9MWX4 leopardus p
45	36	66.7	79	7	Q9MWX1	Q9MWX1 leopardus p

ALIGNMENTS

RESULT 1
O62086 ID O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C31H5.6 PROTEIN.
GN C31H5.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
Craighton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans *;
RL Nature 368:32-38(1994).
DR EMBL; Z93778; CAB07846.1; -.
DR INTERPRO; IPR000379; -.
DR INTERPRO; IPR002925; -.
DR PFAM; PF01738; DLH; 2.
SQ SEQUENCE 446 AA; 50763 MW; 82AD969CDAD753DE CRC64;

Query Match 79.6%; Score 43; DB 5; Length 446;
Best Local Similarity 88.9%; Pred. No. 2;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAA 10
 Db 51 RHNYGSHAA 59
 RESULT 2
 ID Q9LIE5 PRELIMINARY; PRT; 839 AA.
 AC Q9LIE5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
 DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones";
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AF001306; BAB03065.1; -;
 SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 79.6%; Score 43; DB 10; Length 839;
 Best Local Similarity 87.3%; Pred. No. 3.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 274 SRHNYGSF 281
 RESULT 3
 ID O19495 PRELIMINARY; PRT; 89 AA.
 AC O19495;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15.151-5; TISSUE=BURSA;
 RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
 RL Immunogenetics 47:350-354(1998).
 DR EMBL; U91532; AAC15813.1; -;
 DR INTERPRO: IPR000353; -;
 DR PFAM: PF00969; MHC_II_beta; 1.
 KW MH.
 FT NON_TER 1 1
 FT NON_TER 89 89
 SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 70.4%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 3.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 75 RHNYGDF 81
 RESULT 4
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733DID CRC64;

Query Match 66.7%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 25 RHNYGVF 31
 RESULT 5
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3CID CRC64;

Query Match 66.7%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db	25	RHNYGVF	31		
RESULT	6				
P79478					
ID	P79478	PRELIMINARY;	PRT;	39	AA.
AC	P79478;				
DT	01-MAY-1997	(TEMBLrel. 03, Created)			
DT	01-MAY-1997	(TEMBLrel. 03, Last sequence update)			
DT	01-AUG-1998	(TEMBLrel. 07, Last annotation update)			
DE	MHC CLASS II DRB (FRAGMENT).				
OS	Cervus elaphus (Red deer).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;				
OC	Cervidae; Cervinae; Cervus.				
OX	NCBI_TaxID=9860;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Swarbrick P.A., Crawford A.M.;				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; U63081; AAB37781.1; -				
KW	MHC.				
FT	NON_TER	1	1		
FT	NON_TER	39	39		
SQ	SEQUENCE	39	AA; 4806	MM; C2188A16752A3C1D	CRC64;
Query Match	66.7%;	Score 36;	DB 7;	Length 39;	
Best Local Similarity	85.7%;	Pred. No. 3.5;			
Matches	6;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Qy	2	RHNYGSF	8		
Db	25	RHNYGVF	31		
RESULT	7				
P79479					
ID	P79479	PRELIMINARY;	PRT;	39	AA.
AC	P79479;				
DT	01-MAY-1997	(TEMBLrel. 03, Created)			
DT	01-MAY-1997	(TEMBLrel. 03, Last sequence update)			
DT	01-AUG-1998	(TEMBLrel. 07, Last annotation update)			
DE	MHC CLASS II DRB (FRAGMENT).				
OS	Cervus elaphus (Red deer).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;				
OC	Cervidae; Cervinae; Cervus.				
OX	NCBI_TaxID=9860;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Swarbrick P.A., Crawford A.M.;				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; U63082; AAB37782.1; -				
KW	MHC.				
FT	NON_TER	1	1		
FT	NON_TER	39	39		
SQ	SEQUENCE	39	AA; 4806	MM; C2188A16752A3C1D	CRC64;
Query Match	66.7%;	Score 36;	DB 7;	Length 39;	
Best Local Similarity	85.7%;	Pred. No. 3.5;			
Matches	6;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Qy	2	RHNYGSF	8		
Db	25	RHNYGVF	31		
RESULT	8				
Q9TTM4					
ID	Q9TTM4	PRELIMINARY;	PRT;	74	AA.


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RESULT 10
O97835 ID O97835 PRELIMINARY; PRT; 78 AA.
AC O97835;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9677 MW; 653346CE7D1E1388 CRC64;

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Query Match 66.7%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

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RESULT 11
O97839 ID O97839 PRELIMINARY; PRT; 78 AA.
AC O97839;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED AND CORRIDAILE BREED; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017212; BAA36769.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9430 MW; AF8A0B87E34B6832 CRC64;

```

```

Query Match 66.7%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

```

```

RESULT 12
O97844 ID O97844 PRELIMINARY; PRT; 78 AA.
AC O97844;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017220; BAA36777.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9645 MW; 505346CE7D0860CF CRC64;

```

```

Query Match 66.7%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

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```

RESULT 13
O97968 ID O97968 PRELIMINARY; PRT; 78 AA.
AC O97968;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N21.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Aida Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017231; BAA36788.1; -
DR EMBL; AB017204; BAA36761.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9436 MW; 72907E039EC167B2 CRC64;

```

```

Query Match 66.7%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

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Search completed: March 28, 2001, 07:53:07
Job time: 500 sec

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Db      72 RHNYGVF 78

RESULT 14
Q9MWT6
ID      Q9MWT6      PRELIMINARY;      PRT;      78 AA.
AC
DT      01-OCT-2000 (TReMBLrel. 15, Created)
DT      01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT      01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE      MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
GN      LEPA-DRB.
OS      Leopardus pardalis (ocelot).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX      NCBI_TaxID=32538;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT      "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT      Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT      pardalis) and Margay (Leopardus wiedii).";
RL      Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RD      EMBL; AF057894; AAF70946.1; -.
KW      MHC.
FT      NON_TER      1      1
FT      NON_TER      78      78
SQ      SEQUENCE      78 AA; 9559 MW; 77863043708EC5B8 CRC64;

Query Match      66.7%; Score 36; DB 7; Length 78;
Best Local Similarity 85.7%; Pred. NO. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 RHNYGSF 8
Db      71 RHNYGVF 77

RESULT 15
Q9MWT5
ID      Q9MWT5      PRELIMINARY;      PRT;      78 AA.
AC
DT      01-OCT-2000 (TReMBLrel. 15, Created)
DT      01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT      01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE      MHC CLASS II DR ANTIGEN BETA SUBUNIT (FRAGMENT).
GN      LEPA-DRB.
OS      Leopardus pardalis (ocelot).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.
OX      NCBI_TaxID=32538;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yuhki N., Elzirik E., Johnson W.E., O'Brien S.J.;
RT      "Sequence Diversity of Major Histocompatibility Complex Class II DRB
RT      Exon 2 Region of Two Sister Species of the Felidae, Ocelot (Leopardus
RT      pardalis) and Margay (Leopardus wiedii).";
RL      Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RD      EMBL; AF057895; AAF70947.1; -.
KW      MHC.
FT      NON_TER      1      1
FT      NON_TER      78      78
SQ      SEQUENCE      78 AA; 9559 MW; 5076280FF45EC5A7 CRC64;

Query Match      66.7%; Score 36; DB 7; Length 78;
Best Local Similarity 85.7%; Pred. NO. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 RHNYGSF 8
Db      71 RHNYGVF 77

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:48 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-80

Perfect score: 54

Sequence: 1 ARHNYGSPAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	19	W76030
2	51	94.4	10	19	W76024
3	50	92.6	10	19	W76025
4	50	92.6	10	19	W76026
5	50	92.6	10	19	W76027
6	50	92.6	10	19	W76028
7	50	92.6	10	19	W76029
8	50	92.6	10	19	W76010
9	50	92.6	117	19	W76001
10	50	92.6	117	19	W76003
11	50	92.6	117	20	Y06381
12	50	92.6	117	20	Y06387

13	50	92.6	118	20	Y06384
14	50	92.6	118	20	Y06385
15	50	92.6	118	20	Y06386
16	50	92.6	118	20	Y06383
17	50	92.6	130	20	Y06379
18	47	87.0	10	19	W76021
19	46	85.2	10	19	W76037
20	46	85.2	10	19	W76039
21	46	85.2	10	19	W76040
22	46	85.2	10	19	W76022
23	46	85.2	10	19	W76023
24	45	83.3	10	19	W76020
25	42	77.8	110	20	W84099
26	42	77.8	117	20	W84093
27	42	77.8	117	20	W84097
28	41	75.9	8	20	W06371
29	41	75.9	10	19	W76038
30	37	68.5	119	19	Y86109
31	36	66.7	117	16	R79157
32	36	66.7	117	16	R79155
33	36	66.7	117	18	W27357
34	36	66.7	117	18	W27526
35	36	66.7	117	18	W27354
36	36	66.7	119	18	W01578
37	36	66.7	239	20	W73874
38	36	66.7	242	20	W73876
39	34	63.0	30	21	Y81870
40	34	63.0	574	21	Y74960
41	33	61.1	80	12	R13396
42	33	61.1	80	12	R13397
43	33	61.1	89	17	Y14338
44	33	61.1	89	17	Y14306
45	33	61.1	89	17	Y14307

ALIGNMENTS

RESULT 1

W76030
ID W76030 standard; Protein; 10 AA.
XX
AC W76030;
XX
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-H region; CDR; complementarity determining region.
XX
OS Mus sp.
XX
PN W09833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49867.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
| | | | | | | | | |
Db 1 arhnygsfaa 10

RESULT 2
W76024
ID W76024 standard; Protein; 10 AA.
XX
AC W76024;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
DR N-PSDB; V49861.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
SQ Sequence 10 AA;

Query Match 94.4%; Score 51; DB 19; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0044;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
| | | | | | | | | |
Db 1 arhnygsfas 10

RESULT 3
W76025
ID W76025 standard; Protein; 10 AA.
XX
AC W76025;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
DR N-PSDB; V49862.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 41; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

RESULT 4

ID W76026 standard; Protein; 10 AA.

XX AC W76026;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #8.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||

RESULT 5

ID W76027 standard; Protein; 10 AA.

XX AC W76027;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS
 XX Mus sp.
 XX
 XX WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX N-PSDB; V49847.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 XX LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 XX
 XX Disclosure: Page 40; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 XX vitaxin bind selectively to integrin alphavbeta3 and can be used to
 XX inhibit binding of alphavbeta3 to a ligand and thus block
 XX integrin-mediated signal transduction. This is useful in the treatment,
 XX prevention and diagnosis of alphavbeta3-mediated disease, specifically
 XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 XX arthritis, macular degeneration, osteoporosis etc.). The antibodies
 XX contain non-murine framework regions so are suitable for use in humans.
 XX Enhanced types of LM609 have affinity more than 90 times greater than
 XX that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 92.6%; Score 50; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db 1 arhnygsfa 9
 |||||
 RESULT 9
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 XX W76001;
 AC
 XX 02-NOV-1998 (first entry)
 DT
 XX Vitaxin antibody heavy chain variable region protein fragment.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 XX Mus sp.
 OS
 XX

PN WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX N-PSDB; V49820.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 XX LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 XX
 XX Claim 1; Fig 1a; 129pp; English.
 XX
 XX This sequence represents a fragment of the vitaxin antibody variable
 XX heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 XX integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 XX to a ligand and thus block integrin-mediated signal transduction. This is
 XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 XX disease, specifically angiogenesis and restenosis (but also e.g.
 XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 XX osteoporosis etc.). The antibodies contain non-murine framework regions
 XX so are suitable for use in humans. Enhanced types of LM609 have affinity
 XX more than 90 times greater than that of parent the parent antibody.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 92.6%; Score 50; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db 97 arhnygsfa 105
 |||||
 RESULT 10
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX
 XX W76003;
 AC
 XX 02-NOV-1998 (first entry)
 DT
 XX LM609 antibody heavy chain variable region protein fragment.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 XX Mus sp.
 OS
 XX WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.

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XX  Glaser SM, Huse WD;
XX  WPI; 1998-437472/37.
DR  N-PSDB; V49822.
XX
XX  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT  integrin - and related grafted antibodies based on murine monoclonal
PT  LM609, also related nucleic acid, used to treat, prevent or diagnose
PT  angiogenesis or restenosis
XX
XX  Claim 43; Fig 2a; 129pp; English.
XX
XX  This sequence represents the LM609 antibody variable heavy chain region.
CC  LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC  and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC  block integrin-mediated signal transduction. This is useful in the
CC  treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC  specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC  etc.). The antibodies contain non-murine framework regions so are
CC  suitable for use in humans. Enhanced types of LM609 have affinity more
CC  than 90 times greater than that of parent the parent antibody.
XX
XX  Sequence 117 AA;
XX
XX  Query Match 92.6%; Score 50; DB 19; Length 117;
XX  Best Local Similarity 100.0%; Pred. No. 0.083;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 ARHNYGSFA 9
XX  |||||
XX  Db 97 arhnygsfa 105
XX
XX  RESULT 11
XX  Y06381
XX  ID Y06381 standard; Protein; 117 AA.
XX  AC Y06381;
XX  DT 06-SEP-1999 (first entry)
XX  DE Murine monoclonal antibody LM609 VH region.
XX
XX  KW Humanised antibody; antibody humanisation; antibody engineering;
XX  LM609; monoclonal antibody; complementarity determining region;
XX  CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX  cancer; therapy; diagnosis.
XX
XX  OS Mus musculus.
XX  OS WO929888-A1.
XX  PN 17-JUN-1999.
XX  PD
XX  PF 04-DEC-1998; 98WO-US25828.
XX  PR 05-DEC-1997; 97US-0986016.
XX  PA (SCRI ) SCRIPPS RES INST.
XX  PI - Barbas CF, Rader C;
XX  DR WPI; 1999-394979/33.
XX
XX  Production of humanized mouse monoclonal antibodies
PT
XX  PS Disclosure; Page 52-53; 55pp; English.
XX  CC This sequence represents the heavy chain variable region of murine

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CC  monoclonal antibody LM609. LM609 is directed to integrin
CC  alpha-v beta-3. It selectively promotes apoptosis of vascular
CC  cells that have been stimulated to undergo angiogenesis, making it
CC  a tool for cancer diagnosis and therapy. The invention provides
CC  humanised antibodies, especially humanised LM609. In such humanized
CC  antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC  grafted onto a human light chain, and a heavy chain CDR from a mouse
CC  antibody is grafted onto a human antibody heavy chain to produce
CC  libraries from which a humanised murine antibody having the desired
CC  specificity is selected. By preserving the original CDR sequences
CC  such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC  humanisation strategy ensures epitope conservation.
XX
XX  Sequence 117 AA;
XX
XX  Query Match 92.6%; Score 50; DB 20; Length 117;
XX  Best Local Similarity 100.0%; Pred. No. 0.083;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 ARHNYGSFA 9
XX  |||||
XX  Db 97 arhnygsfa 105
XX
XX  RESULT 12
XX  Y06387
XX  ID Y06387 standard; Protein; 117 AA.
XX  AC Y06387;
XX  DT 06-SEP-1999 (first entry)
XX  DE Humanised LM609 antibody VH domain.
XX
XX  KW Humanised antibody; antibody humanisation; antibody engineering;
XX  LM609; monoclonal antibody; complementarity determining region;
XX  CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX  cancer; therapy; diagnosis.
XX
XX  OS Homo sapiens.
XX  OS Synthetic.
XX
XX  FH Key Location/Qualifiers
XX  FT Peptide 1..2
XX  FT /note= "vector-encoded residues"
XX  FT Region 31..35
XX  FT /note= "CDR1"
XX  FT Region 50..66
XX  FT /note= "CDR2"
XX  FT Region 107..117
XX  FT /note= "CDR3"
XX
XX  PN WO929888-A1.
XX  PN 17-JUN-1999.
XX  PD
XX  PF 04-DEC-1998; 98WO-US25828.
XX  PR 05-DEC-1997; 97US-0986016.
XX  PA (SCRI ) SCRIPPS RES INST.
XX  PI Barbas CF, Rader C;
XX  DR WPI; 1999-394979/33.
XX
XX  Production of humanized mouse monoclonal antibodies
PT
XX  PS Disclosure; Page 52; 55pp; English.
XX  CC This sequence represents the heavy chain variable region of a
XX  humanised LM609 antibody. LM609 is directed to human integrin

```


CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX
 XX
 SQ Sequence 117 AA;

Query Match 92.6%; Score 50; DB 20; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 | | | | | | | | | |
 Db 97 arhnygsfa 105

RESULT 13
 Y06384
 ID Y06384 standard; Protein; 118 AA.
 XX
 AC Y06384;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 DE
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 51; 55pp; English.
 XX
 CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX
 XX
 SQ Sequence 118 AA;

Query Match 92.6%; Score 50; DB 20; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.084;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 | | | | | | | | | |
 Db 98 arhnygsfa 106

RESULT 14
 Y06385
 ID Y06385 standard; Protein; 118 AA.
 XX
 AC Y06385;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Humanised LM609 antibody VH domain.
 DE
 KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 31..37
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..107
 FT /note= "CDR3"
 XX
 PN WO9929888-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 PT Production of humanized mouse monoclonal antibodies
 XX
 PS Disclosure; Page 51; 55pp; English.
 XX
 CC This sequence represents the heavy chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;

Query Match 92.6%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ARHNYGSFA 9
Db 98 arhnygsfa 106
|||||

RESULT 15
Y06386
ID Y06386 standard; Protein: 118 AA.
XX
AC Y06386;
XX
DT 06-SEP-1999 (first entry)
XX
DE Humanised LM609 antibody VH domain.
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
OS Synthetic.
XX

Key Location/Qualifiers
FH Peptide 1..2
FT /note= "vector-encoded residues"
FT Region 31..37
FT /note= "CDR1"
FT Region 52..67
FT /note= "CDR2"
FT Region 100..107
FT /note= "CDR3"
XX
PN WO9929888-A1.
XX
PD 17-JUN-1999.
XX
PF 04-DEC-1998; 98WO-US25828.
XX
PR 05-DEC-1997; 97US-0986016.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 1999-394979/33.
XX
PT Production of humanized mouse monoclonal antibodies
XX
PS Disclosure; Page 51-52; 55pp; English.
XX

This sequence represents the heavy chain variable region of a
CC humanised LM609 antibody. LM609 is directed to human integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
SQ Sequence 118 AA;

Query Match 92.6%; Score 50; DB 20; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 98 arhnygsfa 106
|||||

Search completed: March 28, 2001, 06:59:48
Job time: 1384 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:55 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	66.7	94	3	US-09-147-550-14
2	36	66.7	94	3	US-09-147-550-45
3	36	66.7	94	3	US-09-147-550-48
4	36	66.7	94	3	US-09-147-550-77
5	36	66.7	94	3	US-09-147-550-84
6	36	66.7	94	3	US-09-147-550-90
7	36	66.7	94	3	US-09-147-550-101
8	36	66.7	119	3	US-08-767-128-6
9	34	63.0	286	2	US-08-809-267-3
10	34	63.0	286	4	PCT-US95-13662A-3
11	34	63.0	287	2	US-08-741-437-5
12	34	63.0	287	2	US-09-134-593-5
13	32	59.3	15	1	US-08-618-464-7
14	32	59.3	15	3	US-09-107-615-7
15	32	59.3	25	2	US-08-480-190-44
16	32	59.3	25	2	US-08-488-379-44
17	32	59.3	25	4	PCT-US93-07545-44
18	32	59.3	36	1	US-08-053-131-84
19	32	59.3	36	1	US-08-645-641-84
20	32	59.3	36	1	US-07-853-408B-84
21	32	59.3	36	2	US-08-096-762-84
22	32	59.3	36	2	US-08-308-865-84
23	32	59.3	36	4	PCT-US92-10983-84
24	32	59.3	80	1	US-08-264-250A-1
25	32	59.3	89	1	US-08-025-038-30
26	32	59.3	89	1	US-08-039-137-17
27	32	59.3	90	2	US-08-485-133-23
28	32	59.3	94	3	US-09-147-550-12

29 59.3 94 3 US-09-147-550-13 Sequence 13, Appl
30 59.3 94 3 US-09-147-550-15 Sequence 15, Appl
31 59.3 94 3 US-09-147-550-16 Sequence 16, Appl
32 59.3 94 3 US-09-147-550-17 Sequence 17, Appl
33 59.3 94 3 US-09-147-550-18 Sequence 18, Appl
34 59.3 94 3 US-09-147-550-19 Sequence 19, Appl
35 59.3 94 3 US-09-147-550-20 Sequence 20, Appl
36 59.3 94 3 US-09-147-550-21 Sequence 21, Appl
37 59.3 94 3 US-09-147-550-22 Sequence 22, Appl
38 59.3 94 3 US-09-147-550-24 Sequence 24, Appl
39 59.3 94 3 US-09-147-550-25 Sequence 25, Appl
40 59.3 94 3 US-09-147-550-26 Sequence 26, Appl
41 59.3 94 3 US-09-147-550-27 Sequence 27, Appl
42 59.3 94 3 US-09-147-550-28 Sequence 28, Appl
43 59.3 94 3 US-09-147-550-29 Sequence 29, Appl
44 59.3 94 3 US-09-147-550-30 Sequence 30, Appl
45 59.3 94 3 US-09-147-550-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; ORGANISM: BOVINE
US-09-147-550-90

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: ALDA, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101:
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 66.7%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 66.7%; Score 36; DB 3; Length 119;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSEA 9
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Db 97 ARHHYGYA 105

RESULT 9
US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; LITORALIS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,267

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; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 433
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662
; FILING DATE:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-809-267-3

Query Match 63.0%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 10
PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids

; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 433
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662
; FILING DATE:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids

; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US95-13662A-3

Query Match 63.0%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 11
US-08-741-437-5
; Sequence 5, Application US/08741437
; Patent No. 5843665
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
; US-08-741-437-5

Query Match 63.0%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 12
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US-09-134-593-5
; Sequence 5, Application US/09134593
; Patent No. 5981232
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,593
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0148 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 4199
US-09-134-593-5

Query Match 63.0%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
| | | | |
Db 92 HNYGAF 97

RESULT 13
US-08-618-464-7
; Sequence 7, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US

ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: S1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-08-618-464-7

Query Match 59.3%; Score 32; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
| | | | |
Db 11 RHNYG 15

RESULT 14
US-09-107-615-7
; Sequence 7, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIS
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: S1
FEATURE:
NAME/KEY: Peptide
LOCATION: 1.15
US-09-107-615-7

Query Match 59.3%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 11 RHNYG 15

RESULT 15
US-08-480-190-44
Sequence 44, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-44

Query Match 59.3%; Score 32; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 15 RHNYG 19

Search completed: March 28, 2001, 07:01:55
Job time: 1334 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:26 ; Search time 130.08 Seconds
(without alignments)
6.786 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQISINFLHWY 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	90.3	106	2	PL0267
2	65	90.3	123	2	S35479
3	62	86.1	122	2	S40370
4	61	84.7	107	2	S32188
5	60	83.3	96	2	G33730
6	60	83.3	103	2	S19975
7	59	81.9	95	2	PH0867
8	59	81.9	102	2	S26346
9	59	81.9	104	2	B43413
10	59	81.9	107	2	B45722
11	59	81.9	107	2	A45722
12	59	81.9	138	2	A26471
13	58	80.6	62	2	S42265
14	58	80.6	87	2	I52592
15	58	80.6	88	2	S34088
16	58	80.6	88	2	S34087
17	58	80.6	95	2	PH0862
18	58	80.6	107	2	C45722
19	58	80.6	108	2	S19674
20	58	80.6	110	2	S44118
21	58	80.6	117	2	S43528
22	58	80.6	117	2	S42263
23	58	80.6	127	2	S40367
24	58	80.6	129	1	K1HUWK
25	58	80.6	129	2	S52789
26	55	76.4	122	2	D40314
27	54	75.0	92	1	KVRB38
28	54	75.0	93	2	S38564
29	54	75.0	106	2	PC4282

30	54	75.0	107	2	B28044	Ig kappa chain V r
31	54	75.0	107	2	A28044	Ig kappa chain V r
32	54	75.0	107	2	D48677	Ig kappa chain V-J
33	54	75.0	107	2	B49026	Ig kappa chain V r
34	54	75.0	107	2	S69901	Ig kappa chain (cl
35	54	75.0	107	2	S69906	Ig kappa chain (cl
36	54	75.0	108	1	KVMSAR	Ig kappa chain V r
37	54	75.0	108	2	C26405	Ig kappa chain V r
38	54	75.0	108	2	B30551	Ig kappa chain V r
39	54	75.0	108	2	PL0282	Ig kappa chain V r
40	54	75.0	108	2	S38862	Ig kappa chain V r
41	54	75.0	108	2	S69903	Ig kappa chain (cl
42	54	75.0	108	2	S69900	Ig kappa chain (cl
43	54	75.0	108	2	S69902	Ig kappa chain (cl
44	54	75.0	113	2	JL0080	Ig kappa chain pre
45	54	75.0	115	2	A53276	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rohtstein J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A:Reference number: PL0231; MUID:90111618
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 90.3%; Score 65; DB 2; Length 106;
Best Local Similarity 84.6%; Pred. No. 0.0002;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISINFLHWY 13
DB 24 RASQISINFLHWY 36
:|||||||:||||

RESULT 2

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:gl97572; PIDN:AAA39079.1; PID:G554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
 F;1-12/Domain: signal sequence (fragment) #status predicted <SIG>
 F;13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F;28-102/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 65; DB 2; Length 123;
 Best Local Similarity 84.6%; Pred. No. 0.00024;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:||||
 Db 36 RASQISNYLHWY 48

RESULT 3

S40370
 Ig kappa chain - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000.
 C;Accession: S40370
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID:94080891
 A;Accession: S40370
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-122 <KLE>
 A;Cross-references: EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PID:g441429
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 86.1%; Score 62; DB 2; Length 122;
 Best Local Similarity 84.6%; Pred. No. 0.00078;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:||||
 Db 38 RASQISNLFHWY 50

RESULT 4

S32188
 Ig kappa chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C;Accession: S32188
 R;Izui, S.

submitted to the EMBL Data Library, February 1993

A;Reference number: S32185
 A;Accession: S32188
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-107 <IZU>
 A;Cross-references: EMBL:X70090; NID:g288253; PIDN:CAA49695.1; PID:g288254
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-90/Domain: immunoglobulin homology <IMM>

Query Match 84.7%; Score 61; DB 2; Length 107;
 Best Local Similarity 76.9%; Pred. No. 0.001;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||:||||
 Db 24 RASQISNYLHWY 36

RESULT 5

G33730
 Ig kappa chain V region (23.32) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
 C;Accession: G33730
 R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
 A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
 A;Reference number: A33730; MUID:89367325
 A;Accession: G33730
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-96 <LAW>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 60; DB 2; Length 96;
 Best Local Similarity 76.9%; Pred. No. 0.0014;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:||||
 Db 24 RASQISDYLHWY 36

RESULT 6

S19975
 Ig kappa chain V region (M-T408) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C;Accession: S19975
 R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
 submitted to the EMBL Data Library, March 1992
 A;Description: Structural characterization of CD4 mAb.
 A;Reference number: S19963
 A;Accession: S19975
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-103 <WEI>
 A;Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;11-85/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 60; DB 2; Length 103;
 Best Local Similarity 76.9%; Pred. No. 0.0015;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 :|||||:||||
 Db 19 RASQISDYLHWY 31

RESULT 7

PH0867
 Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C;Accession: PH0867
 R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
 J. Exp. Med. 174, 1639-1652, 1991
 A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
 A;Reference number: PH0862; MUID:92078875
 A;Accession: PH0867
 A;Molecule type: DNA
 A;Residues: 1-95 <MAN>
 C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-23/region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-95/Region: complementarity-determining 3

Query Match 81.9%; Score 59; DB 2; Length 95;
 Best Local Similarity 76.9%; Pred. No. 0.002;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||||:|||||
 Db 24 RASQSIGSLHWY 36

RESULT 8
 S26346

Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26346
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <STA>
 A:Cross-references: EMBL:X59211; NID:q52338; PIDN:CAA41921.1; PID:gl334075
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 102;
 Best Local Similarity 84.6%; Pred. No. 0.0022;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||||||:|||||
 Db 22 RASQISNNLHWY 34

RESULT 9
 B43413

Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOW>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 104;
 Best Local Similarity 84.6%; Pred. No. 0.0022;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||||||:|||||
 Db 21 RASQISNNLHWY 33

RESULT 10
 B45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: B45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 107;
 Best Local Similarity 84.6%; Pred. No. 0.0023;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||||||:|||||
 Db 24 RASQISNNLHWY 36

RESULT 11
 A45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C:
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: A45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.9%; Score 59; DB 2; Length 107;
 Best Local Similarity 84.6%; Pred. No. 0.0023;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||||||:|||||
 Db 24 RASQISNNLHWY 36

RESULT 12
 A26471

Ig kappa chain precursor V region (MAK33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C:Accession: A26471
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
 A:Reference number: A91572; MUID:87248058
 A:Accession: A26471
 A:Molecule type: mRNA
 A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <WAT>

Query Match 81.9%; Score 59; DB 2; Length 138;
Best Local Similarity 84.6%; Pred. No. 0.003;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
:|||||:|
Db 44 RASQISINLHWY 56

RESULT 13
S42265
Ig kappa chain V region (O18) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42265
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A:Reference number: S42263; MUID:92043792
A:Accession: S42265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SCO>
A:Cross-references: EMBL:M64856
C:Genetics:
A:Introns: 19/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 80.6%; Score 58; DB 2; Length 62;
Best Local Similarity 76.9%; Pred. No. 0.0019;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
:|||||:|
Db 24 QASQDISNYLWY 36

RESULT 14
I52592
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I52592
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutatio
A:Reference number: I52592; MUID:94264318
A:Accession: I52592
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-87 <RES>
A:Cross-references: GB:S71057; NID:g547053; PIDN:AAB30971.1; PID:g547054
C:Genetics:
A:Gene: IGKV
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 58; DB 2; Length 87;
Best Local Similarity 76.9%; Pred. No. 0.0027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
:|||||:|

Db 17 QASQDISNYLWY 29
RESULT 15
S34088
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34088
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distrib
A:Reference number: S34076; MUID:93170387
A:Accession: S34088
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WAG>
A:Cross-references: EMBL:X67172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 58; DB 2; Length 88;
Best Local Similarity 76.9%; Pred. No. 0.0028;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
:|||||:|
Db 17 QASQDISNYLWY 29

Search completed: March 28, 2001, 07:04:27
Job time: 1065 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:05 ; Search time 72.95 Seconds

(without alignments)
5.693 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQSISNLFHWY 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	58	80.6	129	1 KVIW_HUMAN	P04431 homo sapien
2	54	75.0	92	1 KV09_RABIT	P01690 oryctolagus
3	54	75.0	108	1 KV5K_MOUSE	P01644 mus musculus
4	54	75.0	108	1 KV5L_MOUSE	P01645 mus musculus
5	54	75.0	108	1 KV5M_MOUSE	P01646 mus musculus
6	54	75.0	117	1 KV10_RABIT	P01691 oryctolagus
7	53	73.6	108	1 KVIH_HUMAN	P01594 homo sapien
8	53	73.6	108	1 KV5U_MOUSE	P04946 mus musculus
9	52	72.2	108	1 KVIJ_HUMAN	P01608 homo sapien
10	52	72.2	108	1 KV5J_MOUSE	P01643 mus musculus
11	51	70.8	108	1 KVIH_HUMAN	P01600 homo sapien
12	51	70.8	108	1 KV5N_MOUSE	P01647 mus musculus
13	51	70.8	108	1 KV5O_MOUSE	P01648 mus musculus
14	50	69.4	108	1 KVI1_HUMAN	P01593 homo sapien
15	49	68.1	115	1 KV3I_HUMAN	P04433 homo sapien
16	48	66.7	115	1 KV5I_MOUSE	P01642 mus musculus
17	48	66.7	117	1 KVIJ_HUMAN	P01602 homo sapien
18	48	66.7	129	1 KV3H_HUMAN	P04207 homo sapien
19	47	65.3	107	1 KV04_RABIT	P01685 oryctolagus
20	47	65.3	108	1 KVI1_HUMAN	P01605 homo sapien
21	47	65.3	108	1 KVI1_HUMAN	P01606 homo sapien
22	46.5	64.6	109	1 KV3D_HUMAN	P01622 homo sapien
23	46	63.9	108	1 KV08_RABIT	P01689 oryctolagus
24	46	63.9	108	1 KVI0_HUMAN	P01607 homo sapien
25	46	63.9	111	1 KVI2_RABIT	P01693 oryctolagus
26	45	62.5	107	1 KVI2_HUMAN	P01596 homo sapien
27	45	62.5	108	1 KV07_RABIT	P01688 oryctolagus
28	45	62.5	108	1 KV03_MOUSE	P01674 mus musculus
29	45	62.5	109	1 KV03_MOUSE	P01684 oryctolagus
30	44.5	61.8	109	1 KV3F_HUMAN	P01624 homo sapien
31	44	61.1	104	1 KVI7_RABIT	P01698 oryctolagus
32	44	61.1	108	1 KVI1_HUMAN	P01595 homo sapien
33	44	61.1	108	1 KVI1_HUMAN	P01597 homo sapien

34	44	61.1	108	1 KVI1_HUMAN	P01598 homo sapien
35	44	61.1	108	1 KVI1_HUMAN	P01603 homo sapien
36	44	61.1	108	1 KVI1_HUMAN	P01611 homo sapien
37	44	61.1	108	1 KVI1_HUMAN	P01649 mus musculus
38	44	61.1	108	1 KVI1_HUMAN	P01649 mus musculus
39	44	61.1	129	1 KVI1_HUMAN	P04432 homo sapien
40	43.5	60.4	109	1 KVI3_HUMAN	P01620 homo sapien
41	43	59.7	108	1 KVI0_HUMAN	P01609 homo sapien
42	43	59.7	128	1 KVI3_HUMAN	P06311 homo sapien
43	43	59.7	283	1 LEG1_HAECO	O44126 haemonchus
44	43	59.7	521	1 COX1_APILI	P20374 apis mellif
45	42.5	59.0	108	1 KVI3_HUMAN	P01619 homo sapien

ALIGNMENTS

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RESULT 1
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85014148.
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUNK.
DR HSSP; P01607; IREI.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;
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Query Match 80.6%; Score 58; DB 1; Length 129;
Best Local Similarity 76.9%; Pred. No. 0.0013;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
Db 46 RASQSISNLFHWY 58

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RESULT 2
KV09_RABIT
ID KV09_RABIT STANDARD; PRT; 92 AA.
AC P01690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V REGION 3381 (FRAGMENT)
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 75176905.
RA Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT "Diversity of light chain variable region sequences among rabbit
RT antibodies elicited by the same antigens.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTI BODY TO TYPE III
CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
DR PIR: A01953; KVRB38.
DR INTERPRO: IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 >92
FT NON_TER 92 92
SQ SEQUENCE 92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;

Query Match 75.0%; Score 54; DB 1; Length 92;
Best Local Similarity 76.9%; Pred. No. 0.0046;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLHWY 13
DB 24 QASESISNWLAWY 36

RESULT 3
KV5K_MOUSE
ID KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-V REGION HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idio type.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVM5AR.
DR INTERPRO: IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFFF58E CRC64;

Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0054;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLHWY 13
DB 24 RASQDISNYLWNY 36

RESULT 5
KV5M_MOUSE
ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-V REGION HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFFF597 CRC64;

Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0054;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLHWY 13
DB 24 RASQDISNYLWNY 36

RESULT 4
KV5L_MOUSE
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-V REGION HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idio type.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVM5AR.
DR INTERPRO: IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFFF58E CRC64;

Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0054;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLHWY 13
DB 24 RASQDISNYLWNY 36

RESULT 5
KV5M_MOUSE
ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-V REGION HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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RN (1)
RP SEQUENCE.
RC STRAIN=A/J;
RA MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0054;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
Db 24 RASQDISNYLWY 36

RESULT 6
KV10_RABIT STANDARD; PRT; 117 AA.
AC P01691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V REGION 12F2 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83273646.
RA Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT "cDNA clone encoding a complete rabbit immunoglobulin kappa light
RT chain of b4 allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
CC HYBRIDOMA 12F2; THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
CC AGAINST STREPTOCOCCAL GROUP C VACCINE.
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CC -----
CC EMBL; K01358; AAB59259.1; ALT_TER.
DR PIR; A01954; K4RBF2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
FT NON_TER 1 1
FT SIGNAL <1 6
FT CHAIN 7 117
IG KAPPA CHAIN V REGION 12F2.

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FT DOMAIN 7 29
FT DOMAIN 30 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 106
FT DOMAIN 107 116
FT DISULFID 29 86
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12288 MW; E24A7582389E4439 CRC64;

Query Match 75.0%; Score 54; DB 1; Length 117;
Best Local Similarity 76.9%; Pred. No. 0.0059;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
Db 30 QASQISISTYLSWY 42

RESULT 7
KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-I REGION AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 72189444.
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Sejler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 77022433.
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Latman E.E.,
RA Schwager P., Seigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01862; K1HUAU.
DR HSSP; P01607; 1REI.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 73.6%; Score 53; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0082;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY      1 QASQISNFWLHWY 13
      IIII I I I I I I
Db      24 QASQDISDYNWY 36

RESULT      8
KV5U_MOUSE
ID      KV5U_MOUSE      STANDARD;      PRT;      108 AA.
AC      P04946;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-V REGION NQ5-89.4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 83271467.
RA      Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.:
RT      "mRNA sequences define an unusually restricted IgG response to 2-
RT      phenylloxazalone and its early diversification.";
RL      Nature 304:320-324(1983).
CC      -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; K00745; AAA38690.1; -.
DR      INTERPRO; IPR003006; -.
DR      PFAM; PF00047; ig; 1.
KW      Immunoglobulin V region; Hybridoma.
FT      DOMAIN 1 23 FRAMEWORK 1.
FT      DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN 35 49 FRAMEWORK 2.
FT      DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN 57 88 FRAMEWORK 3.
FT      DOMAIN 89 97 FRAMEWORK 4.
FT      DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.
FT      DISULFID 23 88 BY SIMILARITY.
FT      NON_TER 108 108
SQ      SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DDD CRC64;

Query Match      73.6%; Score 53; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.0082;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 ASQISNFWLHWY 13
      IIII I I I I I I
Db      25 ASQDISDYNWY 36

RESULT      9
KV1P_HUMAN
ID      KV1P_HUMAN      STANDARD;      PRT;      108 AA.
AC      P01608;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-I REGION ROF.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE; 68362076.

Query Match      73.6%; Score 53; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.0082;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 ASQISNFWLHWY 13
      IIII I I I I I I
Db      25 ASQDISDYNWY 36

RESULT      9
KV1P_HUMAN
ID      KV1P_HUMAN      STANDARD;      PRT;      108 AA.
AC      P01608;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-I REGION ROF.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE; 68362076.

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RA      Hilschmann N.:
RT      "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT      Cum.)";
RL      Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN      [2]
RP      REVISIONS TO 39 AND 41.
RA      Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA      Steinmetz-Kayne M., Suter L., Watanabe S.;
RL      (In) Franek F., Shugar D. (eds.);
RL      Gamma globulins: structure and function, pp.57-74, Academic Press,
RL      New York (1969).
CC      -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC      MARKER.
CC      -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR      PIR; A01874; KLHURY.
DR      HSSP; P80362; 1WTL.
DR      INTERPRO; IPR003006; -.
DR      PFAM; PF00047; ig; 1.
KW      Immunoglobulin V region; Bence-Jones protein.
FT      DOMAIN 1 23 FRAMEWORK 1.
FT      DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN 35 49 FRAMEWORK 2.
FT      DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN 57 88 FRAMEWORK 3.
FT      DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN 98 107 FRAMEWORK 4.
FT      DISULFID 23 88 BY SIMILARITY.
FT      NON_TER 108 108
SQ      SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match      72.2%; Score 52; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.012;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QASQISNFWLHWY 13
      IIII I I I I I I
Db      24 QASQDISDYNWY 36

RESULT      10
KV5J_MOUSE
ID      KV5J_MOUSE      STANDARD;      PRT;      108 AA.
AC      P01643;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-V REGION MOPC 173.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE; 76091934.
RA      Schiff C., Fougereau M.;
RT      "Determination of the primary structure of a mouse IgG2a
RT      immunoglobulin. Amino-acid sequence of the light chain.";
RL      Eur. J. Biochem. 59:525-537(1975).
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR      PIR; A01926; KVM573.
DR      INTERPRO; IPR003006; -.
DR      PFAM; PF00047; ig; 1.
KW      Immunoglobulin V region.
FT      DOMAIN 1 23 FRAMEWORK 1.
FT      DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN 35 49 FRAMEWORK 2.
FT      DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN 57 88 FRAMEWORK 3.
FT      DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN 98 108 FRAMEWORK 4.
FT      DISULFID 23 88 BY SIMILARITY.
FT      NON_TER 108 108
SQ      SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

```


Query Match 72.2%; Score 52; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 0.012;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSISNFWY 13
 DB 25 ASQSIGNFLWY 36
 RESULT 11
 ID KV1H_HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION HAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 71032830.
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups.";
 RL Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01868; KIHUHU.
 DR HSSP; P80362; 1WTL.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; ig: 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.019;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFWY 13
 DB 24 RASQISNFWY 36
 RESULT 12
 ID KV5N_MOUSE STANDARD; PRT; 108 AA.
 AC P01647;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-V REGION HP 124E1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.

RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 RT from five monoclonal anti-p-azophenylarsonate antibodies differing
 RT with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR: A01927; KVMSAR.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; ig: 1.
 KW Immunoglobulin V region; Antiarsenate antibody.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
 Best Local Similarity 61.5%; Pred. No. 0.019;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFWY 13
 DB 24 RASQISNFWY 36
 RESULT 13
 ID KV5O_MOUSE STANDARD; PRT; 108 AA.
 AC P01648;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-V REGION HP 91A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RC MEDLINE; 82150934.
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 RT from five monoclonal anti-p-azophenylarsonate antibodies differing
 RT with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR: A01927; KVMSAR.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; ig: 1.
 KW Immunoglobulin V region; Antiarsenate antibody.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
 Best Local Similarity 61.5%; Pred. No. 0.019;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNFWY 13

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CC -----
 CC EMBL; X01668; NOT_ANNOTATED_CDS.
 CC PIR; A01900; K3HUVG.
 CC INTERPRO; IPR003006; -.
 CC PFAM; PF00047; Ig; 1.
 CC Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12575 MW; 2DB47CDA3A17D555 CRC64;

Query Match 68.1%; Score 49; DB 1; Length 115;
 Best Local Similarity 61.5%; Pred. No. 0.045;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||:|:|:|
 Db 44 RASQSVSYLAWY 56

Search completed: March 28, 2001, 07:35:06
 Job time: 143 sec.

Db 24 RASQDINHLNLYWY 36
 :|||:|:|:|
 RESULT 14
 KV31_HUMAN STANDARD; PRT; 108 AA.
 AC P04433;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 69234734.
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RT complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01861; KIHUAG.
 DR HSSP; P01607; 1REI.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 69.4%; Score 50; DB 1; Length 108;
 Best Local Similarity 61.5%; Pred. No. 0.028;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
 :|||:|:|:|
 Db 24 QASQDINHLNLYWY 36

RESULT 15
 KV31_HUMAN STANDARD; PRT; 115 AA.
 AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85087932.
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus.";
 RL Nucleic Acids Res. 12:9229-9236(1984).
 CC -----

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:07 ; Search time 443.95 Seconds
(without alignments)
3.432 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQISINFLHWY 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	80.6	107	4 Q9UL81	Q9ul81 homo sapien
2	53	73.6	108	4 Q9UL77	Q9ul77 homo sapien
3	51	70.8	108	4 Q9UL70	Q9ul70 homo sapien
4	48.5	67.4	101	11 Q9JL78	Q9j178 mus musculus
5	47	65.3	307	3 Q59680	Q59680 schizosacch
6	45	62.5	99	11 Q9JL74	Q9j174 mus musculus
7	43	59.7	108	4 Q9UL83	Q9ul83 homo sapien
8	43	59.7	109	4 Q9UL85	Q9ul85 homo sapien
9	43	59.7	130	8 Q80033	Q80033 exoneurella
10	43	59.7	130	8 Q80034	Q80034 exoneurella
11	43	59.7	131	8 Q79124	Q79124 braunsapis
12	43	59.7	131	8 Q79125	Q79125 brevinea
13	43	59.7	131	8 Q79126	Q79126 exoneurella
14	43	59.7	283	5 Q9NJV0	Q9njv0 haemonchus
15	42	58.3	650	5 Q9TXI6	Q9txi6 caenorhabdi
16	42	58.3	688	8 Q9TK91	Q9tk91 mirabilis j
17	42	58.3	897	5 Q9XZR0	Q9xzc0 caenorhabdi
18	42	58.3	901	5 Q9TXI7	Q9txi7 caenorhabdi
19	41	56.9	108	4 Q9UL79	Q9ul79 homo sapien

20 41 56.9 201 10 Q9SYN3 Q9syn3 arabidopsis
21 41 56.9 202 10 Q9M9G0 Q9m9g0 arabidopsis
22 41 56.9 400 5 O17674 O17674 caenorhabdi
23 40.5 56.2 97 11 Q9JL76 Q9j176 mus musculu
24 40 55.6 166 5 Q96211 Q96211 plasmodium
25 40 55.6 214 11 Q9RIA5 Q9ria5 mus musculu
26 40 55.6 267 8 Q9ML42 Q9ml42 nilaparvata
27 40 55.6 272 4 Q9NUU5 Q9nuu5 homo sapien
28 40 55.6 275 8 Q9MDI7 Q9md17 nilaparvata
29 40 55.6 298 11 Q9QYF0 Q9qyf0 mus musculu
30 40 55.6 413 8 Q9TCH5 Q9tch5 lasloglossu
31 40 55.6 413 8 Q9TCG0 Q9tcg0 lasloglossu
32 40 55.6 493 8 Q34084 Q34084 cecidosea e
33 40 55.6 701 8 Q9TKN4 Q9tkn4 garrya ellii
34 40 55.6 709 8 Q9TK94 Q9tk94 allionia vi
35 40 55.6 5388 5 Q9ULD0 Q9uld0 leishmania
36 39 54.2 130 8 O80035 O80035 exoneurella
37 39 54.2 185 8 O63601 O63601 drosophila
38 39 54.2 187 10 Q9ZWD1 Q9zwd1 arabidopsis
39 39 54.2 334 2 Q9Z785 Q9z785 chlamydia p
40 39 54.2 399 4 Q16529 Q16529 homo sapien
41 39 54.2 593 5 Q9VMR6 Q9vmr6 drosophila
42 39 54.2 664 3 Q9URD2 Q9urd2 schizosacch
43 39 54.2 736 10 Q82754 Q82754 arabidopsis
44 39 54.2 801 3 Q9P3W3 Q9p3w3 schizosacch
45 39 54.2 3317 2 Q9RAH2 Q9rah2 nostoc sp.

ALIGNMENTS

RESULT 1

Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81: TREMBLrel. 13, Created
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -;
DR HSP; P80362; IWTL.
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 80.6%; Score 58; DB 4; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.0055; 0; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISINFLHWY 13

Db 24 RASQISINFLNMY 36

RESULT 2

Q9UL77 PRELIMINARY; PRT; 108 AA.

ID Q9UL77: TREMBLrel. 13, Created

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035037; AAD56273.1; -.
 DR HSSP; P01607; IREI.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 FT NON_TER 1 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 73.6%; Score 53; DB 4; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.042;
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QASQISNLFHWY 13
 :|||||:||||
 Db 24 RASQISSYLNWY 36

RESULT 3
 ID Q9UL70 PRELIMINARY; PRT; 108 AA.
 AC Q9UL70;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035044; AAD56280.1; -.
 DR HSSP; P01607; IREI.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 FT NON_TER 1 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 70.8%; Score 51; DB 4; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.094;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QASQISNLFHWY 13
 :|||||:||||
 Db 24 RASQISSYLNWY 36

RESULT 4

Q9JL78
 ID Q9JL78 PRELIMINARY; PRT; 101 AA.
 AC Q9JL78;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A.CA;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis".
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF206028; AAF69336.1; -.
 FT NON_TER 1 1
 FT NON_TER 101 101
 SQ SEQUENCE 101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;

Query Match 67.4%; Score 48.5; DB 11; Length 101;
 Best Local Similarity 76.9%; Pred. No. 0.24;
 Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 2 ASQSI-SNFLHWY 13
 :|||||:||||
 Db 17 ASSSISSNLHWY 29

RESULT 5
 ID O59680 PRELIMINARY; PRT; 307 AA.
 AC O59680;
 DT 01-JAN-1999 (TReMBLrel. 09, Created)
 DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE PROBABLE CYTOCHROME C1, HEME PROTEIN PRECURSOR.
 GN SPBC29A3.18.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 OC Schizosaccharomycetaceae; Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Volckaert G.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME
 CC B-C1 COMPLEX, WHICH ACCEPTS ELECTRONS FROM RIESKE PROTEIN AND
 CC TRANSFERS ELECTRONS TO CYTOCHROME C IN THE MITOCHONDRIAL
 CC RESPIRATORY CHAIN.
 CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -!- SUBCELLULAR LOCATION: ANCHORED IN THE INNER MITOCHONDRIAL MEMBRANE
 CC WITH ITS N-TERMINUS PROTRUDING INTO THE MITOCHONDRIAL
 CC INTERMEMBRANE SPACE (BY SIMILARITY).
 DR EMBL; AL022299; CAA18395.1; -.
 DR INTERPRO; IPR000345; -.
 DR PFAM; PF02167; Cytochrome_C1; 1.
 DR PRINTS; PR00603; CYTOCHROME_C1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 KW Electron transport; Respiratory chain; Oxidative phosphorylation;
 KW Heme; Mitochondrion; Transmembrane; Transit peptide.
 FT CHAIN 1 62
 FT BINDING 63 307
 FT BINDING 102 102
 FT BINDING 105 105
 FT BINDING 106 106
 FT METAL 106 106
 FT MITOCHONDRION (BY SIMILARITY).
 FT PROBABLE CYTOCHROME C1, HEME PROTEIN.
 FT HEME (COVALENT) (BY SIMILARITY).
 FT HEME (COVALENT) (BY SIMILARITY).
 FT IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

```
FT METAL      225      225      IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSEM    273      287      ANCHORS TO THE MEMBRANE (BY SIMILARITY).
SQ SEQUENCE   307 AA; 34340 MW; FAD8B9D3A9A3C1B3 CRC64;

Query Match      65.3%; Score 47; DB 3; Length 307;
Best Local Similarity 58.3%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHW 12
   : : : : :
Db 246 QAAKDVVNFVLFHW 257

RESULT 6
Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RL acetylglucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206032; AAF69330.1; -.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match      62.5%; Score 45; DB 11; Length 99;
Best Local Similarity 61.5%; Pred. No. 0.99;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHW 13
   : : : : :
Db 16 KASQSVSNVAVY 28

RESULT 7
Q9JL83 PRELIMINARY; PRT; 108 AA.
AC Q9JL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P01607; IREI.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 108 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match      59.7%; Score 43; DB 4; Length 108;
Best Local Similarity 61.5%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQSISNFWLHW 13
   : : : : :
Db 25 ASQSISNFWLHW 36

RESULT 9
Q80033 PRELIMINARY; PRT; 130 AA.
AC Q80033;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CYTOCHROME OXIDASE I (FRAGMENT).
OS Exoneurella lawsoni.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Exoneurella.
OX NCBI_TaxID=78187;
RN [1]
RP SEQUENCE FROM N.A.
RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RL Apoidea; Apidae): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072661; AAC24880.1; -.
FT NON_TER 1
```

DR INTERPRO: IPR000883; -
 KW PFAM: PF00115; COX1; 1.
 KW Mitochondrion.
 FT NON_TER 1 130
 FT 130
 SQ SEQUENCE 130 AA; 15339 MW; 11CF4F1F1EAE22F2 CRC64;

Query Match 59.7%; Score 43; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 ISNPLHWY 13
 ||:||||
 Db 19 ISSFIHWY 26

RESULT 10
 O80034 PRELIMINARY; PRT; 130 AA.
 AC O80034;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 OS Exoneurella tridentata.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 OX NCBI_TaxID=78189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF072663; AAC24882.1; -
 DR INTERPRO: IPR000883; -
 DR PFAM: PF00115; COX1; 1.
 KW Mitochondrion.
 FT NON_TER 1 130
 FT 130
 SQ SEQUENCE 130 AA; 15438 MW; 4B9444ABF5AC3F4F CRC64;

Query Match 59.7%; Score 43; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 ISNPLHWY 13
 ||:||||
 Db 19 ISSFIHWY 26

RESULT 11
 O79124 PRELIMINARY; PRT; 131 AA.
 AC O79124;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 OS Braunsapis unicolor.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Braunsapis.
 OX NCBI_TaxID=78183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;

RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF072659; AAC24878.1; -
 DR INTERPRO: IPR000883; -
 DR PFAM: PF00115; COX1; 1.
 KW Mitochondrion.
 FT NON_TER 1 131
 FT 131
 SQ SEQUENCE 131 AA; 15603 MW; F1407925903C9FE8 CRC64;

Query Match 59.7%; Score 43; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 ISNPLHWY 13
 ||:||||
 Db 19 ISSFIHWY 26

RESULT 12
 O79125 PRELIMINARY; PRT; 131 AA.
 AC O79125;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 OS Brevineura xanthoclypeata.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Brevineura.
 OX NCBI_TaxID=78184;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF072660; AAC24879.1; -
 DR INTERPRO: IPR000883; -
 DR PFAM: PF00115; COX1; 1.
 KW Mitochondrion.
 FT NON_TER 1 131
 FT 131
 SQ SEQUENCE 131 AA; 15508 MW; D5E0508AB020093F CRC64;

Query Match 59.7%; Score 43; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 ISNPLHWY 13
 ||:||||
 Db 19 ISSFIHWY 26

RESULT 13
 O79126 PRELIMINARY; PRT; 131 AA.
 AC O79126;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 OS Exoneurella eremophila.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

```

OC Apoidea: Apidae; Exoneurella.
OX NCBI_TaxID=78186;
RN [1]
RP SEQUENCE FROM N.A.
RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apoidea: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072662; AAC24881.1; -
DR INTERPRO; IPR000883; -
DR PFAM; PF00115; COX1; 1.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 15531 MW; 55B915590EBFCF85 CRC64;

Query Match 59.7%; Score 43; DB 8; Length 131;
Best Local Similarity 75.0%; Pred. No. 2.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 ISNFLHWY 13
DB 19 ISSFIHWY 26

RESULT 14
O9NJVO PRELIMINARY; PRT; 283 AA.
AC O9NJVO;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE GALECTIN
GN HCO-GAL-3B.
OS Haemochus contortus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
OX NCBI_TaxID=6289;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20183859; PubMed-10717307;
RA Greenhalgh C.J., Loukas A., Donald D., Nikolaou S., Newton S.E.;
RT "A family of galectins from haemonchus contortus.";
RL Mol. Biochem. Parasitol. 107:117-121(2000).
DR EMBL; AF105969; AAF63406.1; -
SQ SEQUENCE 283 AA; 32544 MW; F1B2E0DB346BF134 CRC64;

Query Match 59.7%; Score 43; DB 5; Length 283;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 ISNFLHWY 13
DB 2 VSQFLHWY 9

RESULT 15
O9TXI6 PRELIMINARY; PRT; 650 AA.
AC O9TXI6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE HYPOTHETICAL PROTEIN B0025.1B.
GN B0025.1B
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-98519116;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Davidson S., Wohldmann P.;
RT "The sequence of C. elegans cosmid B0025.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97190; AAF23185.1; -
DR INTERPRO; IPR000403; -
DR INTERPRO; IPR001263; -
DR PFAM; PF00454; P13_P14_Kinase; 1.
DR PFAM; PF00613; P13Ka; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; UNKNOWN_1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
SQ SEQUENCE 650 AA; 73799 MW; 6C0514526F3FFDFE CRC64;

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Query Match 58.3%; Score 42; DB 5; Length 650;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 ASQSISNFLHWY 13
DB 240 ASPKVSNIYWH 251

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Search completed: March 28, 2001, 07:53:11
Job time: 504 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:48 ; Search time 154.19 Seconds
(without alignments)
2.883 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQSISNFWY 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*
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19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	13	19 W76031	LM609 grafted anti
2	65	90.3	13	19 W76011	LM609 grafted anti
3	65	90.3	107	19 W76006	LM609 grafted anti
4	65	90.3	107	19 W76002	Vitaxin antibody 1
5	65	90.3	107	19 W76004	LM609 antibody lig
6	61	84.7	105	20 W87456	Jk gene product.
7	61	84.7	105	20 W87458	Humanised anti-alp
8	61	84.7	107	20 W84098	Humanised anti-alp
9	61	84.7	108	20 W84094	Murine vitronectin
10	61	84.7	109	20 Y06380	Murine monoclonal
11	61	84.7	112	20 W84100	Vitronectin alpha-
12	60	83.3	88	21 Y56654	Partial peptide fr

13	60	83.3	107	20 Y30203	The variable light
14	60	83.3	107	20 Y30205	The variable light
15	60	83.3	108	17 W00241	EGF receptor chime
16	60	83.3	124	21 Y56719	Amino acid sequenc
17	60	83.3	128	20 Y30199	Light chain variab
18	60	83.3	214	20 Y30202	Light chain sequen
19	59	81.9	107	13 R25729	Humanised VL regio
20	59	81.9	108	12 R15438	Light chain variab
21	59	81.9	109	20 W89176	Anti-p53 monoclonal
22	59	81.9	127	15 R54093	Sequence of mouse
23	59	81.9	240	12 R15443	Single chain Fv fr
24	58	80.6	75	19 W62818	Amino acid sequenc
25	58	80.6	75	19 W62802	Amino acid sequenc
26	58	80.6	76	20 W60980	Variable kappa lig
27	58	80.6	86	19 W62806	Amino acid sequenc
28	58	80.6	101	13 R22577	Light chain VK10.1
29	58	80.6	104	19 W62821	Amino acid sequenc
30	58	80.6	104	19 W62822	Amino acid sequenc
31	58	80.6	104	19 W62804	Amino acid sequenc
32	58	80.6	105	20 W80968	Kappa light chain
33	58	80.6	105	20 W80974	Kappa light chain
34	58	80.6	105	20 W80978	Kappa light chain
35	58	80.6	108	15 R54258	Anti-HIV gp120 imm
36	58	80.6	108	17 W01281	VL region of HIV n
37	58	80.6	108	21 Y51533	Anti-gp120 antibod
38	58	80.6	108	21 Y98242	Anti-gp120 antibod
39	58	80.6	108	21 Y56675	Anti-IL5 MAB 4A6 1
40	58	80.6	120	21 Y56701	Rat anti-interleuk
41	58	80.6	122	18 W24538	Immunoglobulin rB6
42	58	80.6	238	20 Y21880	Amino acid sequenc
43	58	80.6	241	20 Y21882	Amino acid sequenc
44	57	79.2	108	15 R50219	HSV glycoprotein F
45	57	79.2	108	17 W04333	Light chain of mon

ALIGNMENTS

RESULT 1
ID W76031 standard; Protein; 13 AA.
AC W76031;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-L region CDR1 protein fragment #2.
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX Mus sp.
XX W09833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01826.
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; V49868.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 13 AA:
 SQ
 Query Match 100.0%; Score 72; DB 19; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QASQSISNFWLHWY 13
 Db | | | | | | | | | | | | | |
 1 qasqsisnfwlhw 13
 RESULT 2
 W76011 ID W76011 standard; Protein; 13 AA.
 XX AC W76011;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR1 protein fragment #1.
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-USO1826.
 XX
 PR 30-JAN-1998;
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49848.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Disclosure; Page 40; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 13 AA:
 SQ
 Query Match 90.3%; Score 65; DB 19; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.00919;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQSISNFWLHWY 13
 Db | | | | | | | | | | | | | |
 1 qasqsisnfwlhw 13
 RESULT 3
 W76006 ID W76006 standard; Protein; 107 AA.
 XX AC W76006;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody light chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 ET Misc-difference 49
 FT /label= Arg, Met
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-USO1826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49843.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 19; Fig 7; 129pp; English.
 PS
 CC This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,

CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 19; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLHWY 13
 | | | | | | | | | |
 DB 24 gasqsisnhlhw 36

RESULT 4
 W76002 W76002 standard; Protein; 107 AA.
 XX AC W76002;
 XX DT 02-NOV-1998 (first entry)
 XX DE Vitaxin antibody light chain variable region protein fragment.
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX DR N-PSDB; V49821.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PS Claim 1; Fig 1b; 129pp; English.

CC This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 19; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQSISNFLHWY 13
 | | | | | | | | | |
 DB 24 gasqsisnhlhw 36

RESULT 5
 W76004 W76004 standard; Protein; 107 AA.
 XX AC W76004;
 XX DT 02-NOV-1998 (first entry)
 XX DE LM609 antibody light chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX DR N-PSDB; W76004.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PS Claim 46; Fig 2b; 129pp; English.

CC This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 19; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLHWY 13
 | | | | | | | | | |
 DB 24 gasqsisnhlhw 36

```

RESULT      6
W87456
ID   W87456 standard; Protein; 105 AA.
XX
AC   W87456;
XX
DT   15-MAR-1999 (first entry)
XX
DE   Jk gene product.
XX
KW   Humanised antibody; monoclonal antibody; Mab; antibody engineering;
KW   mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW   cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW   angiogenesis; diabetic retinopathy; inflammation;
KW   macular degeneration; osteoporosis; Paget's disease;
KW   hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW   D12H2LCREI; Jk protein.
XX
OS   Mus sp.
XX
PN   W09840488-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998; 98WO-US04987.
XX
PR   12-MAR-1997; 97US-0039609.
XX
PS   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Johanson KO, Jonak ZL, Taylor AH;
XX
WPI; 1999-034590/03.
DR   N-PSDB; V71803.
XX
XX   New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX   immunotherapeutic treatment of e.g. diabetic retinopathy,
XX   inflammatory disorders, atherosclerosis, restenosis, cancers or
XX   osteoporosis
XX
PS   Example 14; Page 66; 97pp; English.
XX
CC   This polypeptide is encoded by a Jk synthetic gene segment (see
CC   W71803). It was utilising in novel D12H2LCREI humanised light chain
CC   variable region (see W87458), which comprises a human REI framework
CC   and complementarity determining regions from the anti-human alpha-v
CC   beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
CC   antibodies can be used for passive immunotherapy of disorders
CC   mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
CC   and angiogenic associated diseases.
XX
SQ   Sequence 105 AA;

Query Match      84.7%; Score 61; DB 20; Length 105;
Best Local Similarity 84.6%; Pred. No. 0.0073;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY   1 QASQISINFLHWY 13
Db   24 rasqsisnhlhw 36

RESULT      7
W87458
ID   W87458 standard; Protein; 105 AA.
XX
AC   W87458;
XX
DT   15-MAR-1999 (first entry)
XX
DE   Humanised anti-alpha-v beta-3 Mab D12H2LCREI VL.

```

```

XX
KW   Humanised antibody; monoclonal antibody; Mab; antibody engineering;
KW   mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW   cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW   angiogenesis; diabetic retinopathy; inflammation;
KW   macular degeneration; osteoporosis; Paget's disease;
KW   hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW   D12H2LCREI.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   W09840488-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998; 98WO-US04987.
XX
PR   12-MAR-1997; 97US-0039609.
XX
PS   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Johanson KO, Jonak ZL, Taylor AH;
XX
WPI; 1999-034590/03.
DR   N-PSDB; V71805.
XX
XX   New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX   immunotherapeutic treatment of e.g. diabetic retinopathy,
XX   inflammatory disorders, atherosclerosis, restenosis, cancers or
XX   osteoporosis
XX
PS   Example 14; Page 68-69; 97pp; English.
XX
CC   This is the amino acid sequence of the light chain variable region
CC   (VI) of humanised anti-alpha-v beta-3 vitronectin receptor.
CC   monoclonal antibody D12H2LCREI. It is based on a synthetic
CC   humanised kappa chain based on a modified human REI kappa
CC   framework and complementarity determining regions from the murine
CC   anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC   D12 (see W84094). Humanised antibodies of the invention can be used
CC   for passive immunotherapy of a disorder mediated by the alpha-v
CC   beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
CC   related disorders, such as angiogenesis associated with diabetic
CC   retinopathy, atherosclerosis and restenosis, chronic inflammatory
CC   disorders, macular degeneration, rheumatoid arthritis and cancer,
CC   e.g. solid tumour metastasis, and diseases where bone resorption is
CC   associated with pathology such as osteoporosis, hyperparathyroidism,
CC   Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
CC   produced by bone metastasis, bone loss due to immobilisation or sex
CC   hormone deficiency. They can also be used for targeted drug
CC   therapy, and for detection and diagnosis.
XX
SQ   Sequence 105 AA;

Query Match      84.7%; Score 61; DB 20; Length 105;
Best Local Similarity 84.6%; Pred. No. 0.0073;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY   1 QASQISINFLHWY 13
Db   24 rasqsisnhlhw 36

RESULT      8
W84098
ID   W84098 standard; Protein; 107 AA.
XX
AC   W84098;
XX
DT   15-MAR-1999 (first entry)
XX

```

DE	Humanised anti-alpha-v beta-3 MAb D12H2HC 1-0 VL.	
XX		
KW	Humanised antibody; monoclonal antibody; MAb; antibody engineering;	
KW	mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;	
KW	cancer; metastasis; rheumatoid arthritis; atherosclerosis;	
KW	angiogenesis; diabetic retinopathy; inflammation;	
KW	macular degeneration; osteoporosis; Paget's disease;	
KW	hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;	
XX	D12H2HC-10.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Region	24..34
FT		/label= CDR1
FT	Region	50..56
FT		/label= CDR2
FT	Region	89..97
FT		/label= CDR3
XX		
PN	WO9840488-A1.	
XX		
PD	17-SEP-1998.	
XX		
PF	12-MAR-1998; 98WO-US04987.	
XX		
PR	12-MAR-1997; 97US-0039609.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX		
PI	Johanson KO, Jonak ZL, Taylor AH;	
DR	WPI: 1999-034590/03.	
DR	N-PSDB; V71800.	
XX		
PT	New anti alpha_v beta_3 vitronectin receptor antibodies - used for	
PT	immunotherapeutic treatment of e.g. diabetic retinopathy,	
PT	inflammatory disorders, atherosclerosis, restenosis, cancers or	
PT	osteoporosis	
XX		
PS	Claim 2: Page 61-62; 97pp; English.	
XX		
CC	This is the amino acid sequence of the light chain variable region	
CC	(VL) of humanised anti-alpha-v beta-3 vitronectin receptor .	
CC	monoclonal antibody D12H2HC 1-0. It is based on the VL sequence	
CC	(see W84096) of human Kabat subgroup III kappa chain, with	
CC	complementarity determining regions (CDRs) from the murine	
CC	anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody	
CC	D12 (see W84093). 3 Murine framework residues (1, 49 and 60)	
CC	are retained. The humanised light chain can be expressed in host	
CC	cells using nucleic acid molecules (see V71800) of the invention.	
CC	Humanised D12 VH is also provided (see W84097)). The humanised	
CC	antibodies can be used for passive immunotherapy of disorders	
CC	mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or	
CC	angiogenic-related disorders, such as angiogenesis associated	
CC	with diabetic retinopathy, atherosclerosis and restenosis, chronic	
CC	inflammatory disorders, macular degeneration, rheumatoid arthritis	
CC	and cancer, e.g. solid tumour metastasis, and diseases where bone	
CC	resorption is associated with pathology such as osteoporosis,	
CC	hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,	
CC	osteolytic lesions produced by bone metastasis, bone loss due to	
CC	immobilisation or sex hormone deficiency. They can also be used for	
CC	targeted drug therapy, and for detection and diagnosis.	
XX		
SQ	Sequence 107 AA;	

Query Match	84.7%;	Score 61;	DB 20;	Length 107;
Best Local Similarity	84.6%;	Pred No. 0.0074;		
Matches 11; Conservative	1;	Mismatches	1;	Indels 0; Gaps

QY 1 QASQISINFLHWY 13

CC loss due to immobilisation or sex hormone deficiency. They can also
 CC be used for targeted drug therapy, and for detection and diagnosis.

SQ Sequence 108 AA;

Query Match 84.7%; Score 61; DB 20; Length 108;
 Best Local Similarity 84.6%; Pred. No. 0.0075;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASQSISNLFHWY 13
 :||||| ||||
 Db 24 rasqsisnhlhw 36

RESULT 10
 Y06380
 ID Y06380 standard; Protein; 109 AA.

XX AC Y06380;

DT 06-SEP-1999 (first entry)

DE Murine monoclonal antibody LM609 V lambda.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

FH Key Location/Qualifiers

FT Peptide 1..2
 /note= "vector-encoded residues"
 FT Region 24..34
 /note= "CDR1"
 FT Region 50..56
 /note= "CDR2"
 FT Region 89..97
 /note= "CDR3"

XX W09929888-AL.

PD 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V lambda region of
 CC murine monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 109 AA;

Query Match 84.7%; Score 61; DB 20; Length 109;
 Best Local Similarity 84.6%; Pred. No. 0.0076;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASQSISNLFHWY 13
 :||||| ||||
 Db 24 rasqsisnhlhw 36

RESULT 11

W84100
 ID W84100 standard; Protein; 112 AA.

XX AC W84100;

DT 15-MAR-1999 (first entry)

DE Vitronectin alpha-v beta-3 MAB VL.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX OS Mus sp.

XX W09840488-AL.

PD 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

XX N-PSDB; W71802.

XX New anti alpha-v beta-3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX Example 13; Page 64; 97pp; English.

XX This is the amino acid sequence of the region of the murine
 CC monoclonal antibody (MAB) D12 light chain variable region (VL)
 CC that is altered in humanised D12 VL (see also W84098). A
 CC synthetic gene (see V81902) encoding the protein was prepared
 CC from synthetic oligonucleotides and used to prepare an expression
 CC vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3
 CC vitronectin receptor MAB. Humanised D12 MABs can be used for
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic associated
 CC diseases.

XX SQ Sequence 112 AA;

Query Match 84.7%; Score 61; DB 20; Length 112;
 Best Local Similarity 84.6%; Pred. No. 0.0078;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QASQSISNLFHWY 13

Db :||||| ||||
24 rasqsisnlhwy 36

RESULT 12

Y56654
ID Y56654 standard; protein; 88 AA.

XX AC Y56654;

XX DT 15-FEB-2000 (first entry)

XX DE Partial peptide fragment of chimpanzee V kappa cDNA clone 46-5.

XX KW Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity.

XX OS Pan troglodytes.

XX PN WO9955369-A1.

XX PD 04-NOV-1999.

XX PF 28-APR-1999; 99WO-US09131.

XX PR 28-APR-1998; 98US-0083367.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Taylor AH;

XX DR WPI: 2000-023265/02.

XX DR N-PSDB; 239322.

XX PT Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -

XX PS Claim 22; Page 70-71; 123pp; English.

XX SX The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.

XX SQ Sequence 88 AA;

Query Match 83.3%; Score 60; DB 21; Length 88;

Best Local Similarity 84.6%; Pred. No. 0.0087;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13

Db 24 qasqsisnlyslwy 36

RESULT 13

Y30203

ID Y30203 standard; Protein; 107 AA.

XX AC Y30203;

XX DT 01-NOV-1999 (first entry)

XX DE The variable light chain of humanised antibody F4.

XX KW Light chain variable region; chimeric antibody; anti-CD40 antibody;

KW chi220; humoral immune response; T cell dependent antigen;
KW collagen induced arthritis; transplant induced rejection;
KW T cell mediated disorder; autoimmune disease; inflammatory disease;
KW transplantation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9942075-A2.

XX PD 26-AUG-1999.

XX PF 10-FEB-1999; 99WO-US02949.

XX PR 19-FEB-1998; 98US-0026291.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Aruffo AA, Bejorath J, Berry KK, Harris LJ, Hollenbaugh D;

XX PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;

XX DR WPI: 1999-527408/44.

XX DR N-PSDB; 210203.

XX PT Antibody that binds human CD40, for treating T cell mediated
PT disorders

XX PS Claim 21; Page 32-33; 77pp; English.

XX CC The present sequence represents the variable light chain of humanised
CC antibody F4. The antibody is effective in modulating humoral immune
CC response against T cell dependent antigens, collagen induced arthritis
CC and transplant induced rejection. They are also useful for their
CC anti-inflammatory properties. The antibodies have wide therapeutic
CC applications, including autoimmune and inflammatory diseases and
CC transplantation. The antibody can be used in a pharmaceutical composition
CC for treating a patient suffering from a T cell mediated disorder. They
CC can also be used to treat autoimmune diseases, inflammatory diseases,
CC and transplantation.

XX SQ Sequence 107 AA;

Query Match 83.3%; Score 60; DB 20; Length 107;

Best Local Similarity 76.9%; Pred. No. 0.011;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13

Db 24 rasqsisnlyslwy 36

RESULT 14

Y30205

ID Y30205 standard; Protein; 107 AA.

XX AC Y30205;

XX DT 01-NOV-1999 (first entry)

XX DE The variable light chain of humanised antibody L3.17.

XX KW Light chain variable region; chimeric antibody; anti-CD40 antibody;
KW chi220; humoral immune response; T cell dependent antigen;
KW collagen induced arthritis; transplant induced rejection;
KW T cell mediated disorder; autoimmune disease; inflammatory disease;
KW transplantation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9942075-A2.

PD 26-AUG-1999.
 XX
 PE 10-FEB-1999; 99WO-US02949.
 XX
 PR 19-FEB-1998; 98US-0026291.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;
 PI Huse WD, Sisdak AW, Thorne BA, Watkins JD, Wu H;
 XX
 DR WPI; 1999-527408/44.
 DR N-PSDB; Z10205.
 XX
 PT Antibody that binds human CD40, for treating T cell mediated
 PT disorders
 XX
 PS Claim 26; Page 33-34; 77pp; English.
 CC The present sequence represents the variable light chain of humanised
 CC antibody L3.17. The antibody is effective in modulating humoral immune
 CC response against T cell dependent antigens, collagen induced arthritis
 CC and transplant induced rejection. They are also useful for their
 CC anti-inflammatory properties. The antibodies have wide therapeutic
 CC applications, including autoimmune and inflammatory diseases and
 CC transplantation. The antibody can be used in a pharmaceutical composition
 CC for treating a patient suffering from a T cell mediated disorder. They
 CC can also be used to treat autoimmune diseases, inflammatory diseases,
 CC and transplantation.
 XX
 SQ Sequence 107 AA;

Query Match 83.3%; Score 60; DB 20; Length 107;
 Best Local Similarity 76.9%; Pred. No. 0.011;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 Db :|||||:||||
 24 rasqsisnlhwy 36

RESULT 15
 W00241
 ID W00241 standard; Protein; 108 AA.
 AC
 XX W00241;
 XX
 DT 22-NOV-1996 (first entry)
 XX
 DE EGF receptor chimeric MAb chMint5 VL chain.
 XX
 KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;
 KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
 KW immunotoxin; immunocytokine; tumour; cancer.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..97
 FT /label= CDR3
 XX
 PN W09627010-A1.
 XX
 PD 06-SEP-1996.
 XX
 PF 01-MAR-1996; 96WO-EF00805.
 XX
 PR 01-MAR-1995; 95IT-OFI0036.

XX
 PA (ITU-Y) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
 XX
 PI Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;
 PI Ferrer Marsal C, Mele A;
 XX
 DR WPI; 1996-412776/41.
 DR N-PSDB; T33446.
 XX
 PT Murine/human chimeric monoclonal antibody, chMint5 specific for
 PT EGF-R - shows a lower immunogenicity when administered to humans
 XX
 PS Claim 7; Page 18; 28pp; English.
 XX
 CC The amino acid sequence (W00241) of the light chain variable region
 CC (VL) of the epidermal growth factor receptor (EGF-R)-specific mouse-
 CC human chimeric antibody chMint5 was deduced from a cDNA clone
 CC (T33446) obt'd. by PCR amplification of murine Mint5 hybridoma DSM
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
 CC to human C-gamma1 and CK regions. Constructs were expressed in
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than
 CC Mint5 when administered to humans. It can be used in diagnostic
 CC assays or used to produce immunotoxins or immunocytokines useful
 CC for tumour therapy.
 XX
 SQ Sequence 108 AA;

Query Match 83.3%; Score 60; DB 17; Length 108;
 Best Local Similarity 84.6%; Pred. No. 0.011;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
 Db :|||||:||||
 24 rasqsisnlhwy 36

Search completed: March 28, 2001, 06:59:50
 Job time: 1386 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:55 ; Search time 113.49 Seconds
(without alignments)
2.057 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQISNPLHWY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgnl_7/ptodata/1/iaa/5A-COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B-COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6-COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCTUS-COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	60	83.3	96	2	US-08-737-560A-9
2	60	83.3	108	2	US-08-378-939-20
3	59	81.9	100	1	US-08-436-463-19
4	59	81.9	103	1	US-08-436-463-21
5	59	81.9	107	1	US-07-634-278-62
6	59	81.9	107	1	US-07-634-278-63
7	59	81.9	107	1	US-07-634-278-87
8	59	81.9	107	1	US-08-477-728-62
9	59	81.9	107	1	US-08-477-728-63
10	59	81.9	107	1	US-08-477-728-87
11	59	81.9	107	1	US-08-474-040-62
12	59	81.9	107	1	US-08-474-040-63
13	59	81.9	107	1	US-08-474-040-87
14	59	81.9	107	1	US-08-487-200-62
15	59	81.9	107	1	US-08-487-200-63
16	59	81.9	107	1	US-08-487-200-87
17	59	81.9	127	1	US-07-634-278-83
18	59	81.9	127	1	US-08-477-728-83
19	59	81.9	127	1	US-08-474-040-83
20	59	81.9	127	1	US-08-487-200-83
21	59	81.9	127	1	US-08-436-463-4
22	59	81.9	127	1	US-08-436-463-18
23	58	80.6	107	2	US-08-652-558-36
24	58	80.6	107	2	US-08-378-939-14
25	58	80.6	108	1	US-08-276-852-102
26	58	80.6	108	1	US-08-899-575-102
27	58	80.6	108	1	US-08-899-575-102
28	58	80.6	108	2	US-08-378-939-30

29 58 80.6 108 4 PCT-US95-08743-102 Sequence 102, Appl
30 57 79.2 56 1 US-08-162-102C-40 Sequence 40, Appl
31 57 79.2 108 1 US-08-162-102C-25 Sequence 25, Appl
32 57 79.2 108 2 US-08-737-560A-11 Sequence 11, Appl
33 57 79.2 108 4 PCT-US93-08786-25 Sequence 25, Appl
34 55 76.4 107 1 US-08-436-463-20 Sequence 20, Appl
35 55 76.4 107 1 US-08-107-668D-1 Sequence 1, Appl
36 55 76.4 107 1 US-08-472-788A-1 Sequence 1, Appl
37 55 76.4 107 2 US-08-477-531B-1 Sequence 1, Appl
38 55 76.4 107 2 US-07-934-373C-18 Sequence 18, Appl
39 55 76.4 107 2 US-08-082-842A-1 Sequence 1, Appl
40 55 76.4 107 3 US-08-437-642B-18 Sequence 18, Appl
41 55 76.4 107 4 PCT-US93-07832-18 Sequence 18, Appl
42 55 76.4 108 1 US-08-476-039-85 Sequence 85, Appl
43 55 76.4 108 1 US-08-476-349A-85 Sequence 85, Appl
44 55 76.4 108 3 US-08-974-899-3 Sequence 3, Appl
45 55 76.4 109 1 US-07-942-245-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgu-jung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: VK23.32'CL

US-08-737-560A-9

Query Match 83.3%; Score 60; DB 2; Length 96;
Best Local Similarity 76.9%; Pred. No. 0.0031;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:||||
Db 24 RASQISDYLHWY 36

RESULT 2

US-08-378-939-20
; Sequence 20, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: US 07/952640
; APPLICATION NUMBER: 01-DEC-1992
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-20

Query Match 83.3%; Score 60; DB 2; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.0035;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:||||
Db 24 QASQISNLYLHWY 36

RESULT 3

US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto

; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-19

Query Match 81.9%; Score 59; DB 1; Length 100;
Best Local Similarity 84.6%; Pred. No. 0.0047;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:||||
Db 24 RASQISNNLHWY 36

RESULT 4

US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki

; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,463
;; FILING DATE: 26-JUN-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 341255/1992
;; FILING DATE: 28-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: KIMACHI=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 103 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-436-463-21

Query Match 81.9%; Score 59; DB 1; Length 103;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISISNHLHWY 13
Db 22 RASQISISNHLHWY 34

RESULT 5
US-07-634-278-62
;; Sequence 62, Application US/07634278
;; Patent No. 5530101
;; GENERAL INFORMATION:
;; APPLICANT: QUEEN, Cary L.
;; APPLICANT: CO, Man Sung
;; APPLICANT: SCHNEIDER, William P.
;; APPLICANT: LANDOLFI, Nicholas F.
;; APPLICANT: COELINGH, Kathleen L.
;; APPLICANT: SELICK, Harold E.
;; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
;; NUMBER OF SEQUENCES: 113
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourile and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/634,278
;; FILING DATE: 19-DEC-1990
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M

;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 62:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-634-278-62

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISISNHLHWY 13
Db 24 RASQISISNHLHWY 36

RESULT 6
US-07-634-278-63
;; Sequence 63, Application US/07634278
;; Patent No. 5530101
;; GENERAL INFORMATION:
;; APPLICANT: QUEEN, Cary L.
;; APPLICANT: CO, Man Sung
;; APPLICANT: SCHNEIDER, William P.
;; APPLICANT: LANDOLFI, Nicholas F.
;; APPLICANT: COELINGH, Kathleen L.
;; APPLICANT: SELICK, Harold E.
;; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
;; NUMBER OF SEQUENCES: 113
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourile and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/634,278
;; FILING DATE: 19-DEC-1990
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWHY 13
:|||||
DB 24 RASQSISNFWHY 36

RESULT 7

US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634, 278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590, 274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310, 252
; FILING DATE: 13-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWHY 13
:|||||
DB 24 RASQSISNFWHY 36

RESULT 8

US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWHY 13
:|||||
DB 24 RASQSISNFWHY 36

RESULT 9

US-08-477-728-63
; Sequence 63, Application US/08477728

Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
Db 24 RASQSISNLFHWY 36

RESULT 10
US-08-477-728-87
Sequence 87, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
Db 24 RASQSISNLFHWY 36

RESULT 11
US-08-474-040-62
Sequence 62, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-62

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
:|||||||
Db 24 RASQISNNLHWY 36

RESULT 12
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995

;
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-63

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFHWY 13
:|||||||
Db 24 RASQISNNLHWY 36

RESULT 13
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISISNLFHWY 13
:|||||:|||||
Db 24 RASQISISNLFHWY 36

RESULT 14
US-08-487-200-62
Sequence 62, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISISNLFHWY 13
:|||||:|||||
Db 24 RASQISISNLFHWY 36

RESULT 15
US-08-487-200-63
Sequence 63, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-63

Query Match : 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINLHWY 13
Db :|||||
24 RASQISINLHWY 36

Search completed: March 28, 2001, 07:01:57
Job time: 1336 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:27 ; Search time 130.08 Seconds
(without alignments)
5.742 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSSIS 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	87.8	69	PH1080	Ig light chain V r
2	43	87.8	96	G33730	Ig kappa chain V r
3	43	87.8	104	B43413	Ig kappa chain V r
4	43	87.8	106	PL0267	Ig kappa chain V r
5	43	87.8	107	B45722	anti-glycoprotein
6	43	87.8	107	C45722	anti-glycoprotein
7	43	87.8	107	A45722	anti-glycoprotein
8	43	87.8	115	S10146	Ig kappa chain pre
9	43	87.8	138	A26471	Ig kappa chain pre
10	40	81.6	87	PH1082	Ig light chain V r
11	40	81.6	102	S26346	Ig kappa chain V r
12	40	81.6	108	C30502	Ig kappa chain V r
13	40	81.6	115	1 KVM5L7	Ig kappa chain pre
14	40	81.6	123	S35479	Ig kappa chain pre
15	40	81.6	128	FN0445	Ig kappa chain pre
16	39	79.6	67	PH1081	Ig light chain V r
17	39	79.6	103	S11975	Ig kappa chain V r
18	39	79.6	114	S00996	Ig kappa chain pre
19	37	75.5	500	S56276	probable membrane
20	36	73.5	3344	JQ1899	genome polyprotein
21	35	71.4	613	1 Q0BE33	BBF1 protein - hu
22	35	71.4	847	1 S36337	histidine decarbox
23	33	67.3	406	2 B82147	conserved hypothet
24	33	67.3	459	2 T11256	NADH dehydrogenase
25	33	67.3	598	2 T28238	ORF MSV077 hypothe
26	33	67.3	998	2 T04842	protein kinase hom
27	33	67.3	3125	1 GNVSP	genome polyprotein
28	33	67.3	3140	1 GNVSRA	genome polyprotein
29	33	67.3	3140	2 S47508	genome polyprotein

30 33 67.3 3141 1 GNVSPD genome polyprotein
31 32 65.3 290 2 S26028 NADH dehydrogenase
32 32 65.3 365 2 F82398 transcription regu
33 32 65.3 380 2 B47029 methylase llapi -
34 32 65.3 547 1 D64249 hypothetical prote
35 32 65.3 622 2 S35122 site-specific DNA-
36 32 65.3 912 2 T18785 hypothetical prote
37 32 65.3 944 2 T18911 hypothetical prote
38 32 65.3 1150 2 T13824 LK6 protein kinase
39 32 65.3 1317 2 B83346 probable non-ribos
40 32 65.3 1339 2 H81307 restriction modifi
41 32 65.3 3066 1 JQ1661 genome polyprotein
42 32 65.3 3066 1 JQ1662 genome polyprotein
43 31 63.3 112 2 H82197 transcription repr
44 31 63.3 265 2 H64786 ybcM protein - Esc
45 31 63.3 290 2 S26016 NADH dehydrogenase

ALIGNMENTS

RESULT 1

PH1080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.8%; Score 43; DB 2; Length 69;
Best Local Similarity 81.8%; Pred. No. 0.043;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLIRYSSQSSIS 11
Db 17 LLIRYSSQSSIS 27

RESULT 2

G33730
Ig kappa chain V region (23.32) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: G33730
R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325
A:Accession: G33730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 43; DB 2; Length 96;
Best Local Similarity 81.8%; Pred. No. 0.061;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLIRYSSQSSIS 11

Db 46 LLIKYASQSIS 56
 |||:|:|||||

RESULT 3

Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <ROM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 43; DB 2; Length 104;
 Best Local Similarity 81.8%; Pred. No. 0.066;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 |||:|:|||||

Db 43 LLIKYASQSIS 53

RESULT 4

Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0267
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0267
 A:Molecule type: mRNA
 A:Residues: 1-106 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-106/Region: framework 4

Query Match 87.8%; Score 43; DB 2; Length 106;
 Best Local Similarity 81.8%; Pred. No. 0.068;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 |||:|:|||||

Db 46 LLIKYASQSIS 56

RESULT 5

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833

A:Accession: B45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 43; DB 2; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.068;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 |||:|:|||||

Db 46 LLIKYASQSIS 56

RESULT 6

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: C45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833

A:Accession: C45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 43; DB 2; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.068;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 |||:|:|||||

Db 46 LLIKYASQSIS 56

RESULT 7

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fr
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833

A:Accession: A45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 43; DB 2; Length 107;

Best Local Similarity 81.8%; Pred. No. 0.068; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11

Db 46 LLIKYASQSIS 56

RESULT 8

S10146

Ig kappa chain precursor V region (A14) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000

C:Accession: S10146

R:Straubinger, B.; Thiehe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.

Biol. Chem. Hoppe-Seyler 369, 601-607, 1988

A:Title: Two unusual human immunoglobulin V-kappa genes.

A:Reference number: S00996; MUID:89134397

A:Accession: S10146

A:Molecule type: DNA

A:Residues: 1-115 <STR>

A:Cross-references: EMBL:M27751; NID:g185916; PIDN:AAA58913.1; PID:g185917

A:Note: this sequence was determined from the germline gene

C:Genetics: 17/1

A:introns: 17/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

F:43-108/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 87.8%; Score 43; DB 2; Length 115;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11

Db 66 LLIKYASQSIS 76

RESULT 9

A26471

Ig kappa chain precursor V region (MAK33) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C:Accession: A26471

R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine

A:Reference number: A91572; MUID:87248058

A:Accession: A26471

A:Molecule type: mRNA

A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match

Best Local Similarity 87.8%; Score 43; DB 2; Length 139;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11

Db 66 LLIKYASQSIS 76

RESULT 10

PH1082

Ig kappa chain precursor V region (A14) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PH1082

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1082

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-87 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:6-80/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.6%; Score 40; DB 2; Length 87;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11

Db 36 LLIKYASESIS 46

RESULT 11

S26346

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26346

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a proteol

A:Reference number: S26309; MUID:91341421

A:Accession: S26346

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-102 <STA>

A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.6%; Score 40; DB 2; Length 102;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11

Db 44 LLIKYVSQSIS 54

RESULT 12

C30502

Ig kappa chain V region (D444) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C:Accession: C30502

R:Ellat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1

A:Reference number: A30502; MUID:88315787

A:Accession: C30502

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <EIL>

A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 40; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
|||:|:|:|
Db 46 LLIKYASESIS 56

RESULT 13

KVMSL7
Ig kappa chain precursor V region (L7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999
C:Accession: A01925
R:Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences
A:Reference number: A93259; MUID:81220975
A:Accession: A01925
A:Molecule type: DNA
A:Residues: 1-115 <PEG>
A:Cross-references: GB:J00574; NID:g51718; PIDN:CAA24884.1; PID:g758153
A:Note: the sequence was determined from the germline gene
A:Note: there appear to be two possible splice junctions at the 3' end of the intron; the
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match 81.6%; Score 40; DB 1; Length 115;
Best Local Similarity 72.7%; Pred. No. 0.32;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
|||:|:|:|
Db 66 LLIKYASESIS 76

RESULT 14

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a mouse
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 40; DB 2; Length 123;
Best Local Similarity 81.8%; Pred. No. 0.34;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
|||:|:|:|
Db 58 LLIKYVSQSIS 68

RESULT 15

PN0445
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0445
R:Kaluz, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction
A:Reference number: PN0444; MUID:93138402
A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>
A:Cross-references: GB:L02347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-10/Domain: signal sequence #status predicted <SIG>
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 40; DB 2; Length 128;
Best Local Similarity 72.7%; Pred. No. 0.36;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
|||:|:|:|
Db 56 LLIKYASESIS 66

Search completed: March 28, 2001, 07:04:28
Job time: 1066 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:06 ; Search time 72.95 Seconds
(without alignments)
4.817 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSS11

Scoring table:
BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	81.6	115	1 KV51_MOUSE	P01642 mus musculus
2	37	75.5	500	1 YFJL_YEAST	P43601 saccharomyc
3	36	73.5	3344	1 POLG_PPSVH	Q01901 p genome po
4	35	71.4	613	1 UL06_EBV	P03213 Epstein-bar
5	35	71.4	847	1 DCHS_DROME	Q05733 drosophila
6	33	67.3	459	1 NU4M_CERSI	Q03204 ceratotheri
7	33	67.3	459	1 NU4M_RHIUN	Q96068 rhinoceros
8	33	67.3	1786	1 YCFL_ARATH	P56785 arabidopsis
9	33	67.3	3125	1 POLG_PPVNA	P17766 p genome po
10	33	67.3	3140	1 POLG_PPVRA	P17767 p genome po
11	33	67.3	3140	1 POLG_PPVSK	Q84934 p genome po
12	33	67.3	3141	1 POLG_PPVD	P13529 p genome po
13	32	65.3	547	1 Y447_MYCGE	P47685 mycoplasma
14	32	65.3	622	1 MTLI_LACIA	P35516 lactococcus
15	32	65.3	3066	1 POLG_SBMVG	Q90069 s genome po
16	31	63.3	265	1 YBCM_ECOLI	P77634 escherichia
17	31	63.3	290	1 NU1M_ASCSU	P24875 ascaris suu
18	31	63.3	348	1 ABRB_ECOLI	P75747 escherichia
19	31	63.3	453	1 RADA_PSEAE	P96963 pseudomonas
20	31	63.3	542	1 CBPY_CANAL	P30574 candida alb
21	31	63.3	686	1 KNLC_STRPU	Q05090 strongyloce
22	31	63.3	717	1 PAL1_PPUAV	O64963 prunus aviu
23	30	61.2	161	1 YD03_MYCTU	Q10619 mycobacteri
24	30	61.2	185	1 YCXB_BACSU	Q08793 bacillus su
25	30	61.2	332	1 GALR_HAEIN	P31766 haemophilus
26	30	61.2	376	1 PHAE_BORPE	Q00879 bordetella
27	30	61.2	582	1 HEX3_ADE12	P36712 human adeno
28	30	61.2	585	1 HEX3_ADE02	P03279 human adeno
29	30	61.2	585	1 HEX3_ADE05	P12537 human adeno
30	30	61.2	1014	1 CINI_YEAST	P40987 saccharomyc
31	30	61.2	1209	1 THR_DROME	P42286 drosophila
32	30	61.2	1366	1 CA21_HUMAN	P08123 homo sapien
33	29	59.2	145	1 VPRE_HUMAN	P12018 homo sapien

```
RESULT 1
KV51_MOUSE 155 59.2 1 CRT_CLODI P45361 clostridium
AC P01642; 258 59.2 1 TPIS_STRCO Q92320 streptomyce
DT 21-JUL-1986 (Rel. 01, Created) 313 59.2 1 FLGJ_ECOLI P75942 escherichia
DT 21-JUL-1986 (Rel. 01, Last sequence update) 419 59.2 1 MURA_ACICA P33986 acinetobact
DT 15-JUL-1999 (Rel. 38, Last annotation update) 437 59.2 1 MURD_HAEIN P45063 haemophilus
DE IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT). 503 59.2 1 YPTJ_CAEEL Q23469 caenorhabd1
OS Mus musculus (Mouse). 646 59.2 1 GYRB_MYCGA P47720 mycoplasma
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 673 59.2 1 FXR2_HUMAN P51116 homo sapien
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 689 59.2 1 KEJC_DROME Q04652 drosophila
RN [1] 981 59.2 1 YM48_YEAST Q12751 saccharomyc
RP SEQUENCE FROM N.A. 1032 59.2 1 VG07_BPT4 P19061 bacterioph
RX MEDLINE; 81220975. 1070 59.2 1 YHVA_YEAST P38850 saccharomyc
RA Pech M., Hochel J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RL Nature 291:668-670(1981).
CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR: A01925; KVM5U7.
DR INTERPRO: IPR003006;
DR PFAM: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 59 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;
```

ALIGNMENTS

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Query Match 81.6%; Score 40; DB 1; Length 115;
Best Local Similarity 72.7%; Pred. No. 0.1;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSS11
Db 66 LLIRYSSQSS11

RESULT 2
YFJL_YEAST 500 AA.
ID YFJL_YEAST STANDARD; PRT;
AC P43601;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 55.1 KDA PROTEIN IN FABI-PES4 INTERGENIC REGION.
GN YFRO21W.
```

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OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RC MEDLINE; 93400292.
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RL Nat. Genet. 10:261-268(1995).
CC -1- SIMILARITY: TO YEAST YGR223C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D50617; BAA09260.1; -
CC SGD; S0001917; YFR021W.
CC INTERPRO; IPR001680; -
CC PFAM; PF00400; WD40; 2.
CC Hypothetical protein.
CC SEQUENCE 500 AA; 55102 MW; 06B2DFAF842AE933 CRC64;
CC -----
Query Match 75.5%; Score 37; DB 1; Length 500;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LIRYSSOSIS 11
DB 378 MIRYSQKLS 387
-----
RESULT 3
POLG_PRSVH STANDARD; PRT; 3344 AA.
AC Q01901;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPEPTIDE [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Papaya ringspot virus (strain P / mutant HA).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RN SEQUENCE FROM N.A.
RX Wang C.H., Bau H.J., Yeh S.D.;
RT "Comparison of the nuclear inclusion b protein and coat protein genes
RT of five papaya ringspot virus strains distinct in geographic origin
RT and pathogenicity."
RL Phytopathology 84:1205-1210(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE; 93019006.
RA Yeh S.D., Jan F.J., Chiang C.H., Doong T.J., Chen M.C.,
RA Chun P.H., Bau H.J.;
RT "Complete nucleotide sequence and genetic organization of papaya
RT ringspot virus RNA."
RL J. Gen. [redacted] 73:2531-2541(1992).
RN [3]

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RP SEQUENCE OF 2561-3344 FROM N.A.
RX MEDLINE; 93090098.
RT Wang C.H., Yeh S.D.;
RT "Nucleotide sequence comparison of the 3'-terminal regions of severe,
RT mild, and non-papaya infecting strains of papaya ringspot virus.";
RL Arch. Virol. 127:345-354(1992).
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
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CC -----
CC EMBL; X67673; CAA47905.1; -
CC EMBL; S46722; AAB23789.1; -
CC EMBL; X67672; CAA47904.1; -
CC PIR; S24785; S24785.
CC INTERPRO; IPR001205; -
CC INTERPRO; IPR001456; -
CC INTERPRO; IPR001592; -
CC INTERPRO; IPR001730; -
CC INTERPRO; IPR002540; -
CC PFAM; PF00863; Peptidase_C4; 1.
CC PFAM; PF00851; Peptidase_C6; 1.
CC PFAM; PF01577; Poty_P1; 1.
CC PFAM; PF00767; Poty_coat; 1.
CC PFAM; PF00680; RNA_dep_RNA_pol; 1.
CC PRINTS; PR00966; NIAPOTYPPTASE.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 -529
FT CHAIN 530 1149
FT CHAIN 1150 ?
FT CHAIN ? 1401
FT CHAIN 1402 2036
FT CHAIN 2037 2093
FT CHAIN 2094 ?
FT CHAIN ? 2520
FT CHAIN 2521 3037
FT CHAIN 3038 3344
FT BINDING 2156 2156
FT NP_BIND 1486 1493
SQ SEQUENCE 3344 AA; 381040 MW; E90CD7523AC5243D CRC64;
-----
Query Match 73.5%; Score 36; DB 1; Length 3344;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LIRYSSOSIS 11
DB 1737 MIRYSQKQIS 1746

```


SQ SEQUENCE 459 AA; 51719 MW; F25C961D11EC5DPE CRC64;

Query Match 67.3%; Score 33; DB 1; Length 459;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSI 10
 |||:||||:
 Db 177 LLIQYSTQTL 186

RESULT 7
 NUAM_RHIUN STANDARD; PRT; 459 AA.
 AC Q96088;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
 GN MTNDA OR NDA OR NADH4
 OS Rhinoceros unicornis (Greater Indian rhinoceros).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Rhinoceros.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE; 97051708.
 RA Xu X., Janke A., Arnason U.;
 RT "The complete mitochondrial DNA sequence of the greater Indian rhinoceros, Rhinoceros unicornis, and the Phylogenetic relationship among Carnivora, Perissodactyla, and Artiodactyla (+ Cetacea).";
 RL Mol. Biol. Evol. 13:1167-1173(1996).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -----
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 CC -----
 CC EMBL; X97336; CAA66010.1; -;
 DR INTERPRO; IPR000260; -;
 DR INTERPRO; IPR001750; -;
 DR PFAM; PF00361; oxidored_q1; 1.
 DR PFAM; PF01059; oxidored_q5_N; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 459 AA; 51888 MW; 77EF396801AEC3DB CRC64;

Query Match 67.3%; Score 33; DB 1; Length 459;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSI 10
 |||:||||:
 Db 177 LLIQYSTQTL 186

RESULT 8
 YCF1_ARATH STANDARD; PRT; 1786 AA.
 AC P56785;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 213.7 KDA PROTEIN YCF1.
 GN YCF1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Chloroplast.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsals.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
 RT "Complete structure of the chloroplast genome of Arabidopsis thaliana";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: NOT YET KNOWN.
 CC -1- SIMILARITY: TO A SIMILAR ORF IN OTHER PLANTS CHLOROPLAST.
 CC -----
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 CC -----
 CC EMBL; AP000423; BAA84445.1; -;
 DR EMBL; AP000423; BAA84433.1; -;
 KW Chloroplast; Hypothetical protein.
 SQ SEQUENCE 1786 AA; 213727 MW; CFFD2A4D776D7E5D CRC64;

Query Match 67.3%; Score 33; DB 1; Length 1786;
 Best Local Similarity 87.5%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSQS 9
 |||||:
 Db 670 LIRYSQS 677

RESULT 9
 POLG_PPVNA STANDARD; PRT; 3125 AA.
 AC P17766;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN (EC 3.4.22.-) (49 KDA PROTEINASE) (CI); 6 KDA PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA) (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)).
 DE Plum pox potyvirus (isolate NAT) (PPV).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89279232.
 RA Maiss E., Timpe U., Briske A., Jekmann W., Casper R., Himmeler G.,
 RA Mattanovich D., Katinger H.W.D.;
 RT "The complete nucleotide sequence of plum pox virus RNA.";
 RL J. Gen. Virol. 70:513-524(1989).
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT MAY BE INVOLVED IN REPLICATION.
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D13751; BAA02898.1; -;
 DR PIR; JQ0003; GNVSP.
 DR INTERPRO: IPR001205; -;
 DR INTERPRO: IPR001410; -;
 DR INTERPRO: IPR001456; -;
 DR INTERPRO: IPR001592; -;
 DR INTERPRO: IPR001730; -;
 DR INTERPRO: IPR002540; -;
 DR PFAM; PF00270; DEAD; 1;
 DR PFAM; PF00863; Peptidase_C4; 1;
 DR PFAM; PF00851; Peptidase_C6; 1;
 DR PFAM; PF01577; Poty_P1; 1;
 DR PFAM; PF00767; Poty_coat; 1;
 DR PFAM; PF00680; RNA_dep_RNA_pol; 1;
 DR PRINTS; PR00966; NIAPOTVPTASE.
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 301 N-TERMINAL PROTEIN.
 FT CHAIN 302 914 HELPER COMPONENT PROTEINASE.
 FT CHAIN 915 ? PROTEIN P3.
 FT CHAIN ? 1168 6 KDA PROTEIN 1.
 FT CHAIN 1169 1803 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1804 1856 6 KDA PROTEIN 2.
 FT CHAIN 1857 ? GENOME-LINKED PROTEIN.
 FT CHAIN ? 2292 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2293 2810 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 2811 3125 COAT PROTEIN.
 FT BINDING 1919 1919 COVALENT LINKAGE OF VIRAL RNA (BY
 FT NP_BIND 1253 1260 ATP (POTENTIAL)).
 FT SEQUENCE 3125 AA; 354261 MW; ED0DD33C439CB712 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3125;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRVSSQIS 11
 I::I::I::I
 Db 1504 LVRYTKKSIS 1513

RESULT 10
 POLG_PPVRA STANDARD; PRT; 3140 AA.
 ID AC P17767;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
 DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
 DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NTA)
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
 DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
 DE COAT PROTEIN (CP)].
 OS Plum pox potyvirus (strain Rankovic) (PPV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 [1]

RN SEQUENCE FROM N.A.
 RX MEDLINE; 89370814.
 RA Lain S., Riechmann J.L., Garcia J.A.;

RT "The complete nucleotide sequence of plum pox potyvirus RNA.";
 RL Virus Res. 13:157-172(1989).
 RN [2]
 RP SEQUENCE OF 1778-2342 FROM N.A.
 RX MEDLINE; 89268456.
 RA Garcia J.A., Riechmann J.L., Lain S.;
 RT "Proteolytic activity of the plum pox potyvirus N1a-like protein in
 RT Escherichia coli.";
 RL Virology 170:362-369(1989).
 RN [3]
 RP SEQUENCE OF 2263-3140 FROM N.A.
 RA Lain S., Riechmann J.L., Mendez E., Garcia J.A.;
 RT "Nucleotide sequence of the 3' terminal region of plum pox potyvirus
 RT RNA.";
 RL Virus Res. 10:325-342(1988).
 CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M21847; AAA85458.1; -;
 DR EMBL; M26965; AAA47085.1; -;
 DR PIR; A60009; GNVSR.
 DR INTERPRO: IPR001205; -;
 DR INTERPRO: IPR001410; -;
 DR INTERPRO: IPR001456; -;
 DR INTERPRO: IPR001592; -;
 DR INTERPRO: IPR001730; -;
 DR INTERPRO: IPR002540; -;
 DR PFAM; PF00270; DEAD; 1;
 DR PFAM; PF00863; Peptidase_C4; 1;
 DR PFAM; PF00851; Peptidase_C6; 1;
 DR PFAM; PF01577; Poty_P1; 1;
 DR PFAM; PF00767; Poty_coat; 1;
 DR PFAM; PF00680; RNA_dep_RNA_pol; 1;
 DR PRINTS; PR00966; NIAPOTVPTASE.
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 301 N-TERMINAL PROTEIN.
 FT CHAIN 302 914 HELPER COMPONENT PROTEINASE.
 FT CHAIN 915 ? PROTEIN P3.
 FT CHAIN ? 1168 6 KDA PROTEIN 1.
 FT CHAIN 1169 1803 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1804 1856 6 KDA PROTEIN 2.
 FT CHAIN 1857 ? GENOME-LINKED PROTEIN.
 FT CHAIN ? 2292 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2293 2810 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 2811 3140 COAT PROTEIN.
 FT BINDING 1919 1919 COVALENT LINKAGE OF VIRAL RNA (BY
 FT NP_BIND 1253 1260 ATP (POTENTIAL)).
 FT SEQUENCE 3140 AA; 355577 MW; 5F3DBB07982CF3F5 CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3140;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQIS 11
 :||: :|||
 Db 1504 LVRVTKKIS 1513

RESULT 11
 POLG_PPVSQ STANDARD; PRT; 3140 AA.
 AC Q84934; (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
 COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
 DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
 DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
 DE COAT PROTEIN (CP)].
 OS Plum pox polyvirus (strain SK 68) (PPV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.

[1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 94167908.
 RA Palkovics L., Burgyn J., Balazs E.;
 RT "Comparative sequence analysis of four complete primary structures of
 RT plum pox virus strains.";
 RL Virus Genes 7:339-347(1993).
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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 CC EMBL: M92280; AAB05823.1; -
 DR INTERPRO: IPR001205; -
 DR INTERPRO: IPR001410; -
 DR INTERPRO: IPR001456; -
 DR INTERPRO: IPR001592; -
 DR INTERPRO: IPR001730; -
 DR INTERPRO: IPR002540; -
 DR PFAM: PF00270; DEAD; 1.
 DR PFAM: PF00863; Peptidase_C4; 1.
 DR PFAM: PF00851; Peptidase_C6; 1.
 DR PFAM: PF01577; Poty_P1; 1.
 DR PFAM: PF00767; Poty_coat; 1.
 DR PFAM: PF00680; RNA_dep_RNA_pol; 1.
 DR PRINTS: PR00966; NIAPOTYPASE.
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 KW APP-binding.

 FT CHAIN 1 301 N-TERMINAL PROTEIN.
 FT CHAIN 302 914 HELPER COMPONENT PROTEINASE.
 FT CHAIN 915 ? PROTEIN P3.
 FT CHAIN ? 1168 6 KDA PROTEIN 1.

FT CHAIN 1169 1803 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1804 1856 6 KDA PROTEIN 2.
 FT CHAIN 1857 ? GENOME-LINKED PROTEIN.
 FT CHAIN ? 2292 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2293 2810 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 2811 3140 COAT PROTEIN.
 FT BINDING 1919 COVALENT LINKAGE OF VIRAL RNA (BY
 SIMILARITY).
 FT NP_BIND 1253 1260 ATP (POTENTIAL).
 SQ SEQUENCE 3140 AA; 355992 MW; 837A5A692B56436A CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3140;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LIRYSSQIS 11
 :||: :|||
 Db 1504 LVRVTKKIS 1513

RESULT 12
 POLG_PPVD STANDARD; PRT; 3141 AA.
 AC P13529; O84929; P89038;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
 COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
 DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
 DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
 DE COAT PROTEIN (CP)].
 OS Plum pox polyvirus (strain D) (PPV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.

[1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 90098790.
 RA Teycheney P.Y., Taveret G., Delbos R., Raveionandro M., Dunez J.;
 RT "The complete nucleotide sequence of plum pox virus RNA (strain D).";
 RL Nucleic Acids Res. 17:10115-10116(1989).
 RN [2]
 RN SEQUENCE OF 2810-3141 FROM N.A., AND SEQUENCE OF 2812-2828.
 RA Raveionandro M., Varveri C., Delbos R., Dunez J.;
 RT "Nucleotide sequence of the capsid protein gene of plum pox
 RT potyvirus";
 RL J. Gen. Virol. 69:1509-1516(1988).
 RN [3]
 RN REVISIONS TO C-TERMINUS.
 RA le Gall O.;
 RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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CC  EMBL; X16415; CAA34437.1; -.
CC  EMBL; D00298; BAA00210.1; -.
CC  PIR; S06929; GNVSPD.
DR  PIR; JA0078; JA0078.
DR  INTERPRO; IPR001205; -.
DR  INTERPRO; IPR001410; -.
DR  INTERPRO; IPR001456; -.
DR  INTERPRO; IPR001592; -.
DR  INTERPRO; IPR001730; -.
DR  INTERPRO; IPR002540; -.
DR  PFM; PF00270; DEAD; 1.
DR  PFM; PF00863; Peptidase_C4; 1.
DR  PFM; PF00851; Peptidase_C6; 1.
DR  PFM; PF01577; Poty_P1; 1.
DR  PFM; PF00767; Poty_coat; 1.
DR  PFM; PF00680; RNA_dep_RNA_pol; 1.
DR  PRINTS; PR00966; NIAPOTPTASE.
KW  Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW  Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW  ATP-binding.
FT  CHAIN 1 301 N-TERMINAL PROTEIN.
FT  CHAIN 302 915 HELPER COMPONENT PROTEINASE.
FT  CHAIN 916 ? 6 KDA PROTEIN 1.
FT  CHAIN ? 1169 PROTEIN P3.
FT  CHAIN 1170 1804 CYTOPLASMIC INCLUSION PROTEIN.
FT  CHAIN 1805 1857 6 KDA PROTEIN 2.
FT  CHAIN 1858 ? GENOME-LINKED PROTEIN.
FT  CHAIN ? 2293 NUCLEAR INCLUSION PROTEIN A.
FT  CHAIN 2294 ? 2811 NUCLEAR INCLUSION PROTEIN B.
FT  CHAIN 2812 3141 COAT PROTEIN.
FT  BINDING 1920 1920 COVALENT LINKAGE OF VIRAL RNA (BY
FT  NP_BIND 1254 1261 SIMILARITY).
FT  SEQUENCE 3141 AA; 355569 MW; 6C3641C404414DBB CRC64;

Query Match 67.3%; Score 33; DB 1; Length 3141;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LIRYSSQSI 11
Db 1505 LVRYTKKSIS 1514

RESULT 13
Y447_MYCGE
ID Y447_MYCGE STANDARD; PRT; 547 AA.
AC P47685;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL PROTEIN MG447.
GN MG447.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE; 96026346.
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]

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SEQUENCE OF 107-215 FROM N.A.  

  STRAIN=ATCC 33530 / G-37;  

  MEDLINE; 94075230.  

  RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;  

  RT "A survey of the Mycoplasma genitalium genome by using random  

  sequencing.";  

  RL J. Bacteriol. 175:7918-7930(1993).  

  CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  

  CC -----  

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  CC -----  

  CC EMBL; U39726; AAC72467.1; -;  

  CC EMBL; U39731; AAB01637.1; -;  

  CC EMBL; U01788; AAD10610.1; -;  

  CC TIGR; MG447; -;  

  CC INTERPRO; IPR002528; -;  

  CC PFM; PF01554; UPF0013; 1.  

  KW Hypothetical protein; Transmembrane.  

  FT TRANSMEM 33 53 POTENTIAL.  

  FT TRANSMEM 107 127 POTENTIAL.  

  FT TRANSMEM 145 165 POTENTIAL.  

  FT TRANSMEM 203 223 POTENTIAL.  

  FT TRANSMEM 231 251 POTENTIAL.  

  FT TRANSMEM 263 283 POTENTIAL.  

  FT TRANSMEM 298 318 POTENTIAL.  

  FT TRANSMEM 351 371 POTENTIAL.  

  FT TRANSMEM 397 417 POTENTIAL.  

  FT TRANSMEM 432 452 POTENTIAL.  

  FT TRANSMEM 470 490 POTENTIAL.  

  FT TRANSMEM 499 519 POTENTIAL.  

  FT SEQUENCE 547 AA; 62052 MW; E6D115C419A2E81B CRC64;

Query Match 65.3%; Score 32; DB 1; Length 547;  

Best Local Similarity 60.0%; Pred. No. 30;  

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LIRYSSQSI 10
Db 249 LVRYSSSLGV 258

RESULT 14
MTLL_LACLA
ID MTLL_LACLA STANDARD; PRT; 622 AA.
AC P35516;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE MODIFICATION METHYLASE LLAI (EC 2.1.1.72) (ADENINE-SPECIFIC  

DE METHYLTRANSFERASE LLAI) (M.LLAI).  

OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  

OC Plasmid pTR2030.  

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  

OC Lactococcus.  

RN [1]  

RP SEQUENCE FROM N.A.  

RX MEDLINE; 91294179.  

RA Hill C., Miller L.A., Klaenhammer T.R.;  

RT "In vivo genetic exchange of a functional domain from a type II A  

RT methylase between lactococcal plasmid pTR2030 and a virulent  

RT bacteriophage.";  

RL J. Bacteriol. 173:4363-4370(1991).  

CC -!- FUNCTION: METHYLATION OF SPECIFIC ADENINE RESIDUES; REQUIRED FOR  

CC BOTH RESTRICTION AND MODIFICATION ACTIVITIES. MAY RECOGNIZE A  

CC NONPALINDROMIC SEQUENCE.  

CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE =


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CC S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPURINE.
 CC -1- SIMILARITY: CONTAINS TWO COPIES OF A SEGMENT OF FOUR AMINO ACIDS
 CC WHICH IS CHARACTERISTIC OF ADENINE-SPECIFIC METHYLASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U17233; AAA65073.1; -
 CC PIR; A47029; A47029.
 CC REBASE; RB01188; L1A1.
 CC INTERPRO; IPR002052; -
 CC INTERPRO; IPR002294; -
 CC PFAM; PF02086; Methyltransf12; 2.
 CC PRINTS; PR00505; D12NM7FRASE.
 CC PROSITE; PS00092; N6_MTASE; 1.
 CC Transferase; Methyltransferase; Restriction system; Repeat; Plasmid.
 CC SEQUENCE 622 AA; 72512 MW; 69A817F46BE9C772 CRC64;
 CC -----
 CC Query Match 65.3%; Score 32; DB 1; Length 622;
 CC Best Local Similarity 60.0%; Pred. No. 35;
 CC Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 LLRYSSQSI 10
 CC :|:|:|:|
 CC Db 281 VLVSYSNQS 290
 CC -----
 CC RESULT 15
 CC POLG_SBMVG STANDARD; PRT; 3066 AA.
 CC ID POLG_SBMVG STANDARD; PRT; 3066 AA.
 CC AC Q90069;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
 CC DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (PI); HELPER
 CC COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
 CC 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
 CC DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
 CC (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
 CC DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
 CC DE COAT PROTEIN (CP)].
 CC OS Soybean mosaic virus (strain G2) (SMV).
 CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 CC OC Potyvirus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE; 92356085.
 CC RA Jayaram C., Hill J.H., Miller W.A.;
 CC RT "Complete nucleotide sequences of two soybean mosaic virus strains
 CC differentiated by response of soybean containing the Rsv resistance
 CC gene.";
 CC RL J. Gen. Virol. 73:2067-2077(1992).
 CC CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION
 CC CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S42280; CAB28008.1; -
 CC INTERPRO; IPR001205; -
 CC INTERPRO; IPR001410; -
 CC INTERPRO; IPR001456; -
 CC INTERPRO; IPR001592; -
 CC INTERPRO; IPR001650; -
 CC INTERPRO; IPR001730; -
 CC INTERPRO; IPR002540; -
 CC PFAM; PF00270; DEAD_1;
 CC PFAM; PF00863; Peptidase_C4; 1.
 CC PFAM; PF00851; Peptidase_C6; 1.
 CC PFAM; PF01577; Poty_P1; 1.
 CC PFAM; PF00767; Poty_coat; 1.
 CC PFAM; PF00680; RNA_dep_RNA_pol; 1.
 CC PFAM; PF00271; helicase_C1;
 CC PRINTS; PR00966; NIAPOTYPTASE.
 CC KW Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 CC KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 CC KW ATP-binding.
 CC FT CHAIN 1 ? N-TERMINAL PROTEIN.
 CC FT CHAIN ? ? HELPER COMPONENT PROTEINASE.
 CC FT CHAIN ? ? PROTEIN P3.
 CC FT CHAIN ? ? 6 KDA PROTEIN 1.
 CC FT CHAIN ? ? CYTOPLASMIC INCLUSION PROTEIN.
 CC FT CHAIN ? ? 6 KDA PROTEIN 2.
 CC FT CHAIN ? ? GENOME-LINKED PROTEIN.
 CC FT CHAIN ? ? NUCLEAR INCLUSION PROTEIN A.
 CC FT CHAIN ? ? NUCLEAR INCLUSION PROTEIN B.
 CC FT CHAIN ? 3066 COAT PROTEIN.
 CC FT NP_BIND 1249 1256 ATP (POTENTIAL).
 CC SQ SEQUENCE 3066 AA; 349538 MW; 2188A79DBD155399 CRC64;
 CC -----
 CC Query Match 65.3%; Score 32; DB 1; Length 3066;
 CC Best Local Similarity 55.6%; Pred. No. 2e+02;
 CC Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 3 IRYSSQSI 11
 CC :|:|:|:|:|
 CC Db 1501 VRYNKQSVS 1509

Search completed: March 28, 2001, 07:35:09

Job time: 146 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:11 ; Search time 443.95 Seconds
(without alignments)
2.904 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSI 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	71.4	675	10 Q9M0X5	Q9M0X5 arabidopsis
2	35	71.4	847	5 Q9V5I3	Q9V5I3 drosophila
3	35	71.4	3344	12 P90213	P90213 papaya ring
4	34	69.4	141	2 Q9KEA6	Q9KEA6 bacillus ha
5	34	69.4	3056	12 Q65892	Q65892 bean yellow
6	33	67.3	132	10 Q9SMA8	Q9SMA8 oryza sativ
7	33	67.3	406	2 Q9KQW4	Q9KQW4 vibrio chol
8	33	67.3	422	2 Q9KXB5	Q9KXB5 escherichia
9	33	67.3	422	9 Q9XJL2	Q9XJL2 bacterioph
10	33	67.3	598	12 Q9YWL5	Q9YWL5 melanoplus
11	33	67.3	684	10 Q9SBC6	Q9SBC6 arabidopsis
12	33	67.3	998	10 Q9SVG2	Q9SVG2 arabidopsis
13	33	67.3	3140	12 Q84925	Q84925 plum pox po
14	33	67.3	3140	12 Q9PYF0	Q9PYF0 plum pox vi
15	32	65.3	163	3 O13291	O13291 arthroderma
16	32	65.3	225	10 Q9M063	Q9M063 arabidopsis
17	32	65.3	262	8 Q9XMU4	Q9XMU4 tetrahymena
18	32	65.3	365	2 Q9KL23	Q9KL23 vibrio chol
19	32	65.3	428	5 O18656	O18656 brugia mala

20	32	65.3	545	10 Q9ZQ32	Q9ZQ32 arabidopsis
21	32	65.3	912	5 Q17532	Q17532 caenorhabdi
22	32	65.3	944	5 Q9XVFI	Q9XVFI caenorhabdi
23	32	65.3	1000	5 Q9V540	Q9V540 drosophila
24	32	65.3	1037	10 Q9SIP2	Q9SIP2 arabidopsis
25	32	65.3	1090	5 Q9VGI5	Q9VGI5 drosophila
26	32	65.3	1115	4 Q9ULL0	Q9ULL0 homo sapien
27	32	65.3	1142	5 Q9VGI4	Q9VGI4 drosophila
28	32	65.3	1150	5 Q94548	Q94548 drosophila
29	32	65.3	1250	2 Q9JN06	Q9JN06 campylobact
30	32	65.3	1339	2 Q9PNP0	Q9PNP0 campylobact
31	32	65.3	3066	12 Q9IBP2	Q9IBP2 soybean mos
32	31	63.3	112	2 Q34419	Q34419 vibrio chol
33	31	63.3	235	10 Q9XHF3	Q9XHF3 zea mays (m
34	31	63.3	254	5 Q44877	Q44877 caenorhabdi
35	31	63.3	283	2 Q9RA04	Q9RA04 rhodococcus
36	31	63.3	297	5 Q22171	Q22171 caenorhabdi
37	31	63.3	326	12 Q96718	Q96718 chlorella v
38	31	63.3	345	10 Q9LY23	Q9LY23 arabidopsis
39	31	63.3	363	5 Q16921	Q16921 caenorhabdi
40	31	63.3	379	10 Q23457	Q23457 arabidopsis
41	31	63.3	402	2 Q9KP98	Q9KP98 vibrio chol
42	31	63.3	424	4 Q9UH98	Q9UH98 homo sapien
43	31	63.3	428	3 Q13817	Q13817 schizosacch
44	31	63.3	435	11 Q9QZE2	Q9QZE2 mus musculu
45	31	63.3	435	11 Q9JMJ3	Q9JMJ3 mus musculu

ALIGNMENTS

RESULT 1
Q9M0X5 PRELIMINARY; PRT; 675 AA.
AC Q9M0X5;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE RECEPTOR PROTEIN KINASE-LIKE PROTEIN.
GN AT4G05200.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vill D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dadhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL161503; CAB81062.1; -
KW Kinase
SQ SEQUENCE 675 AA; 75348 MW; 8F4525263199CDE8 CRC64;

Query Match 71.4%; Score 35; DB 10; Length 675;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLIRYSSQSI 10
:::|::|::|
Db 126 MVRYSNQSI 134

RESULT 2
Q9V5I3 PRELIMINARY; PRT; 847 AA.
ID Q9V5I3

AC Q9V513;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HDC PROTEIN.
 GN HDC.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003830; AAF58623.1;
 DR FLYBASE; FBgn0005619; Hdc.
 DR INTERPRO: IPR002129;
 DR PFAM: PF00282; pyridoxal_dec; 1.
 DR PRINTS; PR00800; VHDCRBOXLASE.
 DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
 SQ SEQUENCE 847 AA; 94035 MW; C04F32F01C176951 CRC64;

Query Match 71.4%; Score 35; DB 5; Length 847;
 Best Local Similarity 81.8%; Pred. No. 55;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLRYSSQSIS 11

Db 762 LLRYSSQSIS 772

RESULT 3
 P90213

ID P90213 PRELIMINARY; PRT; 3344 AA.
 AC P90213;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PRSV YK POLYPROTEIN.
 OS Papaya ringspot virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=12205;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YK FROM TAIWAN;
 RL Wang C.H., Yeh S.D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X97251; CAA65886.1;
 DR MEROPS; C04.001;
 DR MEROPS; C06.001;
 DR MEROPS; S30.001;
 DR INTERPRO: IPR001205;
 DR INTERPRO: IPR001254;
 DR INTERPRO: IPR001410;
 DR INTERPRO: IPR001456;
 DR INTERPRO: IPR001592;
 DR INTERPRO: IPR001650;
 DR INTERPRO: IPR001730;
 DR INTERPRO: IPR002540;
 DR PFAM; PF00271; helicase_C; 1.
 DR PFAM; PF00680; RNA_dep_RNA_pol; 1.
 DR PFAM; PF00767; Poty_coat; 1.
 DR PFAM; PF00851; Peptidase_C6; 1.
 DR PFAM; PF00863; Peptidase_C4; 1.
 DR PFAM; PF01577; Poty_P1; 1.
 DR PRINTS; PR00966; NIAPOTYPTASE.
 KW Polyprotein.
 SQ SEQUENCE 3344 AA; 380584 MW; 7BFF421E092C4E85 CRC64;
 Query Match 71.4%; Score 35; DB 12; Length 3344;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LIRYSSQSIS 11
 Db 1737 MIRYSQAVS 1746
 RESULT 4
 ID Q9KEA6 PRELIMINARY; PRT; 141 AA.
 AC Q9KEA6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE BH0947 PROTEIN.
 GN BH0947.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RA Takami H., Nakasone K., Takaki Y.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP001510; BAB04666.1;
 SQ SEQUENCE 141 AA; 15618 MW; 58C490C4A57D201A CRC64;

Query Match 69.4%; Score 34; DB 2; Length 141;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 LLRYSSQS 9
Db 23 LLRYFSQS 31

RESULT 5
Q65892 PRELIMINARY; PRT; 3056 AA.
AC Q65892;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE POLYPROTEIN.
OS Bean yellow mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RA Nakamura S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1679-3056 FROM N.A.
RC STRAIN=MB4;
RA Nakamura S., Honkura R., Ugaki M., Ohshima M., Ohashi Y.;
RT "Nucleotide sequence of the 3'-terminal region of bean yellow mosaic
RT virus RNA and resistance to viral infection in transgenic Nicotiana
RT benthamiana expressing its coat protein gene.";
RL Ann. Phytopathol. Soc. Jpn. 60:295-304(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RA Nakamura S., Honkura R., Iwai T., Ugaki M., Ohashi Y.;
RT "The complete nucleotide sequence of bean yellow mosaic virus genomic
RT RNA.";
RL Ann. Phytopathol. Soc. Jpn. 62:472-477(1996).
DR EMBL; D83749; BAA12099.1; -.
DR MEROPS; C04.001; -.
DR MEROPS; C06.001; -.
DR MEROPS; S30.001; -.
DR INTERPRO; IPR001205; -.
DR INTERPRO; IPR001254; -.
DR INTERPRO; IPR001410; -.
DR INTERPRO; IPR001456; -.
DR INTERPRO; IPR001592; -.
DR INTERPRO; IPR001730; -.
DR INTERPRO; IPR002540; -.
DR PFAM; PF00270; DEAD; 1.
DR PFAM; PF00680; RNA_dep_RNA_pol; 1.
DR PFAM; PF00767; Poty_coat; 1.
DR PFAM; PF00851; Peptidase_C6; 1.
DR PFAM; PF00863; Peptidase_C4; 1.
DR PFAM; PF01577; Poty_PL; 1.
DR PRINTS; PR00966; NIAPOTYPASE.
KW Polyprotein.
SQ SEQUENCE 3056 AA; 347574 MW; AFFBEOB50F12D9CF CRC64;

Query Match 69.4%; Score 34; DB 12; Length 3056;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLRYSSQS 11
Db 1478 LLRYTQSVS 1487

RESULT 6
Q9SMA8 PRELIMINARY; PRT; 132 AA.
ID Q9SMA8
AC Q9SMA8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE ZWH0001.1 (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. INDICA;
RA Hong G., Zhao W.;
RT "Oryza sativa genomic DNA, chromosome 4, clone: b6015.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117264; CAB55385.1; -.
FT NON_TER 1
SQ SEQUENCE 132 AA; 14829 MW; 480E20C36B16AD0C CRC64;

Query Match 67.3%; Score 33; DB 10; Length 132;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLRYSSQS 11
Db 101 LLRYQSRVS 111

RESULT 7
Q9KQW4 PRELIMINARY; PRT; 406 AA.
ID Q9KQW4
AC Q9KQW4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE HYPOTHETICAL PROTEIN VC1884.
GN VC1884.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RL Nature 406:477-483(2000).
DR EMBL; AE004263; AAF95032.1; -.
DR TIGR; VC1884; -.
SQ SEQUENCE 406 AA; 43747 MW; 4879D14D30442588 CRC64;

Query Match 67.3%; Score 33; DB 2; Length 406;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLRYSSQS 11
Db 216 LLRYDAQTIS 225

RESULT 8
Q9KXB5 PRELIMINARY; PRT; 422 AA.
ID Q9KXB5
AC Q9KXB5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

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DT 01-OCT-2000 (TREMBLrel..15, Last annotation update)
DE HYPOTHETICAL 45.5 KDA PROTEIN.
GN H0141.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7;
RA Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kimura S.,
RA Kurokawa K., Ishii K., Hattori M., Tatsuno I., Abe H., Iida T.,
RA Yamamoto K., Onishi M., Hayashi T., Yasunaga T., Honda T.,
RA Sasakawa C., Shinagawa H.;
RT "Complete nucleotide sequence of the prophage VT2-Sakai carrying the
RT verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
RT derived from the Sakai outbreak.";
RL Genes Genet. Syst. 74:227-239(1999).
DR EMBL; AF000422; BAA94169.1; -.
KW Hypothetical protein.
SQ SEQUENCE 422 AA; 45496 MW; 146BB1299BE985B0 CRC64;

Query Match 67.3%; Score 33; DB 2; Length 422;
Best Local Similarity 60.0%; Pred. NO. 72;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 10
Db 387 LTIRYSNQNV 396

RESULT 9
Q9XJL2 PRELIMINARY; PRT; 422 AA.
AC Q9XJL2;
DT 01-NOV-1999 (TREMBLrel..12, Created)
DT 01-NOV-1999 (TREMBLrel..12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel..13, Last annotation update)
DE HYPOTHETICAL 45.5 KDA PROTEIN.
GN L0125.
OS Bacteriophage 933W, and Bacteriophage VT2-Sa.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA phages.
OX NCBI_TaxID=10730, 97081;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RX MEDLINE=99173898; PubMed=10074068;
RA Plunkett G., III, Rose D.J., Durfee T.J., Blattner F.R.;
RT "Sequence of Shiga toxin 2 phage 933W from Escherichia coli O157:H7;
RT Shiga toxin as a phage late-gene product.";
RL J. Bacteriol. 181:1767-1778(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RA Plunkett G., III;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
RT "Sequence analysis of Stx2-Converting phage VT2-Sa shows a great
RT divergence in early regulation and replication regions.";
RL DNA Res. 6:235-240(1999).
DR EMBL; AF125520; AAD25468.1; -.
DR EMBL; AF000363; BAA84345.1; -.
KW Hypothetical protein.

SQ SEQUENCE 422 AA; 45496 MW; 146BB1299BE985B0 CRC64;

Query Match 67.3%; Score 33; DB 2; Length 422;
Best Local Similarity 60.0%; Pred. NO. 72;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 10
Db 387 LTIRYSNQNV 396

RESULT 9
Q9XJL2 PRELIMINARY; PRT; 422 AA.
AC Q9XJL2;
DT 01-NOV-1999 (TREMBLrel..12, Created)
DT 01-NOV-1999 (TREMBLrel..12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel..13, Last annotation update)
DE HYPOTHETICAL 45.5 KDA PROTEIN.
GN L0125.
OS Bacteriophage 933W, and Bacteriophage VT2-Sa.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA phages.
OX NCBI_TaxID=10730, 97081;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RX MEDLINE=99173898; PubMed=10074068;
RA Plunkett G., III, Rose D.J., Durfee T.J., Blattner F.R.;
RT "Sequence of Shiga toxin 2 phage 933W from Escherichia coli O157:H7;
RT Shiga toxin as a phage late-gene product.";
RL J. Bacteriol. 181:1767-1778(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RA Plunkett G., III;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
RT "Sequence analysis of Stx2-Converting phage VT2-Sa shows a great
RT divergence in early regulation and replication regions.";
RL DNA Res. 6:235-240(1999).
DR EMBL; AF125520; AAD25468.1; -.
DR EMBL; AF000363; BAA84345.1; -.
KW Hypothetical protein.

SQ SEQUENCE 422 AA; 45496 MW; 146BB1299BE985B0 CRC64;

Query Match 67.3%; Score 33; DB 2; Length 422;
Best Local Similarity 60.0%; Pred. NO. 72;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 10
Db 387 LTIRYSNQNV 396

RESULT 10
Q9YWL5 PRELIMINARY; PRT; 598 AA.
AC Q9YWL5;
DT 01-MAY-1999 (TREMBLrel..10, Created)
DT 01-MAY-1999 (TREMBLrel..10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel..10, Last annotation update)
DE ORF MSV077 HYPOTHETICAL PROTEIN.
GN MSV077.
OS Melanoplus sanguinipes entomopoxvirus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=83191;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUCSON;
RX MEDLINE=99102612; PubMed=9847359;
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
RL J. Virol. 73:533-552(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TUCSON;
RX Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063866; AAC97632.1; -.
SQ SEQUENCE 598 AA; 70312 MW; A52B887D6A451FFF CRC64;

Query Match 67.3%; Score 33; DB 12; Length 598;
Best Local Similarity 54.5%; Pred. NO. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 11
Db 563 ILVRYASQIFS 573

RESULT 11
Q9SBC6 PRELIMINARY; PRT; 684 AA.
AC Q9SBC6;
DT 01-MAY-2000 (TREMBLrel..13, Created)
DT 01-MAY-2000 (TREMBLrel..13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel..14, Last annotation update)
DE RECEPTOR-LIKE PROTEIN KINASE.
GN RKCI.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Ohtake Y., Takahashi T., Komeda Y.;
RT "Expression analysis of Arabidopsis thaliana genes encoding receptor-
RT like protein kinases.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF084037; AAC95354.1; -.
DR INTERPRO; IPR000719; -.

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DR INTERPRO: IPR001245; -
 DR INTERPRO: IPR002290; -
 DR INTERPRO: IPR002902; -
 DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF01657; DUF26; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Kinase.
 SQ SEQUENCE 684 AA; 76080 MW; 1AD4A6025FC8756D CRC64;

Query Match 67.3%; Score 33; DB 10; Length 684;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQSIS 11
 I:||||:|
 DB 123 LVRYSNKSF 132

RESULT 12
 Q9SVG2 PRELIMINARY; PRT; 998 AA.

AC Q9SVG2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PROTEIN KINASE-LIKE PROTEIN.
 GN F21P8.140 OR AT4G23250.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

SEQUENCE FROM N.A.
 RA Bevan M., Massenet O., Clabault G., Quigley F., Mache R., Bancroft I.,
 RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

[2]
 SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

[3]
 SEQUENCE FROM N.A.
 RA Massenet O., Clabault G., Quigley F., Mache R., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
 SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL022347; CAA18472.1; -
 DR EMBL: AL161559; CAB79280.1; -

DR HSSP: P00523; 2PTK
 DR INTERPRO: IPR000719; -
 DR INTERPRO: IPR002290; -

DR PFAM: PF00069; pkinase; 1.
 DR PFAM: PF01657; DUF26; 2.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 KW Kinase.

SQ SEQUENCE 998 AA; 111644 MW; 7F6BBFD7A572B924 CRC64;

Query Match 67.3%; Score 33; DB 10; Length 998;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQSIS 11
 I:||||:|
 DB 123 LVRYSNKSF 132

RESULT 13
 Q84925 PRELIMINARY; PRT; 3140 AA.

AC Q84925;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE COAT PROTEIN (FRAGMENTIS).

OS Plum pox potyvirus (strain SK 68) (PPV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=103927;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN-DERIVED FROM SOUR CHERRY MAINTAINED ON NICOTIANA CLEVELANDII;
 RA Maiss E., Deborre G., Jekmann W., Casper R.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL: X81083; CAA56974.1; -
 DR INTERPRO: IPR001254; -

DR INTERPRO: IPR001410; -
 DR INTERPRO: IPR001730; -

DR PRINTS: PR00966; NIAPOTYPTASE.
 KW Coat protein.

FT CHAIN 1 >308 P1.
 FT NON_CONS 308 309 HCPR.

FT CHAIN 309 >766
 FT NON_CONS 766 767 P3.

FT CHAIN 767 >1116
 FT NON_CONS 1116 1117 6K1.

FT CHAIN 1117 >1168
 FT NON_CONS 1168 1169 CI.

FT CHAIN 1169 >1803
 FT NON_CONS 1803 1804 6K2.

FT CHAIN 1804 >1856
 FT NON_CONS 1856 1857 VPG.

FT CHAIN 1857 >2049
 FT CHAIN 1857 >2292 NIA.

FT CHAIN 2292 2293 NIB.
 FT CHAIN 2293 >2810

FT NON_CONS 2810 2811 COAT PROTEIN.
 FT CHAIN 2811 >3140

FT NON_TER 3140 3140
 SQ SEQUENCE 3140 AA; 355547 MW; F18674C2EFBB8598 CRC64;

Query Match 67.3%; Score 33; DB 12; Length 3140;
 Best Local Similarity 60.0%; Pred. No. 5.5e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQSIS 11
 I:||||:|
 DB 1504 LVRYTKKSIS 1513

RESULT 14
 Q9PYF0 PRELIMINARY; PRT; 3140 AA.

AC Q9PYF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE POLYPROTEIN.
 OS Plum pox virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=12211;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M;
 RA Saenz P., Cervera M., Dallot S., Quiot L., Quiot J.B., Riechmann J.,
 RA Garcia J.;
 RT Identification of a plum pox potyvirus pathogenicity determinant in
 RT the sequence encoding the carboxyl terminal region of protein P3.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243957; CAB51641.1; -
 DR INTERPRO: IPR001205; -
 DR INTERPRO: IPR001254; -
 DR INTERPRO: IPR001410; -
 DR INTERPRO: IPR001456; -
 DR INTERPRO: IPR001592; -
 DR INTERPRO: IPR001730; -
 DR INTERPRO: IPR002540; -
 DR PFAM; PF00680; RNA_dep_RNA_pol; 1.
 DR PFAM; PF00767; Poty_coat; 1.
 DR PFAM; PF00851; Peptidase_C6; 1.
 DR PFAM; PF00863; Peptidase_C4; 1.
 DR PFAM; PF01577; Poty_P1; 1.
 DR PRINTS; PR00966; NIAPOTYPTASE.
 KW Polyprotein.
 FT CHAIN 1 308 P1 PROTEIN.
 FT CHAIN 309 766 HC PROTEIN.
 FT CHAIN 767 1116 P3 PROTEIN.
 FT CHAIN 1117 1168 6K1 PROTEIN.
 FT CHAIN 1169 1803 CI PROTEIN.
 FT CHAIN 1804 1856 6K2 PROTEIN.
 FT CHAIN 1857 2292 N1A PROTEIN.
 FT CHAIN 2293 2810 N1B PROTEIN.
 FT CHAIN 2811 3140 COAT PROTEIN.
 SQ SEQUENCE 3140 AA; 355670 MW; 25AB3502E7DBC6C6 CRC64;

Query Match 67.3%; Score 33; DB 12; Length 3140;
 Best Local Similarity 60.0%; Pred. No. 5.5e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSOSIS 11

DB 1504 LVRTRKSIS 1513

RESULT 15
 013291
 ID 013291 PRELIMINARY; PRT; 163 AA.
 AC 013291;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CHITIN SYNTHASE 1.
 OS Arthroderma persicolor.
 OC Eukaryota; Fungi; Ascomycota; Onygenales; Arthrodermataceae;
 OC Arthroderma.
 OX NCBI_TaxID=65487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VUT-77160;
 RA Kano R., Nakamura Y., Watari T., Watanabe S., Takahashi H.,
 RA Tsujimoto H., Hasegawa A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB006983; BAA22260.1; -
 DR INTERPRO: IPR002923; -
 DR PFAM; PF01644; Chitin_synth; 1.
 DR PRODOM; PD002998; -; 1.
 SQ SEQUENCE 163 AA; 18124 MW; A9ADD249AFBBB46 CRC64;

Query Match 65.3%; Score 32; DB 3; Length 163;
 Best Local Similarity 77.8%; Pred. No. 45;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IRYSSOSIS 11

1111111

DB 108 IRYSSFSVS 116

Search completed: March 28, 2001, 07:53:18
 Job time: 511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:50 ; Search time 154.19 Seconds
(without alignments)
2.439 Million cell updates/sec

Title: US-09-016-061-84
Perfect score: 49
Sequence: 1 LLIRYSSQSSIS 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*
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2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
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5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
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8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
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21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	11	W76032	LM609 grafted anti
2	44	89.8	11	W76012	LM609 grafted anti
3	43	87.8	88	Y56553	Partial peptide fr
4	43	87.8	105	W87456	JK gene product.
5	43	87.8	105	W87458	Humanised anti- α p
6	43	87.8	106	R41234	Monoclonal antibod
7	43	87.8	107	R25729	Humanised VL regio
8	43	87.8	107	R38601	HYH light chain.
9	43	87.8	107	W58482	Murine HYH antibod
10	43	87.8	107	W84098	Humanised anti- α p
11	43	87.8	108	W04333	Light chain of mon
12	43	87.8	108	W84094	Murine vitronectin

13	43	87.8	109	15	R52033	Light chain variab
14	43	87.8	109	20	Y06380	Murine monoclonal
15	43	87.8	112	20	W84100	Vitronectin alpha-
16	43	87.8	127	15	R54093	Sequence of mouse
17	43	87.8	128	21	Y56718	Amino acid sequenc
18	41	83.7	107	19	W76002	Vitaxin antibody 11
19	41	83.7	107	19	W76004	LM609 antibody lig
20	40	81.6	104	19	W26795	Anti-gp54 MAb 48-1
21	40	81.6	106	19	W71241	Light chain variab
22	40	81.6	107	14	R32129	Anti-IL2R beta ant
23	40	81.6	107	14	R37612	hIL2R Ab L chain v
24	40	81.6	107	14	R37610	B-B10 MAb L chain
25	40	81.6	107	15	R50190	Light chain variab
26	40	81.6	107	18	W08948	Kappa light chain
27	40	81.6	107	20	Y26979	Light chain variab
28	40	81.6	107	21	Y70604	Vkappa region of h
29	40	81.6	108	17	W00241	EGF receptor chime
30	40	81.6	127	15	R50187	Light chain variab
31	40	81.6	127	15	R50191	Light chain variab
32	40	81.6	127	15	R50192	Light chain variab
33	40	81.6	127	18	W08945	Kappa light chain
34	40	81.6	127	18	W08946	Kappa light chain
35	40	81.6	127	18	W08941	Kappa light chain
36	40	81.6	127	18	W08943	Kappa light chain
37	40	81.6	127	20	Y26980	Light chain variab
38	40	81.6	127	20	Y26981	Light chain variab
39	40	81.6	127	20	Y26982	Light chain variab
40	40	81.6	239	14	R34511	Fv(TU25). Homo sa
41	40	81.6	240	17	W05133	Single chain antib
42	40	81.6	240	19	W71243	scFv comprising he
43	40	81.6	240	19	W26799	Anti-gp54 MAb 48-1
44	40	81.6	245	21	Y70605	scFv fragment of h
45	40	81.6	651	17	W05135	scFv(225)-ETA fus1

ALIGNMENTS

RESULT 1

W76032
ID W76032 standard; Protein; 11 AA.
XX
AC W76032;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR2 protein fragment #2.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49869.

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIRYSQSIS 11
 |||||
 Db 1 llirysqsis 11

RESULT 2
 W76012
 ID W76012 standard; Protein; 11 AA.
 AC W76012;
 DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-L region CDR2 protein fragment #1.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49849.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Disclosure; Page 40; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 11 AA;

Query Match 89.8%; Score 44; DB 19; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0032;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LLIRYSQSIS 11
 |||||
 Db 1 llirysqsis 11

RESULT 3
 Y56653
 ID Y56653 standard; protein; 88 AA.
 XX
 AC Y56653;
 XX

DT 15-FEB-2000 (first entry)
 XX
 DE Partial peptide fragment of chimpanzee V kappa cDNA clone 46-4.
 XX
 KW Complementarity determining region; antibody; primate; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity.
 XX
 OS Pan troglodytes.
 XX
 PN WO9955369-A1.
 XX

PD 04-NOV-1999.
 XX
 PF 28-APR-1999; 99WO-US09131.
 XX
 PR 28-APR-1998; 98US-0083367.
 XX

PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Taylor AH;
 XX

DR WPI; 2000-023265/02.
 DR N-PSDB; Z39321.
 XX

PT Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -
 XX
 PS Claim 22; Page 70; 123pp; English.

XX
 CC The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.
 XX

SQ Sequence 88 AA;

Query Match 87.8%; Score 43; DB 21; Length 88;
 Best Local Similarity 81.8%; Pred. No. 0.062; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 0;

QY 1 LLIRYSQSIS 11
 |||:|:||||
 Db 46 llikyasqsis 56

RESULT 4

W87456
 ID W87456 standard; Protein; 105 AA.
 XX
 AC W87456;
 XX
 XX 15-MAR-1999 (first entry)
 DT
 DE Jk gene product.
 XX
 XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI; Jk protein.
 XX
 XX Mus sp.
 OS
 XX W09840488-A1.
 PN
 XX 17-SEP-1998.
 PD
 XX 12-MAR-1998; 98WO-US04987.
 PF
 XX 12-MAR-1997; 97US-0039609.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Johanson KO, Jonak ZL, Taylor AH;
 PI
 XX WPI; 1999-034590/03.
 DR
 XX N-PSDB; V71803.
 DR
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 XX Example 14; Page 66; 97pp; English.
 PS
 XX This polypeptide is encoded by a Jk synthetic gene segment (see
 CC W71803). It was utilising in novel D12H2LCREI humanised light chain
 CC variable region (see W87458), which comprises a human REI framework
 CC and complementarity determining regions from the anti-human alpha-v
 CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the 'alpha-v beta-3 vitronectin receptor, e.g. restenosis
 CC and angiogenic associated diseases.
 XX
 XX Sequence 105 AA;

Query Match 87.8%; Score 43; DB 20; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.076; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 0;

QY 1 LLIRYSQSIS 11
 |||:|:||||
 Db 46 llikyasqsis 56

RESULT 5

W87458

ID W87458 standard; Protein; 105 AA.
 XX
 AC W87458;
 XX
 XX 15-MAR-1999 (first entry)
 DT
 DE Humanised anti-alpha-v beta-3 MAB D12H2LCREI VL.
 XX
 XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX W09840488-A1.
 PN
 XX 17-SEP-1998.
 PD
 XX 12-MAR-1998; 98WO-US04987.
 PF
 XX 12-MAR-1997; 97US-0039609.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Johanson KO, Jonak ZL, Taylor AH;
 PI
 XX WPI; 1999-034590/03.
 DR
 XX N-PSDB; V71805.
 DR
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 XX Example 14; Page 68-69; 97pp; English.
 PS
 XX This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2LCREI. It is based on a synthetic
 CC humanised kappa chain based on a modified human REI kappa
 CC framework and complementarity determining regions from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see W84094). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.
 XX
 XX Sequence 105 AA;

Query Match 87.8%; Score 43; DB 20; Length 105;
 Best Local Similarity 81.8%; Pred. No. 0.076;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 |||:|:||||
 Db 46 llikyasqsis 56

RESULT 6
 ID R41234 standard; Protein; 106 AA.
 XX
 AC R41234;
 XX
 DT 18-MAR-1994 (first entry)
 XX
 DE Monoclonal antibody BW2121 V-gene light chain coding region.
 XX
 KW Monoclonal antibody; tumour; melanoma; ss.
 XX
 OS Mus musculus.
 XX
 PN EP561183-A.
 XX
 PD 22-SEP-1993.
 XX
 PF 25-FEB-1993; 93EP-0102895.
 XX
 PR 19-MAR-1992; 92DE-4208795.
 XX
 PA (BEHW) BEHRINGWERKE AG.
 XX
 PI Bosslet K, Dippold W, Seemann G;
 XX
 DR WPI: 1993-296513/38.
 DR N-PSDB; Q48766.
 XX
 PT Hybridoma 2121 (dsm acc 2036) and monoclonal antibody BW 2121 -
 PT specifically bind to gangliosides GD3 and GQ1B, useful for prodn.
 PT and diagnosis of melanoma or tumours expressing GD3 and GQ1B
 XX
 PS Claim 2; Page 6; 9pp; German.
 XX
 CC The monoclonal antibody BW2121 can be used for the detection of
 CC melanomas and other tumours expressing GD3 and GQ1b. The monoclonal
 CC antibody may also be used as part of a pharmaceutical composition or
 CC diagnostic kit.
 XX
 SQ Sequence 106 AA;

Query Match 87.8%; Score 43; DB 14; Length 106;
 Best Local Similarity 81.8%; Pred. No. 0.077; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 0;

QY 1 LLIRYSSQSIS 11
 |||:|||||
 Db 46 llikysesis 56

RESULT 7
 ID R25729 standard; Protein; 107 AA.
 XX
 AC R25729;
 XX
 DT 13-JAN-1993 (first entry)
 XX
 DE Humanised VL region of the mouse CMV5 antibody.
 XX
 KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW 9H; light chain; variable region; framework; human; wol.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "CDR"
 FT Region 50..56
 FT /note= "CDR"
 FT Region 89...97

FT Misc-difference /note= "CDR"
 FT 49
 FT /note= "mutated residue"
 XX
 PN WO9211018-A.
 XX
 PD 09-JUL-1992.
 XX
 PF 19-DEC-1991; 91WO-US09711.
 XX
 PR 19-DEC-1990; 90US-0634278.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Co MS, Coellingh KL, Landolfi NF, Queen CL, Schneider WP;
 XX
 DR WPI: 1992-249842/30.
 XX
 CC New immunoglobulin(s) having murine CDRs in human framework
 CC regions - have lower antigenicity; useful for treating e.g. HSV,
 CC CMV, T-cell disorders, myeloid disorders and auto-immune
 CC conditions
 XX
 PS Claim 40; Fig 27A; 141pp; English.
 XX
 CC The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human Wol framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the gH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant
 CC DNA and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also R25721-32.
 XX
 SQ Sequence 107 AA;

Query Match 87.8%; Score 43; DB 13; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.078;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
 |||:|||||
 Db 46 llikysqsis 56

RESULT 8
 R38601
 ID R38601 standard; peptide; 107 AA.
 XX
 AC R38601;
 XX
 DT 28-OCT-1993 (first entry)
 XX
 DE HYH light chain.
 XX
 KW Antibody; variable domain; light; L; heavy; H; consensus;
 KW affinity; antigen; immunogenicity; humanisation; framework.
 XX
 OS Homo sapiens.
 XX
 PN WO9311794-A.
 XX
 PD 24-JUN-1993.
 XX
 PF 14-DEC-1992; 92WO-US10906.
 XX
 PR 13-DEC-1991; 91US-0808464.
 XX
 PA (XOMA) XOMA CORP.

XX Fishwild DM, Kohn FR, Little RG, Studnicka GM;
XX WPI: 1993-213827/26.
XX Antibodies prepn. used for treatment of auto-immune diseases - by
XX replacement of critical residues to reduce immunogenicity but
XX retain binding affinity, etc.
XX Disclosure: Page 84; 160pp; English.
XX The amino acid sequences of the light and heavy chains of the
XX variable domains from antibodies HYH [HYHEI-10 Fab-lysozyme complex]
XX (R38601 and R38608, respectively), MCPC [Iga Fab MCP603-phosphocholine
XX complex] (R38602-03 and R38609-10, respectively), NEWN [Ig Fab' NEW]
XX (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
XX R38612, respectively) may be used to determine an alignment from which
XX appropriate changes may be made.
XX Unlike other methods of humanisation, which advocate the
XX replacement of entire antibody framework regions with those of human
XX antibodies, this method involves only the introduction of human
XX residues into those positions not critical for antigen binding.
XX This ensures that the binding properties of the modified antibody
XX are not diminished.
XX Sequence 107 AA;

Query Match 87.8%; Score 43; DB 14; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.078;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 llikyasqsis 56
|||:|||||

RESULT 9
W58482
ID W58482 standard; protein; 107 AA.
AC W58482;
XX 18-AUG-1998 (first entry)
XX Murine HVH antibody light chain variable domain.
XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
XX depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
XX autoimmune disease; rheumatoid arthritis; type I diabetes.
XX Mus sp.
XX US5770196-A.
XX 23-JUN-1998.
XX 07-JUN-1995; 95US-0472788.
XX 23-JUN-1993; 93US-0082842.
XX 13-DEC-1991; 91US-0808464.
XX 14-DEC-1992; 92WO-US10906.
XX 07-JUN-1995; 95US-0472788.
XX (XOMA) XOMA CORP.
XX Studnicka GM;
XX WPI: 1998-376744/32.
XX Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
XX with humanised variable regions

PS Disclosure: Column 43-44; 77pp; English.
XX A method has been developed of depleting CD5+ cells in an animal. The
XX method comprises administering a cytotoxic protein containing a modified
XX immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
XX molecule or an immunoconjugate or fusion protein containing an anti-CD5
XX Ig molecule, and where the modified Ig variable domain comprises at
XX least one of (a) a modified light chain variable region (see W58478 or
XX W58480), and (b) a modified heavy chain variable region (see W58479 or
XX W58481), where W58478 and W58479 are humanised forms of the H65 light
XX and heavy chain variable domains with low risk amino acid substitutions
XX [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
XX W58481 are humanised forms of the H65 light and heavy chain variable
XX domains with moderate risk amino acid substitutions and are present in
XX humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
XX treating autoimmune diseases, especially systemic lupus erythematosus,
XX rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
XX represents the murine HVH antibody light chain variable domain.
XX Sequence 107 AA;

Query Match 87.8%; Score 43; DB 19; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.078;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 llikyasqsis 56
|||:|||||

RESULT 10
W84098
ID W84098 standard; protein; 107 AA.
XX W84098;
XX 15-MAR-1999 (first entry)
XX Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL.
XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
XX cancer; metastasis; rheumatoid arthritis; atherosclerosis;
XX angiogenesis; diabetic retinopathy; inflammation;
XX macular degeneration; osteoporosis; Paget's disease;
XX hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
XX D12HZHC-10.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Region 24..34
XX /label= CDR1
XX Region 50..56
XX /label= CDR2
XX Region 89..97
XX /label= CDR3
XX WO9840488-A1.
XX 17-SEP-1998.
XX 12-MAR-1998; 98WO-US04987.
XX 12-MAR-1997; 97US-0039609.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Johanson KO, Jonak ZL, Taylor AH;
XX WPI: 1999-034590/03.

DR N-PSDB; V71800.
 XX New anti alpha v beta 3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Claim 2; Page 61-62; 97pp; English.
 XX
 CC This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence
 CC (see W84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions (CDRs) from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see W84095). 3 Murine framework residues (1, 49 and 60)
 CC are retained. The humanised light chain can be expressed in host
 CC cells using nucleic acid molecules (see V71800) of the invention.
 CC Humanised D12 VH is also provided (see W84097). The humanised
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
 CC angiogenic-related disorders, such as angiogenesis associated
 CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
 CC inflammatory disorders, macular degeneration, rheumatoid arthritis
 CC and cancer, e.g. solid tumour metastasis, and diseases where bone
 CC resorption is associated with pathology such as osteoporosis,
 CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.
 XX
 SQ Sequence 107 AA;

Query Match 87.8%; Score 43; DB 20; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.078;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
 |||:|:||||
 Db 46 llikyasqsis 56

RESULT 11
 W04333
 ID W04333 standard; peptide; 108 AA.
 AC W04333;

DT 23-JUN-1997 (first entry)

DE Light chain of monoclonal antibody 4B4-1-1.

XX Antibody; human; heavy chain; variable region; light chain; MAb; 4-1BB;
 KW tumour necrosis factor receptor; membrane protein; accessory molecule;
 KW T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;
 KW immunosuppressive agent; autoimmune disease; rejection response; therapy;
 KW organ transplantation.

OS Synthetic.

XX Key Location/Qualifiers
 FH Region 24..34
 FT Region /note= "complementarity determining region 1"
 FT Region 50..56
 FT Region /note= "complementarity determining region 2"
 FT Region 89..97
 FT Region /note= "complementarity determining region 3"

XX W09632495-A1.

XX 17-OCT-1996.

XX

PF 06-APR-1996; 96WO-KR00045.
 XX
 PR 08-APR-1995; 95KR-0008176.
 XX
 PA (GLDS) LG CHEM LTD.
 XX
 PI Kang CY, Kim JG;
 XX
 DR WPI; 1996-477145/47.
 DR N-PSDB; T38510.
 XX
 CC Monoclonal antibody specific for human 4-1BB - useful as
 CC immunospecific agent for treating autoimmune diseases and preventing
 CC organ transplant rejection
 PT
 PT
 XX Claim 2; Page 23; 37pp; English.
 PS
 XX
 CC W04332 and W04333 represent fragments of the variable regions of the
 CC heavy and light chains of the antibody of the invention. This sequence is
 CC encoded by nucleotides 1 to 324 of the coding sequence shown in T38510.
 CC The antibody of the invention (designated 4B4-1-1) is a monoclonal
 CC antibody (MAb) specific for human 4-1BB. 4-1BB encodes a member of the
 CC tumour necrosis factor receptor family of integral membrane proteins.
 CC 4-1BB is an accessory molecule expressed on the surface of T-cells in the
 CC initial stage of activation. The accessory molecules on the T-cell bind
 CC to the corresponding ligand on the antigen-presenting cell and this
 CC accelerates the activation of the T- and antigen-presenting cells,
 CC thereby promoting various immune responses. The MAb is specific for human
 CC 4-1BB, which is selectively expressed on activated T-cells. The MAb is
 CC useful as an immunosuppressive agent. It can be used for the treatment of
 CC autoimmune diseases, such as rheumatoid arthritis, and for preventing
 CC rejection response after organ transplantation.
 XX
 SQ Sequence 108 AA;

Query Match 87.8%; Score 43; DB 17; Length 108;
 Best Local Similarity 81.8%; Pred. No. 0.079;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
 |||:|:||||
 Db 46 llikyasqsis 56

RESULT 12
 W84094
 ID W84094 standard; Protein; 108 AA.
 AC W84094;

DT 15-MAR-1999 (first entry)

DE Murine vitronectin alpha-v beta-3 receptor MAB VL region.

XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX Mus sp. Location/Qualifiers
 OS Key 24..34
 FH Region /label= CDR1
 FT Region 50..56
 FT Region /label= CDR2
 FT Region 89..97
 FT Region /label= CDR3

XX W09840488-A1.

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XX PD 17-SEP-1998.
XX PF 12-MAR-1998; 98WO-US04997.
XX PR 12-MAR-1997; 97US-0039609.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Johanson KO, Jonak ZL, Taylor AH;
XX DR WPI; 1999-034590/03.
XX DR N-PSDB; V71798.
XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX PT immunotherapeutic treatment of e.g. diabetic retinopathy,
XX PT inflammatory disorders, atherosclerosis, restenosis, cancers or
XX PT osteoporosis
XX PS Example 13; Page 59-60; 97pp; English.
XX CC This is the amino acid sequence of the light chain variable region
XX CC (VL) of the anti-human alpha-v beta-3 vitronectin receptor murine
XX CC monoclonal antibody D12, as deduced from isolated cDNA (see
XX CC W71798). D12 VH (see W84093) and VL show sequence similarity to
XX CC Kabat VH subgroup I (see W84095) and Kabat VL subgroup III (see
XX CC W84096), respectively. Humanised VH (see W84097) and VL (see
XX CC W84098) were constructed by combining the framework regions of the
XX CC human V region consensus sequences with complementarity determining
XX CC regions of D12 (keeping some preferred murine framework residues).
XX CC The humanised antibodies are specifically reactive with the human
XX CC alpha-v beta-3 protein receptor and capable of neutralising the
XX CC receptor. They can be used for passive immunotherapy of a disorder
XX CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
XX CC disorders or angiogenic-related disorders, such as angiogenesis
XX CC associated with diabetic retinopathy, atherosclerosis and
XX CC restenosis, chronic inflammatory disorders, macular degeneration,
XX CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
XX CC diseases where bone resorption is associated with pathology such as
XX CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
XX CC of malignancy, osteolytic lesions produced by bone metastasis, bone
XX CC loss due to immobilisation or sex hormone deficiency. They can also
XX CC be used for targeted drug therapy, and for detection and diagnosis.
XX SQ Sequence 108 AA;

Query Match 87.8%; Score 43; DB 20; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.079;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
DB 46 LLIKYASQSIS 56

RESULT 13
R52033
ID R52033 standard; Protein; 109 AA.
XX AC R52033;
XX XX
XX 26-SEP-1996 (first entry)
XX DE Light chain variable region of murine antibody 3Hfm.
XX KW antibody; humanised; murine; human; heavy chain; light; variable;
XX KW framework region; complementarity determining region; reshaping;
XX KW modelling; surface residue; modify.
XX OS Mus sp.
XX XX
XX FH Key Location/Qualifiers

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ET Region 1..23
FT /label= framework_region_1
FT /note= "FR 1"
FT 24..34
FT /label= complementarity_determining_region_1
FT /note= "CDR 1"
FT 35..49
FT /label= FR_2
FT 50..56
FT /label= CDR_2
FT 57..88
FT /label= FR_3
FT 89..97
FT /label= CDR_3
FT 98..109
FT /label= FR_4
XX EP592106-A1.
XX PD 13-APR-1994.
XX PF 07-SEP-1993; 93EP-0307051.
XX PR 09-SEP-1992; 92US-0942245.
XX PA (PEDE/) PEDERSEN J T.
XX PA (IMMU-) IMMUNOGEN INC.
XX PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
XX WPI; 1994-120230/15.
XX DR Method of resurfacing of rodent antibodies to produce humanised
XX PT antibody forms - for producing non-human antibodies with improved
XX PT therapeutic efficiency by presenting human surface on V-region
XX PS Example 1; Fig 3A; 230pp; English.
XX CC The present sequence is that of the light chain variable (LC VR) region
XX CC of murine antibody 3Hfm. This sequence was aligned with 11 other known
XX CC antibody LC VRs and a set of framework positions of surface exposed amino
XX CC acid residues was determined. This information can be used in a method to
XX CC determine how to modify a rodent antibody or fragment by resurfacing in
XX CC order to produce a humanised rodent antibody. Residues (determined from
XX CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
XX CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
XX CC combinations of surface residues in the murine sequences were found in
XX CC the human sequences and vice versa. However the residues in individual
XX CC positions appear to be conserved.
XX SQ Sequence 109 AA;

Query Match 87.8%; Score 43; DB 15; Length 109;
Best Local Similarity 81.8%; Pred. No. 0.08;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
DB 46 LLIKYASQSIS 56

RESULT 14
Y06380
ID Y06380 standard; Protein; 109 AA.
XX AC Y06380;
XX XX
XX 06-SEP-1999 (first entry)
XX DE Murine monoclonal antibody LM609 V lambda.
XX KW Humanised antibody; antibody humanisation; antibody engineering;

```


KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.
 XX

OS Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 24..34
 FT /note= "CDR1"
 FT Region 50..56
 FT /note= "CDR2"
 FT Region 89..97
 FT /note= "CDR3"

XX WO9929888-A1.

PN 17-JUN-1999.

PD 04-DEC-1998; 98WO-US25828.

PF 05-DEC-1997; 97US-0986016.

PR (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

DR Production of humanized mouse monoclonal antibodies

PT Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V lambda region of

CC murine monoclonal antibody LM609. LM609 is directed to integrin

CC alpha-v beta-3. It selectively promotes apoptosis of vascular

CC cells that have been stimulated to undergo angiogenesis, making it

CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized

CC antibodies, a light chain CDR from a mouse antibody such as LM609 is

CC grafted onto a human light chain, and a heavy chain CDR from a mouse

CC antibody is grafted onto a human antibody heavy chain to produce

CC libraries from which a humanised murine antibody having the desired

CC specificity is selected. By preserving the original CDR sequences

CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the

CC humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

SQ

Query Match 87.8%; Score 43; DB 20; Length 109;
 Best Local Similarity 81.8%; Pred. No. 0.08;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIRYSQSIS 11

Db 46 llikyasqsis 56

RESULT 15

W84100

ID W84100 standard; Protein; 112 AA.

XX W84100;

XX 15-MAR-1999 (first entry)

DE Vitronectin alpha-v beta-3 MAB VL.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
 XX

OS Mus sp.

XX WO9840488-A1.

PN 17-SEP-1998.

PD 12-MAR-1998; 98WO-US04987.

PF 12-MAR-1997; 97US-0039609.

PR (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

PN-PSDB; V71802.

XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for

PT immunotherapeutic treatment of e.g. diabetic retinopathy,

PT inflammatory disorders, atherosclerosis, restenosis, cancers or

PT osteoporosis

XX Example 13; Page 64; 97pp; English.

XX This is the amino acid sequence of the region of the murine

CC monoclonal antibody (MAB) D12 light chain variable region (VL)

CC that is altered in humanised D12 VL (see also W84098). A

CC synthetic gene (see V81902) encoding the protein was prepared

CC from synthetic oligonucleotides and used to prepare an expression

CC vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3

CC vitronectin receptor MAB. Humanised D12 MABs can be used for

CC passive immunotherapy of disorders mediated by the alpha-v beta-3

CC vitronectin receptor, e.g. restenosis and angiogenic associated

CC diseases.

XX Sequence 112 AA;

SQ

Query Match 87.8%; Score 43; DB 20; Length 112;
 Best Local Similarity 81.8%; Pred. No. 0.082;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIRYSQSIS 11

Db 46 llikyasqsis 56

Search completed: March 28, 2001, 06:59:52
 Job time: 1388 sec

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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-728-83

Query Match 100.0%; Score 55; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
Db 109 QQSNSWPHT 117
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Search completed: March 28, 2001, 07:01:58
Job time: 1337 sec

APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPH 9
Db 89 QQSNSWPH 97

RESULT 14
US-07-634-278-83
Sequence 83, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-83

Query Match 100.0%; Score 55; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPH 9
Db 109 QQSNSWPH 117

RESULT 15
US-08-477-728-83
Sequence 83, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728

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; Sequence 63, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. NO. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 13
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; US-08-487-200-63

; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. NO. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 12
US-08-487-200-63

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SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 9
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 10
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9

; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 7
US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; APPLICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 8
US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||||
Db 89 QQSNSWPHT 97

RESULT 5
US-07-728-62
Sequence 62, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
|||||||
Db 89 QQSNSWPHT 97

RESULT 6
US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:

QY 1 QQNSWPHT 9
Db 89 QQNSWPHT 97
RESULT 2
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQNSWPHT 9
Db 89 QQNSWPHT 97

RESULT 3
US-07-634-278-63
; Sequence 63, Application US/07634278

; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 100.0%; Score 55; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQNSWPHT 9
Db 89 QQNSWPHT 97

RESULT 4
US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:58 ; Search time 113.49 Seconds
(without alignments)
1.424 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQSNWPHT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgnl_7/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgnl_7/ptodata/1/1aa/6_COMB.pep:*
- 4: /cgnl_7/ptodata/1/1aa/PCTUS_COMB.pep:*
- 5: /cgnl_7/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	55	100.0	100	1	US-08-436-463-19
2	55	100.0	107	1	US-07-634-278-62
3	55	100.0	107	1	US-07-634-278-63
4	55	100.0	107	1	US-07-634-278-87
5	55	100.0	107	1	US-08-477-728-62
6	55	100.0	107	1	US-08-477-728-63
7	55	100.0	107	1	US-08-477-728-87
8	55	100.0	107	1	US-08-474-040-62
9	55	100.0	107	1	US-08-474-040-63
10	55	100.0	107	1	US-08-474-040-87
11	55	100.0	107	1	US-08-487-200-62
12	55	100.0	107	1	US-08-487-200-63
13	55	100.0	107	1	US-08-487-200-87
14	55	100.0	127	1	US-07-634-278-83
15	55	100.0	127	1	US-08-477-728-83
16	55	100.0	127	1	US-08-474-040-83
17	55	100.0	127	1	US-08-487-200-83
18	55	100.0	127	1	US-08-436-463-4
19	49	89.1	107	1	US-08-436-463-20
20	49	89.1	107	1	US-08-107-669D-1
21	49	89.1	107	1	US-08-472-788A-1
22	49	89.1	107	2	US-08-477-531B-1
23	49	89.1	107	2	US-08-082-842A-1
24	49	89.1	109	1	US-07-942-245-4
25	49	89.1	143	2	US-08-653-402B-8
26	44	80.0	103	1	US-08-436-463-21
27	44	80.0	127	1	US-08-436-463-18
28	42	76.4	240	2	US-07-956-399-2

US-08-436-463-19

29	41	74.5	13	1	US-08-221-580-7	Sequence 7, Appli
30	41	74.5	13	4	PCT-US95-04018-69	Sequence 69, Appli
31	41	74.5	107	1	US-08-192-102-3	Sequence 3, Appli
32	41	74.5	107	1	US-08-324-799-3	Sequence 3, Appli
33	41	74.5	107	2	US-08-192-861A-3	Sequence 3, Appli
34	40	72.7	9	2	US-08-476-176B-55	Sequence 55, Appli
35	40	72.7	9	3	US-08-127-721A-55	Sequence 55, Appli
36	40	72.7	9	3	US-08-485-246A-55	Sequence 55, Appli
37	40	72.7	106	2	US-08-800-198-4	Sequence 4, Appli
38	40	72.7	106	3	US-09-296-595-4	Sequence 4, Appli
39	40	72.7	107	2	US-08-476-176B-4	Sequence 4, Appli
40	40	72.7	107	3	US-08-127-721A-4	Sequence 4, Appli
41	40	72.7	107	3	US-08-485-246A-4	Sequence 4, Appli
42	40	72.7	127	2	US-08-476-176B-6	Sequence 6, Appli
43	40	72.7	127	2	US-08-476-176B-8	Sequence 8, Appli
44	40	72.7	127	2	US-08-476-176B-10	Sequence 10, Appli
45	40	72.7	127	3	US-08-127-721A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-436-463-19

Sequence 19, Application US/08436463

Patent No. 5760185

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko

APPLICANT: MAEDA, Hiroaki

APPLICANT: NISHIYAMA, Kiyoto

APPLICANT: TOKIYOSHI, Sachio

TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT

TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

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CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,463

FILING DATE: 26-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 341255/1992

FILING DATE: 28-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: KIMACHI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 100 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-463-19

Query Match 100.0%; Score 55; DB 1; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.006;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
XX with humanised variable regions
PS Disclosure; Column 43-44; 77pp; English.
XX
CC A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunconjugate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at
CC least one of (a) a modified light chain variable region (see W58478 or
CC W58480), and (b) a modified heavy chain variable region (see W58479 or
CC W58481), where W58478 and W58479 are humanised forms of the H65 light
CC and heavy chain variable domains with low risk amino acid substitutions
CC [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC W58481 are humanised forms of the H65 light and heavy chain variable
CC domains with moderate risk amino acid substitutions and are present in
CC humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
CC treating autoimmune diseases, especially systemic lupus erythematosus,
CC rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC represents the murine HYH antibody light chain variable domain.
XX
SQ Sequence 107 AA;

Query Match 89.1%; Score 49; DB 19; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.082;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 qgsnswpyt 97

RESULT 15
ID R15438
XX R15438 standard; Protein; 108 AA.
AC
XX R15438;
XX
DT 25-FEB-1992 (first entry)
DE
DE Light chain variable region of MAB 1A6.
KW HRV; ICAM-1; antigen-binding fragment; inflammation;
KW auto-immune disease.
XX
OS Homo sapiens.
XX
XX EP459577-A.
XX
PD 04-DEC-1991.
XX
XX 25-MAY-1991; 91EP-0201243.
XX
XX 01-JUN-1990; 90US-0532001.
XX
XX (MERI) MERCK & CO INC.
XX
XX Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
XX WPI; 1991-355850/49.
XX
XX Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion
PT molecule (ICAM-1)
XX
XX Claim 1; Page 19; 28pp; English.
XX
XX This is one of six antibody fragments from MAB's specific for domain
CC 1 of ICAM-1. MAB 1A6 also specifically blocks the major group of
CC human rhinovirus from binding to and infecting HeLa cells. The
CC peptide fragments can be used to treat or prevent rhinovirus

CC infection. See R15437-R15443.
XX
SQ Sequence 108 AA;

Query Match 89.1%; Score 49; DB 12; Length 108;
Best Local Similarity 88.9%; Pred. No. 0.082;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 qgsnswpyt 97

Search completed: March 28, 2001, 06:59:53
Job time: 1389 sec

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 49 /label= Arg, Met
 FT
 XX
 XX WO9833919-A2.
 XX
 XX 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB; V49843.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 19; Fig 7; 129pp; English.
 XX
 XX This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 89.1%; Score 49; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.082;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNWPHT 9
 Db 89 qqsgswpht 97

RESULT 12
 W76002
 ID W76002 standard; Protein; 107 AA.
 XX
 AC W76002;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody light chain variable region protein fragment.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

RESULT 10
 R38601
 ID R38601 standard; peptide; 107 AA.
 XX
 AC R38601;
 XX
 AC
 DT 28-OCT-1993 (first entry)
 XX
 DE HTH light chain.
 XX
 XX Antibody; variable domain; light; L; heavy; H; consensus;
 KW affinity; antigen; immunogenicity; humanisation; framework.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO9311794-A.
 XX
 PD 24-JUN-1993.
 XX
 PF 14-DEC-1992; 92WO-US10906.
 XX
 PR 13-DEC-1991; 91US-0808464.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 XX
 DR WPI: 1993-213827/26.
 XX
 XX Antibodies prep. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.
 XX
 PS Disclosure; Page 84; 160pp; English.
 XX
 XX The amino acid sequences of the light and heavy chains of the
 CC variable domains from antibodies HYH [HYHEL-10 Fab-lysozyme complex]
 CC (R38601 and R38608, respectively), MCP [IgA Fab MCP603-phosphocholine
 CC complex] (R38602-03 and R38609-10, respectively), NEWM [Ig Fab' NEWM
 CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
 CC R38612, respectively) may be used to determine an alignment from which
 CC appropriate changes may be made.
 CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.
 XX
 SQ Sequence 107 AA;

Query Match 89.1%; Score 49; DB 14; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.082;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNWPHT 9
 Db 89 qqsnswpht 97

RESULT 11
 W76006
 ID W76006 standard; Protein; 107 AA.
 XX
 AC W76006;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody light chain variable region protein fragment.

CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.

XX
 SQ Sequence 127 AA;

Query Match 100.0%; Score 55; DB 15; Length 127;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
 Db 109 qqsnswpht 117
 |||||

RESULT 8
 W76034
 ID W76034 standard; Protein; 9 AA.
 AC W76034;
 XX
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR3 protein fragment #3.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX Mus sp.
 OS
 XX
 XX WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX

XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX N-PSDB; V49871.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC prevention-mediated signal transduction. This is useful in the treatment,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 9 AA;

Query Match 89.1%; Score 49; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
 Db 1 qgstswpht 9
 |||||

RESULT 9
 W76013
 ID W76013 standard; Protein; 9 AA.
 XX
 AC W76013;
 XX

XX 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR3 protein fragment #1.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX Mus sp.
 OS
 XX
 XX WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US01826.
 XX
 XX 30-JAN-1997; 97US-0791391.
 XX

XX (IXSY-) IXSYS INC.
 XX
 XX Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX N-PSDB; V49850.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC prevention-mediated signal transduction. This is useful in the treatment,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 9 AA;

Query Match 89.1%; Score 49; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
 Db 1 qqsngswpht 9
 |||||

CC humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

Query Match 100.0%; Score 55; DB 20; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
Db 89 qgsnswpht 97

RESULT 6
Y06382
ID Y06382 standard; Protein; 109 AA.

XX Y06382;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VL domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
LM609; monoclonal antibody; complementarity determining region;
CDR grafting; mouse; integrin; apoptosis; angiogenesis;
cancer; therapy; diagnosis.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..2
FT Region /note= "vector-encoded residues"
FT Region 24..34
FT Region /note= "CDR1"
FT Region 50..56
FT Region /note= "CDR2"
FT Region 89..97
FT Region /note= "CDR3"

XX W09929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 50; 55pp; English.

XX This sequence represents the light chain variable region of a
humanised LM609 antibody. LM609 is directed to human integrin
alpha-v beta-3. It selectively promotes apoptosis of vascular
cells that have been stimulated to undergo angiogenesis, making it
a tool for cancer diagnosis and therapy. The invention provides
humanised antibodies, especially humanised LM609. In such humanized
antibodies, a light chain CDR from a mouse antibody such as LM609 is
grafted onto a human light chain, and a heavy chain CDR from a mouse
antibody is grafted onto a human antibody heavy chain to produce
libraries from which a humanised murine antibody having the desired
specificity is selected. By preserving the original CDR sequences
such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

Query Match 100.0%; Score 55; DB 20; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
Db 89 qgsnswpht 97

RESULT 7

R54093
ID R54093 standard; Protein; 127 AA.

XX R54093;

XX 29-DEC-1994 (first entry)

XX Sequence of mouse V-kappa showing the sequences of recombinant
DE anti-FHV-1 antibody CDRs 1, 2 and 3.

XX Feline herpes virus; FHV-1; monoclonal antibody; CDR;
complementarity determining region.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..20
FT Region /label= leader
FT Region 21..43
FT Region /label= FR1
FT Region 44..54
FT Region /label= CDR1
FT Region 55..70
FT Region /label= FR2
FT Region 71..76
FT Region /label= CDR2
FT Region 77..108
FT Region /label= FR3
FT Region 109..117
FT Region /label= CDR3
FT Region 118..127
FT Region /label= FR4

XX W09412661-A.

XX 09-JUN-1994.

XX 25-NOV-1993; 93WO-JP01724.

XX 28-NOV-1992; 92JP-0341255.

XX (KAGA) CHEMA SERO THERAPEUTIC RES INST.

XX Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

XX WPI; 1994-200288/24.

XX N-PSDB; Q64167.

XX Feline monoclonal antibody and recombinant antibodies specific
PT for FHV-1 - for detection, treatment and prevention of FHV-1
PT infection.

XX Disclosure; Page 18-19; 53pp; Japanese.

XX The inventors claim a monoclonal antibody against feline herpes
virus (FHV-1). They also claim a recombinant antibody against FHV-1
and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
used in the detection, treatment and prevention of FHV-1. The
sequences of the CDRs in the VH of the recombinant anti-FHV-1

CC DNA¹ and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also R25721-32.

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 55; DB 13; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 Db |||||
 89 qqsnswpht 97

RESULT 4

Y06388
 ID Y06388 standard; Protein; 109 AA.

XX AC Y06388;

DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VL domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Homo sapiens.
 OS Synthetic.

XX FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 24..34
 FT /note= "CDR1"
 FT Region 50..56
 FT /note= "CDR2"
 FT Region 89..97
 FT /note= "CDR3"

XX PN W09929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 52; 55pp; English.

XX CC This sequence represents the light chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired

CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 109 AA;

Query Match 100.0%; Score 55; DB 20; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 Db |||||
 89 qqsnswpht 97

RESULT 5

Y06380
 ID Y06380 standard; Protein; 109 AA.

XX AC Y06380;

DT 06-SEP-1999 (first entry)

XX DE Murine monoclonal antibody LM609 v lambda.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "vector-encoded residues"
 FT Region 24..34
 FT /note= "CDR1"
 FT Region 50..56
 FT /note= "CDR2"
 FT Region 89..97
 FT /note= "CDR3"

XX PN W09929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 49-50; 55pp; English.

XX CC This sequence represents the light chain v lambda region of
 CC murine monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the

PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QQNSNSWPHT 9
 Db | | | | | | | | |

Db 1 qqnsnswpht 9

RESULT 2
 ID Y06372
 AC Y06372 standard; Peptide; 9 AA.

XX
 XX Y06372;
 DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VL CDR3.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; Integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

OS
 XX WO9929888-A1.

XX
 XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized-mouse monoclonal antibodies

XX Disclosure; Page 45; 55pp; English.

XX This sequence represents complementarity determining region 3
 CC (LCB3) of the light chain of murine monoclonal antibody LM609.
 CC LM609 is directed to integrin alpha-v beta-3. It selectively
 CC promotes apoptosis of vascular cells stimulated to undergo
 CC angiogenesis, making it a tool for cancer diagnosis and therapy.
 CC The invention provides humanised antibodies, especially humanised
 CC LM609. In such humanized antibodies, a light chain CDR from a

CC mouse antibody such as LM609 is grafted onto a human light chain,
 CC and a heavy chain CDR from a mouse antibody is grafted onto a human
 CC antibody heavy chain to produce libraries from which a humanised
 CC murine antibody having the desired specificity is selected. By
 CC preserving the original CDR sequences such as the HCDR3 and LCDR3
 CC sequences of LM609, the humanisation strategy ensures epitope
 CC conservation.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QQNSNSWPHT 9
 Db | | | | | | | | |

Db 1 qqnsnswpht 9

RESULT 3
 R25729
 ID R25729 standard; Protein; 107 AA.

XX AC R25729;

XX 13-JAN-1993 (first entry)

XX Humanised VL region of the mouse CMV5 antibody.

XX Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW gH; light chain; variable region; framework; human; Wol.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 24..34

FT /note= "CDR"

FT Region 50..56

FT /note= "CDR"

FT Region 89..97

FT /note= "CDR"

FT Misc-difference 49

FT /note= "mutated residue"

XX WO9211018-A.

XX 09-JUL-1992.

XX 19-DEC-1991; 91WO-US09711.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;

XX WPI; 1992-249842/30.

XX New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions

XX Claim 40; Fig 27A; 141pp; English.

XX The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human Wol framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the gH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:52 ; Search time 154.19 Seconds
(without alignments)
1.996 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QOSNSWPH 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT: *
- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT: *
- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT: *
- 5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT: *
- 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT: *
- 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT: *
- 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT: *
- 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT: *
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- 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT: *
- 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT: *
- 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT: *
- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT: *
- 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT: *
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- 17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT: *
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- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT: *
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT: *
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	19 W76033	LM609 grafted anti
2	55	100.0	9	20 W06372	Murine monoclonal
3	55	100.0	107	13 R25729	Humanised VL regio
4	55	100.0	109	20 Y06388	Humanised LM609 an
5	55	100.0	109	20 Y06380	Murine monoclonal
6	55	100.0	109	20 Y06382	Humanised LM609 an
7	55	100.0	127	15 R54093	Sequence of mouse
8	49	89.1	9	19 W76034	LM609 grafted anti
9	49	89.1	9	19 W76013	LM609 grafted anti
10	49	89.1	107	14 R38601	HYH light chain.
11	49	89.1	107	19 W76006	LM609 grafted anti
12	49	89.1	107	19 W76002	Vitaxin antibody 1

13	49	89.1	107	19 W76004	LM609 antibody lig
14	49	89.1	107	19 W58482	Murine HYH antibod
15	49	89.1	108	12 R15438	Light chain variab
16	49	89.1	109	15 R52033	Light chain variab
17	49	89.1	143	18 W19580	Mouse anti-idiotyp
18	49	89.1	240	12 R15443	Single chain Fv fr
19	46	83.6	105	20 W87456	JK gene product.
20	46	83.6	105	20 W87458	Humanised anti-alp
21	46	83.6	107	20 W84098	Humanised anti-alp
22	46	83.6	108	20 W84094	Murine vitronectin
23	46	83.6	112	20 W84100	vitronectin alpha-
24	42	76.4	10	20 W89161	Anti-p53 monoclonal
25	42	76.4	20	20 W89169	Anti-p53 monoclonal
26	42	76.4	107	14 R32129	Anti-IL2R beta ant
27	42	76.4	109	20 W89176	Anti-p53 monoclonal
28	42	76.4	240	14 R34510	Fv(TU27). Homo sa
29	41	74.5	9	19 W76036	LM609 grafted anti
30	41	74.5	9	19 W44180	Monoclonal antibod
31	41	74.5	104	19 W26795	Anti-gp54 MAb 48-1
32	41	74.5	107	18 W28531	Humanised CA2 ligh
33	41	74.5	107	19 W40820	Light chain variab
34	41	74.5	107	20 Y23243	Light chain variab
35	41	74.5	108	16 R79884	Anti-EGFR antibody
36	41	74.5	127	19 W44176	Monoclonal antibody
37	41	74.5	240	19 W26799	Anti-gp54 MAb 48-1
38	40	72.7	9	20 Y26992	CDR3 domain reshap
39	40	72.7	23	20 Y12061	Human 5' EST secre
40	40	72.7	106	19 W71241	Light chain variab
41	40	72.7	107	15 R50190	Light chain variab
42	40	72.7	107	17 R88718	Mouse antibody kap
43	40	72.7	107	20 Y26979	Light chain variab
44	40	72.7	107	21 Y70604	Vkappa region of h
45	40	72.7	127	15 R50187	Light chain variab

ALIGNMENTS

RESULT 1

W76033
ID W76033 standard; Protein; 9 AA.
XX
AC W76033;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR3 protein fragment #2.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN W09833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; V49870.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

AC O13548;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE YPR99CP.
GN YPR099C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albertmann K., Allen E., Ansong W.,
RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Bolstein D.,
RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
RA Delliuss H., Dipaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,
RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
RA Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,
RA Johnston M., Kaiman S., Kleine K., Komp C., Kurdi O., Lashkari D.,
RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
RA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,
RA Newtich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
RA Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,
RA Schroeder M., Solcu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S.,
RA Viereedeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
RA Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Nelson J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Waterston R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Jia Y., Cherry J.M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32445; AAB68088.1; -;
SQ SEQUENCE 118 AA; 13360 MW; 16DDC5E2B31655D5 CRC64;

Query Match 65.5%; Score 36; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NSWPH 8

Db 53 NSWPH 57

RESULT 15

Q27824

ID Q27824
AC Q27824;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE SERINE COLLAGENASE 1 PRECURSOR (EC 3.4.21.32) (BRACHYURIN)
DE (COLLAGENOLYTIC PROTEASE).
OS Uca pugnator (Atlantic sand-fiddler crab) (Celuca pugnator).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Ocypodoidea; Ocypodidae; Celuca.
OX NCBI_TaxID=6772;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOPANCREAS;
RX MEDLINE=96212234; PubMed=8626718;
RA Tsu C.A., Craik C.S.;
RT "Substrate recognition by recombinant serine collagenase 1 from Uca pugnator.";
RL J. Biol. Chem. 271:11563-11570(1996).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS, WITH BROAD SPECIFICITY
CC FOR PEPTIDE BONDS. DEGRADATES NATIVE COLLAGEN AT ABOUT 75% OF THE
CC LENGTH OF THE MOLECULE FROM THE N-TERMINUS. LOW ACTIVITY ON SMALL
CC MOLECULE SUBSTRATES OF BOTH TRYPSIN AND CHYMOTRYPSIN.
DR EMBL; U49931; AAC47030.1; -;
DR HSP; P00771; IAZZ.
DR INTERPRO; IPR001254; -;
DR INTERPRO; IPR001314; -;
DR PFAM; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Signal; Hydrolase.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 45 270 SERINE COLLAGENASE 1.
SQ SEQUENCE 270 AA; 28170 MW; C084D974968ED687 CRC64;

Query Match 65.5%; Score 36; DB 5; Length 270;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NSWPH 8

Db 54 NSWPH 58

Search completed: March 28, 2001, 07:53:21
Job time: 514 sec

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Db 195 QKSNSWGH 202
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RESULT 10.
Q9NQS7 PRELIMINARY; PRT; 919 AA.
AC Q9NQS7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE INNER CENTROMERE PROTEIN INCENP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Adams R.R., Eckley D.M., Mackay A., Earnshaw W.C.;
RT "Characterization and expression of the human INCENP gene.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
DR EMBL; AF282265; AAF87584.1; -.
SQ SEQUENCE 919 AA; 105536 MW; 8F93024E411087C6 CRC64;

Query Match 67.3%; Score 37; DB 4; Length 919;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SNSWPH 8
      .:|||||
Db 398 NNSWPH 403

RESULT 11
Q9XCE0 PRELIMINARY; PRT; 94 AA.
AC Q9XCE0;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE MUCONOLACTONE ISOMERASE.
GN CATC.
OS Mycobacterium smegmatis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC2-155;
RX MEDLINE=99328972; PubMed=10400584;
RA Fernandes N.D., Wu Q.-L., Kong D., Puyang X., Garg S., Husson R.N.;
RT "A mycobacterial extracytoplasmic sigma factor involved in survival
following heat shock and oxidative stress.";
RL J. Bacteriol. 181:4266-4274(1999).
DR EMBL; AF144091; AAD41808.1; -.
KW Isomerase.
SQ SEQUENCE 94 AA; 10966 MW; D2D71632A2F2FF0 CRC64;

Query Match 65.5%; Score 36; DB 2; Length 94;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 8
      .:|||||
Db 35 QRSWKPH 42

RESULT 12
Q9Z9Y5 PRELIMINARY; PRT; 96 AA.
ID Q9Z9Y5
AC Q9Z9Y5;

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DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE MUCONOLACTONE ISOMERASE (EC 5.3.3.4).
GN CATCI.
OS Frateuria sp. ANA-18.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Frateuria.
OX NCBI_TaxID=70412;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANA-18;
RX MEDLINE=99132292; PubMed=9931486;
RA Murakami S., Takashima A., Takemoto J., Takenaka S., Shinke R.,
RA Aoki K.;
RT "Cloning and sequence analysis of two catechol-degrading gene clusters
from the aniline-assimilating bacterium Frateuria species ANA-18.";
RL Gene 226:189-198(1999).
DR EMBL; AB009343; BAA75206.1; -.
KW Isomerase.
SQ SEQUENCE 96 AA; 11034 MW; 3D01BC0314DB6856 CRC64;

Query Match 65.5%; Score 36; DB 2; Length 96;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 8
      .:|||||
Db 35 QKSQKPH 42

RESULT 13
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P01607; IREI.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 65.5%; Score 36; DB 4; Length 109;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSNSWP 7
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Db 89 QQYNSWP 95

RESULT 14
O13548 PRELIMINARY; PRT; 118 AA.
ID O13548

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
DR EMBL; AE003547; AAF50133.1; -;
DR FLYBASE; FBgn0036103; CG7958.
SQ SEQUENCE 1109 AA; 116491 MW; 4FD726183EB5642AC CRC64;

Query Match 69.1%; Score 38; DB 5; Length 1109;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQNSWPHPT 9
Db 591 QMNTNWPHPT 599

RESULT 8
Q9ZVX6 PRELIMINARY; PRT; 1109 AA.
ID Q9ZVX6
AC Q9ZVX6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE TMV RESISTANCE PROTEIN.
GN FL2A24.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC FL2A24 genomic sequence.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005167; AAC64218.1; -;
DR INTERPRO; IPR000157; -;
DR INTERPRO; IPR000767; -;
DR INTERPRO; IPR001611; -;
DR INTERPRO; IPR001617; -;
DR INTERPRO; IPR002182; -;
DR PFAM; PF00560; LRR; 3.
DR PFAM; PF00931; NB-ARC; 2.
DR PFAM; PF01582; TIR; 1.
DR PRINTS; PR00364; DISEASERSIST.
SQ SEQUENCE 1109 AA; 125679 MW; 865678FBC55DE694 CRC64;

Query Match 69.1%; Score 38; DB 10; Length 1109;
Best Local Similarity 66.7%; Pred. No. 69;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQNSWPHPT 9
Db 900 QOQHSWEHT 908

RESULT 9
Q9VJS8 PRELIMINARY; PRT; 656 AA.
ID Q9VJS8
AC Q9VJS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANON-D52 PROTEIN.
DE ANON-D52.
GN ANON-D52.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195(2000).
DR EMBL; AE003555; AAF50421.1; -;
DR FLYBASE; FBgn0010431; anon-D52.
SQ SEQUENCE 656 AA; 75789 MW; DB4311709EDEF52 CRC64;

Query Match 67.3%; Score 37; DB 5; Length 656;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQNSWPHPT 8

DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE T1111.17 PROTEIN.
 GN T1111.17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RA "Arabidopsis thaliana chromosome I BAC T1111 genomic sequence."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC012680; AAF18557.1; -;
 DR INTERPRO: IPR001611; -;
 DR PFAM; PF00560; LRR; 3;
 DR PRINTS; PRO0019; LEURICHRPT.
 SQ SEQUENCE 581 AA; 64828 MW; 5E6FAC53FDF49FD4 CRC64;

Query Match 70.9%; Score 39; DB 10; Length 581;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QOSNSWPH 8
 I I I I I
 DB 244 QSSNLWPH 251

RESULT 5
 ID Q25679 PRELIMINARY; PRT; 278 AA.
 AC Q25679;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE HOX1 GENE.
 GN HOX1.
 OS Podocoryne carnea.
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
 OC Hydractiniidae; Podocoryne.
 OX NCBI_TaxID=6096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95301097; PubMed=7781898;
 RA Aerne B., Baeder C.D., Schmid V.;
 RT "Life stage and tissue-specific expression of the homeobox gene cnox1-
 PC of the hydrozoan Podocoryne carnea."
 RL Dev. Biol. 169:547-556(1995).
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; X81455; CAA57211.1; -;
 DR HSSP; P14653; 1B72.
 DR INTERPRO; IPR001356; -;
 DR PFAM; PF00046; homeobox.1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW Homeobox; Nuclear protein; DNA-binding.
 SQ SEQUENCE 278 AA; 32680 MW; 259BD1156B271BA8 CRC64;

Query Match 69.1%; Score 38; DB 5; Length 278;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SNSWPH 9
 I I I I I
 DB 256 SNSWPH 262

RESULT 6
 ID Q01350 PRELIMINARY; PRT; 497 AA.
 AC Q01350;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE GAG PROTEIN.
 GN GAG.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90136512; PubMed=2559313;
 RA Tchurikov N.A., Gerasimova T.I., Johnson T.K., Barbakar N.I.,
 RA Kenzior A.L., Georgiev G.P.;
 RT "Mobile elements and transposition events in the cut locus of
 RT Drosophila melanogaster."
 RL Mol. Gen. Genet. 219:241-248(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tchurikov N.A., Ponomarenko N.A., Krasnov A.N.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U89994; AAB50147.1; -;
 DR FLYBASE; FBgn0010302; Burdock.
 SQ SEQUENCE 497 AA; 56804 MW; 6498A941089BCD4A CRC64;

Query Match 69.1%; Score 38; DB 5; Length 497;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QOSNSWP 7
 I I I I I
 DB 381 QQQNSWP 387

RESULT 7
 ID Q9VTB9 PRELIMINARY; PRT; 1109 AA.
 AC Q9VTB9;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE CG7958 PROTEIN.
 GN CG7958.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003555; AAF50437.1; -
 DR FLYBASE: FBgn0035879; CG7112.
 DR INTERPRO: IPR000195; -
 DR PFAM: PF00566; TBC; 1.
 SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 80.0%; Score 44; DB 5; Length 1194;
 Best Local Similarity 77.8%; Pred. NO. 6.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHPT 9

Db 461 QOSSSWPYT 469

RESULT 2
 Q9M9E4 ID Q9M9E4 PRELIMINARY; PRT; 413 AA.
 AC Q9M9E4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE F3p9-22.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F3p9 from chromosome I";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;

QY 1 QOSNSWPHPT 9

Db 145 QONNQWHT 153

RESULT 4
 Q9SEK3 ID Q9SEK3 PRELIMINARY; PRT; 581 AA.
 AC Q9SEK3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC013430; AAF71805.1; -
 SQ SEQUENCE 413 AA; 45745 MW; 2F0D48E28FAF6A43 CRC64;

Query Match 70.9%; Score 39; DB 10; Length 413;
 Best Local Similarity 75.0%; Pred. NO. 18;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNSWPHPT 8

Db 76 QSSNLWPH 83

RESULT 3
 P89903 ID P89903 PRELIMINARY; PRT; 523 AA.
 AC P89903;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE FROM AFRICAN GREEN MONKEY, TANTALUS SPECIES (SIVTAN) PROVIRAL DNA,
 DE COMPLETE GENOME.
 GN GAG.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TANTALUS-1;
 RX MEDLINE=97223354; PubMed=9123848;
 RA Soares M.A., Robertson D.L., Hui H., Allan J.S., Shaw G.M., Hahn B.H.;
 RT "A full-length and replication-competent proviral clone of SIVAGM from
 RT tantalus monkeys";
 RL Virology 228:394-399(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TANTALUS-1;
 RA Soares M.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U58991; AAC57051.1; -
 DR HSSP: P03351; 1E1A.
 DR INTERPRO: IPR000071; -
 DR INTERPRO: IPR000721; -
 DR INTERPRO: IPR001878; -
 DR PFAM: PF00098; zf-CCHC; 2.
 DR PFAM: PF00540; gag_p17; 1.
 DR PFAM: PF00607; gag_p24; 1.
 DR PRINTS: PR00234; HIVMATR1X.
 DR PRINTS: PR00939; C2HCZNFINGER.
 SQ SEQUENCE 523 AA; 57688 MW; F623CED7277681AA CRC64;

Query Match 70.9%; Score 39; DB 12; Length 523;
 Best Local Similarity 66.7%; Pred. NO. 22;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNSWPHPT 9

Db 145 QONNQWHT 153

RESULT 4
 Q9SEK3 ID Q9SEK3 PRELIMINARY; PRT; 581 AA.
 AC Q9SEK3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:18 ; Search time 443.95 Seconds
(without alignments)
2.376 Million cell updates/sec

Title: US-09-016-061-86
Perfect score: 55
Sequence: 1 QQSNSWPH 9

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organalle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	44	80.0	1194	5 Q9VSI2	Q9vsi2 drosophila
2	39	70.9	413	10 Q9M9D4	Q9m9d4 arabidopsis
3	39	70.9	523	12 P89903	P89903 chimpanzee
4	39	70.9	581	10 Q9SFK3	Q9sfk3 arabidopsis
5	38	69.1	278	5 Q25679	Q25679 podocoryne
6	38	69.1	497	5 Q01350	Q01350 drosophila
7	38	69.1	1109	5 Q9VTB9	Q9vtb9 drosophila
8	38	69.1	1109	10 Q9ZVX6	Q9zvx6 arabidopsis
9	37	67.3	656	5 Q9VSJ8	Q9vsj8 drosophila
10	37	67.3	919	4 Q9NQS7	Q9nqs7 homo sapien
11	36	65.5	94	2 Q9XCE0	Q9xce0 mycobacteri
12	36	65.5	96	2 Q9Z9Y5	Q9z9y5 frateuria
13	36	65.5	109	4 Q9UL85	Q9ul85 homo sapien
14	36	65.5	118	3 Q13548	Q13548 saccharomyc
15	36	65.5	270	5 Q27824	Q27824 uca pugilac
16	36	65.5	640	5 Q9XWZ6	Q9xwz6 caenorhabdi
17	36	65.5	978	6 Q9XS93	Q9xs93 canis famil
18	35	63.6	145	2 P73353	P73353 synecocyst
19	35	63.6	374	11 Q88768	Q88768 rattus norv

20	35	63.6	374	11	Q9QUI9	Q9qui9 rattus norv
21	35	63.6	419	11	Q63629	Q63629 rattus norv
22	35	63.6	428	2	Q9KSE5	Q9kse5 vibrio chol
23	35	63.6	750	10	Q41103	Q41103 phaseolus v
24	34	61.8	151	5	Q18581	Q18581 nabis sp. m
25	34	61.8	151	5	Q23702	Q23702 ctenolepism
26	34	61.8	151	5	Q02473	Q02473 stylochus z
27	34	61.8	151	5	P91717	P91717 dugesia tig
28	34	61.8	164	12	Q9WSZ2	Q9wsz2 human herpe
29	34	61.8	224	12	Q87449	Q87449 chimpanzee
30	34	61.8	224	12	Q9Q068	Q9q068 chimpanzee
31	34	61.8	224	12	Q9Q066	Q9q066 chimpanzee
32	34	61.8	224	12	Q9Q065	Q9q065 chimpanzee
33	34	61.8	224	12	Q9Q064	Q9q064 chimpanzee
34	34	61.8	224	12	Q9Q063	Q9q063 chimpanzee
35	34	61.8	224	12	Q9Q062	Q9q062 chimpanzee
36	34	61.8	224	12	Q9Q061	Q9q061 chimpanzee
37	34	61.8	224	12	Q9Q060	Q9q060 chimpanzee
38	34	61.8	224	12	Q9Q059	Q9q059 chimpanzee
39	34	61.8	224	12	Q9Q058	Q9q058 chimpanzee
40	34	61.8	224	12	Q9Q057	Q9q057 chimpanzee
41	34	61.8	224	12	Q9Q056	Q9q056 chimpanzee
42	34	61.8	224	12	Q9Q055	Q9q055 chimpanzee
43	34	61.8	224	12	Q9Q054	Q9q054 chimpanzee
44	34	61.8	224	12	Q9Q053	Q9q053 chimpanzee
45	34	61.8	224	12	Q9Q049	Q9q049 chimpanzee

ALIGNMENTS

RESULT 1

Q9VSI2 ID Q9VSI2 PRELIMINARY; PRT; 1194 AA.
AC Q9VSI2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE CG7112 PROTEIN.
GN CG7112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.N., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

DR PFAM; PF00098; zf-CCHC; 2.
DR PRINTS; PR00234; HIV1MATRIX.
DR PRINTS; PR00939; C2HC2NFINGER.
KW AIDS; Core protein; Polyprotein.
FT CHAIN 1 141 CORE PROTEIN P17.
FT CHAIN 142 519 CORE PROTEINS P24 AND P15.
SQ SEQUENCE 519 AA; 58143 MW; 85A3AC06BCCDCA38 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 519;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNSWPH 8
|||
Db 145 QQGNWVH 152

Search completed: March 28, 2001, 07:35:11
Job time: 148 sec

Query Match 61.8%; Score 34; DB 1; Length 459;
 Best Local Similarity 71.4%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 3 SNSWPH 9
 DB 188 TNSWAHT 194

RESULT 14
 TYTR_TRYCR STANDARD; PRT; 492 AA.
 AC P28593;
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TRYPAOTHIONE REDUCTASE (EC 1.6.4.8) (TR) (N1,N8-
 BIS(GLUTATHIONYL)SPERMIDINE REDUCTASE).
 GN TPR.
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91187059.
 RA Sullivan F.X., Walsh C.T.;
 RT "Cloning, sequencing, overproduction and purification of
 trypanothione reductase from Trypanosoma cruzi.";
 RL Mol. Biochem. Parasitol. 44:145-148(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SILVIO;
 RX MEDLINE; 95255281.
 RA Borges A., Cunningham M.L., Tover J., Fairlamb A.H.;
 RT "Site-directed mutagenesis of the redox-active cysteines of
 Trypanosoma cruzi trypanothione reductase.";
 RL Eur. J. Biochem. 228:745-752(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
 RX MEDLINE; 94211757.
 RA Lantwin C.B., Schlichting I., Kabsch W., Pai E.F., Krauth-Siegel R.L.;
 RT "The structure of Trypanosoma cruzi trypanothione reductase in the
 oxidized and NADPH reduced state.";
 RL Proteins 18:161-173(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE; 96367082.
 RA Zhang Y., Bond C.S., Bailey S., Cunningham M.L., Fairlamb A.H.,
 Hunter W.N.;
 RT "The crystal structure of trypanothione reductase from the human
 pathogen Trypanosoma cruzi at 2.3-A resolution.";
 RL Protein Sci. 5:52-61(1996).
 CC -1- FUNCTION: TRYPAOTHIONE IS THE PARASITE ANALOG OF GLUTATHIONE;
 CC THIS ENZYME IS THE EQUIVALENT OF GLUTATHIONE REDUCTASE.
 CC -1- CATALYTIC ACTIVITY: NADPH + TRYPAOTHIONE = NADP(+) + REDUCED
 CC TRYPAOTHIONE.
 CC -1- COFACTOR: FAD.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
 CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
 CC OXIDOREDUCTASES CLASS-I.
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 CC EMBL; M38051; AAA63547.1; -
 CC EMBL; Z13958; CAA78360.1; -

DR PIR; S30204; S30204.
 DR PDB; 1NDA; 30-SEP-94.
 DR PDB; 1AOG; 17-SEP-97.
 DR INTERPRO; IPR001100; -
 DR INTERPRO; IPR001327; -
 DR INTERPRO; IPR001864; -
 DR PFAM; PF00070; PYL_redox; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNRDRTASEI.
 DR PRINTS; PR00470; TRYPANRDTASE.
 DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
 KW Redox-active center; Oxidoreductase; Flavoprotein; FAD; NADP;
 KW 3D-structure. 7 37 FAD (ADP PART) (PROBABLE).
 FT NP_BIND 53 58 REDOX-ACTIVE.
 FT DISULFID 317 327 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 461 461 BY SIMILARITY.
 FT ACT_SITE 95 95 K -> N (IN STRAIN SILVIO).
 FT VARIANT 140 140 E -> A (IN STRAIN SILVIO).
 FT VARIANT 156 156 N -> H (IN STRAIN SILVIO).
 FT VARIANT 353 353 N -> T (IN STRAIN SILVIO).
 FT VARIANT 402 403 NI -> KV (IN STRAIN SILVIO).
 FT VARIANT 441 441 V -> I (IN STRAIN SILVIO).
 SQ SEQUENCE 492 AA; 53868 MW; 4AF179952A20750F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 492;
 Best Local Similarity 83.3%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNSWPH 8
 DB 161 SGSWPH 166

RESULT 15
 GAG_SIVAT STANDARD; PRT; 519 AA.
 ID GAG_SIVAT
 AC P05892;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P17, P24, AND P15].
 GN GAG.
 OS Simian immunodeficiency virus (TYO-1 isolate) (SIV-AGM).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88232906.
 RA Fukasawa M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H.,
 RA Miki K., Kitamura T., Hayami M.;
 RT "Sequence of simian immunodeficiency virus from African green monkey,
 a new member of the HIV/SIV group.";
 RL Nature 333:457-461(1988).
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
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 CC -----
 CC EMBL; X07805; CAA30657.1; -
 DR PIR; A30045; POLJG4.
 DR HSP; P05888; 1AAF.
 DR HIV; X07805; GAGSAGMTY.
 DR INTERPRO; IPR000071; -
 DR INTERPRO; IPR000721; -
 DR INTERPRO; IPR001878; -
 DR PFAM; PF00540; gag_p17; 1.
 DR EMBL; X07805; gag_p24; 1.

```

KW Aromatic amino acid biosynthesis; Multifunctional enzyme;
KW Oxidoreductase; Lyase; Transferase; Kinase; NADP; ATP-binding.
FT DOMAIN 1 383 3-DEHYDROQUINATE SYNTHASE.
FT DOMAIN 395 840 EPSP SYNTHASE.
FT DOMAIN 867 1042 SHIKIMATE KINASE.
FT DOMAIN 1043 1284 3-DEHYDROQUINASE.
FT DOMAIN 1297 1581 SHIKIMATE DEHYDROGENASE.
FT ACT_SITE 827 827 POTENTIAL.
FT NP_BIND 875 882 ATP (POTENTIAL).
FT ACT_SITE 1189 1189 BY SIMILARITY.
FT ACT_SITE 1217 1217 FORMS A SCHIFF-BASE INTERMEDIATE (BY SIMILARITY).
SQ SEQUENCE 1581 AA; 178043 MW; 417A84356061170F CRC64;

Query Match 65.5%; Score 36; DB 1; Length 1581;
Best Local Similarity 71.4%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNSWPHT 9
DB 1176 NNSWPYT 1182
:||||:|

RESULT 11
POLR_OYMW STANDARD; PRT; 1776 AA.
AC P20127;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).
OS Ononis yellow mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90021186.
RA Ding S.W., Keese P., Gibbs A.;
RT "Nucleotide sequence of the ononis yellow mosaic tymovirus genome.";
RL Virology 172:555-563(1989).
CC -----
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CC -----
CC EMBL: J04375; AAA46796.1;
CC PIR: J0106; RWPYV.
CC INTERPRO: IPR000606;
CC PFAM: PF0143; Viral_helicase1;
KW Transferase; RNA-directed RNA polymerase; Polyprotein; ATP-binding.
FT NP_BIND 899 906 ATP (BY SIMILARITY).
SQ SEQUENCE 1776 AA; 198127 MW; 1C2E37B9EC3A5333 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 1776;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNSWPH 8
DB 1191 SNKWPYH 1196
|||||

RESULT 12
KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION' BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 86174817.
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSP; P80362; LWTL.
DR INTERPRO: IPR003006;
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQNSWPHT 9
DB 89 QQNSWPYT 97
|||:|:|:|

RESULT 13
NUAM_PELSU STANDARD; PRT; 459 AA.
AC O79677;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
GN ND4.
OS Pelomedusa subrufa (African side-necked turtle).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
RN [1]
RP SEQUENCE FROM N.A.
RA Zardoya R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -----
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CC -----
CC EMBL: AF039066; AAD05057.1;
CC INTERPRO: IPR000260;
CC INTERPRO: IPR001750;
CC PFAM: PF00361; oxidored_q1; 1.
CC PFAM: PF01059; oxidored_q5_N; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 459 AA; 51629 MW; 89BC451BD09482CC CRC64;

```

OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FDA 574;
RX MEDLINE; 92165839.
RA Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
RA Lindberg M., Hoeek M.;
RT "Molecular characterization and expression of a gene encoding a
RT Staphylococcus aureus collagen adhesin.";
RL J. Biol. Chem. 267:4766-4772(1992).
RN [2]
RP ERRATUM.
RA Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
RA Lindberg M., Hoeek M.;
RL J. Biol. Chem. 269:11672-11672(1994).
RN [3]
RP COLLAGEN-BINDING DOMAIN.
RC STRAIN-FDA 574;
RX MEDLINE; 94032261.
RA Patti J.M., Boles J.O., Hoeek M.;
RT "Identification and biochemical characterization of the ligand
RT binding domain of the collagen adhesin from Staphylococcus aureus.";
RL Biochemistry 32:11428-11435(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.
RX MEDLINE; 97475225.
RA Symersky J., Patti J.M., Carson M., House-Pompeo K., Teale M.,
RA Moore D., Jin L., Schneider A., Delucas L.J., Hoeek M.,
RA Narayana S.V.L.;
RT "Structure of the collagen-binding domain from a Staphylococcus
RT aureus adhesin.";
RL Nat. Struct. Biol. 4:833-838(1997).
CC -1- FUNCTION: MEDIATES ATTACHMENT OF STAPHYLOCOCCAL CELLS TO
CC COLLAGEN-CONTAINING SUBSTRATA.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. CELL WALL.
CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
CC IN THE REGION OF THE MEMBRANE ANCHOR.
CC -----
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CC -----
DR EMBL; M81736; AAA20874.1; -
DR PDB; 1AMX; 24-JUN-98.
DR INTERPRO; IPR001899; -
DR PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
KW Signal; Repeat; Transmembrane; Cell wall; 3D-structure.
FT SIGNAL 1 29 POTENTIAL..
FT CHAIN 30 1183 COLLAGEN ADHESIN.
FT DOMAIN 30 1157 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1158 1177 MEMBRANE ANCHOR (POTENTIAL).
FT DOMAIN 1178 1183 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 318 COLLAGEN-BINDING.
FT DOMAIN 533 1093 3 X 187 AA APPROXIMATE TANDEM REPEATS.
FT DOMAIN 1093 1157 LYS/PRO-RICH (CELL WALL-SPANNING).
FT DOMAIN 1151 1156 CONSERVED IN GRAM-POSITIVE COCCI SURFACE
FT PROTEINS.
FT REPEAT 533 719 B1.
FT REPEAT 720 906 B2.
FT REPEAT 907 1093 B3.
SQ SEQUENCE 1183 AA; 133066 MW; B6A1CC072E575D76 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 1183;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QSNWSPHT 9
:|:|:|

Db 666 ESNWTHHT 673
RESULT 10
AROL_PNECA STANDARD; PRT; 1581 AA.
AC Q12659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PENTAFUNCTIONAL AROM POLYPEPTIDE [INCLUDES: 3-DEHYDROQUINATE SYNTHASE
DE (EC 4.6.1.3); 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-
DE DEHYDROQUINASE); SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25); SHIKIMATE
DE KINASE (EC 2.7.1.71); 3-PHOSPHOSHAKIMATE 1-CARBOXYVINYLTRANSFERASE
DE (EC 2.5.1.19) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP
DE SYNTHASE) (EPSPS)].
GN AROM.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Fungi Incertae sedis; Pneumocystidaceae;
OC Pneumocystis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94172285.
RA Banerji S., Wakefield A.E., Allen A.G., Maskell D.J., Peters S.E.,
RA Hopkin J.M.;
RT "The cloning and characterization of the arom gene of Pneumocystis
RT carinii.";
RL J. Gen. Microbiol. 139:2901-2914(1993).
CC -1- FUNCTION: THE AROM POLYPEPTIDE CATALYSES 5 CONSECUTIVE ENZYMATIC
CC REACTIONS IN PRECHORISMATE POLYAROMATIC AMINO ACID BIOSYNTHESIS.
CC -1- CATALYTIC ACTIVITY: 7-PHOSPHO-3-DEOXY-ARABINO-HEPTULOSONATE -
CC 3-DEHYDROQUINATE + ORTHOPHOSPHATE.
CC -1- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE -> 3-DEHYDROSHIKIMATE + H(2)O.
CC -1- CATALYTIC ACTIVITY: SHIKIMATE + NADP(+) -> 5-DEHYDROSHIKIMATE +
CC NADPH.
CC -1- CATALYTIC ACTIVITY: ADP + SHIKIMATE -> ADP + SHIKIMATE 3-PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHAKIMATE -
CC ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHAKIMATE.
CC -1- PATHWAY: SECOND TO SIXTH STEPS IN THE BIOSYNTHESIS OF CHORISMATE
CC WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE
CC PATHWAY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
CC DEHYDROQUINATE SYNTHASE FAMILY.
CC -1- SIMILARITY: IN THE 3RD SECTION; BELONGS TO THE SHIKIMATE KINASE
CC FAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SHIKIMATE
CC DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL; L18918; AAA17839.1; -
DR INTERPRO; IPR000623; -
DR INTERPRO; IPR001381; -
DR INTERPRO; IPR001986; -
DR INTERPRO; IPR002658; -
DR INTERPRO; IPR002907; -
DR PFAM; PF01761; DHQ_synthase; 1.
DR PFAM; PF01487; DHQ_inase_I; 1.
DR PFAM; PF02075; EPSP_synthase; 1.
DR PFAM; PF01202; SKI; 1.
DR PFAM; PF01488; Shikimate_DH; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
DR PROSITE; PS01028; DEHYDROQUINASE_I; 1.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.

30-MAY-2000 (Rel. 39, Last annotation update)
 KETOL-ACID REDUCTOISOMERASE PRECURSOR (EC 1.1.1.86) (ACETOHYDROXY-ACID
 REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE).
 ILV-2.
 Neurospora crassa.
 Eukaryote; Fungi; Ascomycota; Sordariales; Sordariaceae; Neurospora.
 [1]
 SEQUENCE FROM N.A.
 MEDLINE; 93013010.
 Sista H., Bowman B.;
 "Characterization of the ilv-2 gene from Neurospora crassa encoding
 alpha-keto-beta-hydroxyacyl reductoisomerase.";
 Gene 120:115-118(1992).
 CC -1- CATALYTIC ACTIVITY: 2,3-DIHYDROXYISOLEVALERATE + NADP(+) =
 2-ACETOLACTATE + NADPH (ALSO: 2,3-DIHYDROXYACID-3-METHYLVALERATE
 + NADP(+)) - 2-ACETO-2-HYDROXYBUTYRATE + NADPH).
 CC -1- COFACTOR: REQUIRES MAGNESIUM.
 CC -1- PATHWAY: SECOND STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
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 CC
 EMBL; M84189; AAC00797.1; -;
 PIR; JC1428; JC1428.
 DR HSP; Q01292; 1YVE.
 DR INTERPRO; IPR000506; -;
 DR PFAM; PF01450; ILVC; 1.
 DR Oxidoreductase; Branched-chain amino acid biosynthesis; Magnesium;
 KW NADP; Mitochondrion; Transit peptide.
 KW TRANSIT 1 26 MITOCHONDRION (POTENTIAL).
 FT CHAIN 27 400 KETOL-ACID REDUCTOISOMERASE.
 FT NP_BIND 90 99 NADPH (POTENTIAL).
 FT ACT_SITE 177 177 POTENTIAL.
 FT SEQUENCE 400 AA; 44508 MW; D8AA4C0A3F4BD7CB CRC64;
 Query Match 65.5%; Score 36; DB 1; Length 400;
 Best Local Similarity 71.4%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 QSNSWPH 8
 Db 156 QSETWPH 162
 RESULT 8
 KKIT CANFA
 ID KIT_CANFA STANDARD; PRT; 975 AA.
 AC Q97799;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MAST/STEM CELL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (SCFR)
 DE (PROTO-ONCOGENE TYROSINE-PROTEIN KINASE KIT) (C-KIT).
 GN KIT.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 99142897.
 RA Ma W., Longley B.J., Wang X., Blount J.L., Langley K., Caughey G.H.;
 RT "Clustering of activating mutations in c-kit's juxtamembrane coding
 region in canine mast cell neoplasms.";
 RL J. Invest. Dermatol. 112:165-170(1999).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL

GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 3-KINASE (PI3K).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE DOMAINS.
 CC
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 CC
 EMBL; AF044249; AAD02327.1; -;
 DR HSP; P08631; 2HCK.
 DR INTERPRO; IPR000719; -;
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00069; pkinase; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Transmembrane; Immunoglobulin domain.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 975 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
 FT DOMAIN 25 519 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 520 542 POTENTIAL.
 FT DOMAIN 543 975 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 588 936 PROTEIN KINASE.
 FT NP_BIND 594 602 ATP (BY SIMILARITY).
 FT BINDING 622 622 ATP (BY SIMILARITY).
 FT ACT_SITE 791 791 BY SIMILARITY.
 FT MOD_RES 822 822 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 96 96 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 147 147 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 370 370 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 466 466 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 489 489 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 975 AA; 109335 MW; 8F570BDB9F05B1CB CRC64;
 Query Match 65.5%; Score 36; DB 1; Length 975;
 Best Local Similarity 85.7%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 QSNSWPH 8
 Db 261 QSNSWHH 267
 RESULT 9
 CNA_STAAU
 ID CNA_STAAU STANDARD; PRT; 1183 AA.
 AC Q53654;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE COLLAGEN ADHESIN PRECURSOR.
 GN CNA.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;

RT Igm anti-gamma globulins (Lay/Pom) with shared idiotypic
 RT specificities.";
 RL Scand. J. Immunol. 5:677-684(1976).
 CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01871; KIHULY.
 DR HSSP; P01607; IREI.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 25 49
 FT DOMAIN 30 56
 FT DOMAIN 35 88
 FT DOMAIN 37 88
 FT DOMAIN 39 97
 FT DOMAIN 40 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 65.5%; Score 36; DB 1; Length 108;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNWPH 9
 || i: || i
 Db 89 QQYNNWPT 97

RESULT 5
 KV3F_HUMAN
 ID KV3F_HUMAN STANDARD; PRT; 109 AA.
 AC P01624;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION POM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 76276460.
 RA Klapper D.G., Capra J.D.;
 RT "The amino acid sequence of the variable regions of the light chains
 RT from two idiotypically cross reactive Igm anti-gamma globulins.";
 RL Ann. Immunol. (Paris) 127C:261-271(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01897; K3HUPM.
 DR HSSP; P01789; 2MCP.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 109;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSNWPH 9
 || i: || i
 Db 90 QQYNNWPT 98

RESULT 6
 COGS_UCAPU
 ID COGS_UCAPU STANDARD; PRT; 226 AA.
 AC P00771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE BRACHYURIN (EC 3.4.21.32) (COLLAGENOLYTIC PROTEASE).
 OS Uca pugnator (Atlantic sand fiddler crab) (Celica pugnator).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Ocyropoidea; Ocypodidae; Celica.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEPATOPANCREAS;
 RX MEDLINE; 81040004.
 RA Grant G.A., Henderson K.O., Eisen A.Z., Bradshaw R.A.;
 RT "Amino acid sequence of a collagenolytic protease from the
 RT hepatopancreas of the fiddler crab, Uca pugnator.";
 RL Biochemistry 19:4653-4659(1980).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS), AND REVISIONS.
 RC TISSUE=HEPATOPANCREAS;
 RX MEDLINE; 97299771.
 RA Perona J.J., Tsu C.A., Craik C.S., Fletterick R.J.;
 RT "Crystal structure of an ecotin-collagenase complex suggests a model
 RT for recognition and cleavage of the collagen triple helix.";
 RL Biochemistry 36:5381-5392(1997).
 CC -1- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING
 CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS, WITH BROAD SPECIFICITY
 CC FOR PEPTIDE BONDS. DEGRADES NATIVE COLLAGEN AT ABOUT 75% OF THE
 CC LENGTH OF THE MOLECULE FROM THE N-TERMINUS. LOW ACTIVITY ON SMALL
 CC MOLECULE SUBSTRATES OF BOTH TRYPSIN AND CHYMOTRYPSIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR PIR; A00958; KCUF.
 DR PDB; 1AZZ; 25-FEB-98.
 DR INTERPRO; IPR001254; -.
 DR INTERPRO; IPR001314; -.
 DR PFAM; PF00089; trypsin; 1.
 DR PRINTS; PR00722; chymotrypsin.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Collagen degradation; 3D-structure.
 FT DISULFID 26 42
 FT DISULFID 151 164
 FT DISULFID 174 200
 FT ACT_SITE 41 41
 FT ACT_SITE 87 87
 FT ACT_SITE 178 178
 FT CONFLICT 91 91
 FT CONFLICT 147 148
 FT CONFLICT 175 175
 FT CONFLICT 185 185
 SQ SEQUENCE 226 AA; 23511 MW; E45591CAF332C8C CRC64;

Query Match 65.5%; Score 36; DB 1; Length 226;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NSWPH 8
 || || || ||
 Db 10 NSWPH 14

RESULT 7
 ILV5_NEUCR
 ID ILV5_NEUCR STANDARD; PRT; 400 AA.
 AC P38674;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12 / AN387;
 RX MEDLINE; 93273744.
 RA Wissenbach U., Unden G.;
 RT "Physical map location of the new *artPIOMJ* genes of *Escherichia coli*,
 encoding a periplasmic arginine transport system.";
 RL J. Bacteriol. 175:3687-3688(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE; 97061202.
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horuchi T.;
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 FOR ARGinine.
 CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 (ABC TRANSPORTERS).
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 DR EMBL; X86160; CAA60101.1; -
 DR EMBL; AE000188; AAC73951.1; -
 DR EMBL; D90724; BAA35578.1; -
 DR PIR; S31694; S31694.
 DR ECOGENE; EGI1624; ARTP.
 DR INTERPRO; IPR001617; -
 DR PRAM; PF00005; ABC_trap; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW Amino-acid transport; Transport; ATP-binding; Inner membrane.
 FT NP_BIND 35 42 ATP (POTENTIAL).
 FT CONFLICT 94 95 WP -> CA (IN REF. 1).
 FT CONFLICT 121 121 R -> S (IN REF. 1).
 SQ SEQUENCE 242 AA; 27022 MW; D5B50062E523413A CRC64;

Query Match 69.1%; Score 38; DB 1; Length 242;
 Best Local Similarity 75.0%; Pred. No. 6.2;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QQSNWSPH 8
 DB 89 QQYNLWPH 96

RESULT 3
 CTCLACILW STANDARD; PRT; 96 AA.
 AC Q33947;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MUONOLACTONE DELTA-ISOMERASE 1 (EC 5.3.3.4) (MIASE 1).
 GN CATCI.
 OS Acinetobacter lwoffii.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K24;
 RX MEDLINE; 97405925.
 RA Kim S.I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
 RA Park Y.K., Lee Y.N., Ha K.-S.;
 RT "Cloning and characterization of two *cata* genes in *Acinetobacter*
 RT lwoffii K24.";
 RL J. Bacteriol. 179:5226-5231(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K24;
 RX MEDLINE; 98139907.
 RA Kim S.I., Leem S.-H., Choi J.-S., Ha K.-S.;
 RT "Organization and transcriptional characterization of the *cataI* gene
 cluster in *Acinetobacter lwoffii* K24.";
 RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
 CC -1- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE -
 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.
 CC -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
 AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
 CC -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
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 or send an email to license@isb-sib.ch).
 DR EMBL; U77658; AAC46227.1; -
 KW Aromatic hydrocarbons catabolism; Isomerase.
 SQ SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;

Query Match 65.5%; Score 36; DB 1; Length 96;
 Best Local Similarity 62.5%; Pred. No. 5.4;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QQSNWSPH 8
 DB 35 QKSGKWP 42

RESULT 4
 KVIM_HUMAN STANDARD; PRT; 108 AA.
 ID KVIM_HUMAN
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION LAY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RN SEQUENCE.
 RP MEDLINE; 77038198.
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:09 ; Search time 72.95 Seconds
(without alignments)
3.941 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQNSNWPHT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	76.4	115	1 KV5I_MOUSE	P01642 mus musculus
2	38	69.1	242	1 ARTP_ECOLI	P30858 escherichia
3	36	65.5	96	1 CTCL_ACILW	O33947 acinetobact
4	36	65.5	108	1 KVIM_HUMAN	P01605 homo sapien
5	36	65.5	109	1 KV3F_HUMAN	P01624 homo sapien
6	36	65.5	226	1 COGS_UCAPU	P00771 uca pugilat
7	36	65.5	400	1 ILV5_NEUCR	P38674 neurospora
8	36	65.5	975	1 KKIT_CANFA	O97799 canis famil
9	36	65.5	1183	1 CNA_STAAR	O53654 staphylococ
10	36	65.5	1581	1 AR01_PNECA	Q12659 p pentafunc
11	36	65.5	1776	1 POLR_GYMV	P20127 ononis yell
12	34	61.8	108	1 KV3H_HUMAN	P04430 homo sapien
13	34	61.8	459	1 NUAM_PELSU	O79677 pelomedusa
14	34	61.8	492	1 TYTR_TRYCR	P28593 trypanosoma
15	34	61.8	519	1 GAG_SIVAT	P05892 simian immu
16	34	61.8	520	1 GAG_SIVAT	P27972 simian immu
17	33	60.0	87	1 YMC_BPPH1	P10435 bacterioph
18	33	60.0	129	1 KV3H_HUMAN	P04207 homo sapien
19	33	60.0	235	1 PSP_MOUSE	P07743 mus musculus
20	33	60.0	243	1 ARTP_HAEIN	P45092 haemophilus
21	33	60.0	254	1 VG12_BPMIL5	Q05328 mycobacteri
22	33	60.0	513	1 BMP6_HUMAN	P22004 homo sapien
23	33	60.0	521	1 GAG_SIVAG	P27978 simian immu
24	33	60.0	675	1 COP1_ARATH	P43254 arabidopsis
25	33	60.0	762	1 AOCX_BOVIN	Q29437 bos taurus
26	33	60.0	762	1 AOCY_BOVIN	O46406 bos taurus
27	33	60.0	822	1 DEXT_STRSL	Q59979 streptococ
28	32	58.2	192	1 Y3_SOCMV	P15633 soybean chl
29	32	58.2	194	1 VG37_HAEIN	P44231 haemophilus
30	32	58.2	253	1 RL6_YEAST	P05736 saccharomyc
31	32	58.2	266	1 ELI_PIG	P00772 sus scrofa
32	32	58.2	287	1 DLX3_MOUSE	Q64205 mus musculus
33	32	58.2	301	1 NKR5_HUMAN	P43631 homo sapien

34	32	58.2	304	1	NKR6_HUMAN	P43632 homo sapien
35	32	58.2	304	1	NKR7_HUMAN	Q14952 homo sapien
36	32	58.2	304	1	NKR9_HUMAN	Q14953 homo sapien
37	32	58.2	310	1	YHCQ_ECOLI	P46482 escherichia
38	32	58.2	341	1	NKR2_HUMAN	P43628 homo sapien
39	32	58.2	348	1	NKR0_HUMAN	P43627 homo sapien
40	32	58.2	348	1	NKR1_HUMAN	P43626 homo sapien
41	32	58.2	471	1	UFOL_MAIZE	P16166 zea mays (m
42	32	58.2	618	1	MUTL_SALTY	P14161 salmonella
43	32	58.2	723	1	RRPO_TNVA	P22958 tobacco nec
44	32	58.2	727	1	CATA_SALTY	P17750 salmonella
45	32	58.2	752	1	PSAA_ODOSI	P19479 odontella s

ALIGNMENTS

RESULT 1
KV5I_MOUSE STANDARD; PRT: 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81220975.
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -1- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPICE JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR; A01925; KVM5L7.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 76.4%; Score 42; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQNSNP 7
| | | | |
Db 109 QQNSNP 115

RESULT 2
ARTP_ECOLI STANDARD; PRT: 242 AA.
ID ARTP_ECOLI
AC P30858; P77355;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ARGININE TRANSPORT ATP-BINDING PROTEIN ARTP.
GN ARTP.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
 F:36-110/Domain: immunoglobulin homology <IMM>
 F:43-108/Disulfide bonds: #status predicted

Query Match 76.4%; Score 42; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 0.98;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWP 7
 |||||
 Db 109 QQSNSWP 115

RESULT 13

PN0445
 Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PN0445
 R:Kalaza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
 Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction
 A:Reference number: PN0444; MUID:93138402

A:Accession: PN0445
 A:Molecule type: mRNA
 A:Residues: 1-128 <KAL>

A:Cross-references: G8:102347
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-10/Domain: signal sequence #status predicted <SIG>
 F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
 F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 128;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWP 9
 |||||
 Db 99 QQTNSWPT 107

RESULT 14

S40343

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)
 C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40343
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891

A:Accession: S40343
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA

A:Residues: 1-128 <KLE>
 A:Cross-references: EMBL:X72453; NID:9441374; PID:9441375
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 40; DB 2; Length 128;
 Best Local Similarity 66.7%; Pred. No. 2.5;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWP 9
 |||||
 Db 109 QQYNNWPT 117

RESULT 15

C40201

artifactual warning sequence (translated ALU class C) - human

C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
 C:Accession: C40201

R:Claverie, J.M.

A:Reference number: A40201

A:Accession: C40201

A:Molecule type: DNA

A:Residues: 1-613 <CLA>

R:Claverie, J.M.

Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potential artifacts
 A:Reference number: A40200; MUID:92241891

A:Contents: annotation

C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of the sequence.

C:Comment: Any significant similarity of a predicted protein sequence to a portion of the sequence is noted.

Query Match 72.7%; Score 40; DB 4; Length 613;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNSWP 8
 |||||
 Db 588 SNSWP 593

Search completed: March 28, 2001, 07:04:29
 Job time: 1067 sec

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 46; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 0.17;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |

DB 87 QOSNTWPYT 95

RESULT 8

IG kappa chain V region - mouse (fragment)
B43413

C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177
A:Accession: B43413
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 44; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |

DB 86 QOSNSWPLT 94

RESULT 9

IG kappa chain V region (D444) - mouse
C30502

C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: C30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787
A:Accession: C30502
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <EIL>
A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 44; DB 2; Length 108;
Best Local Similarity 77.8%; Pred. No. 0.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |

DB 89 QOTNSWPHT 97

RESULT 10

A26471
IG kappa chain precursor V region (MAK33) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 80.0%; Score 44; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
| | | | | | | | | |

DB 109 QOSNSWPLT 117

RESULT 11

PHI082

IG light chain V region (clone 165.54) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PHI082
R:Tillman, D.M.; Joo, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PHI082
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-87 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]FI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:6-80/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWP 7
| | | | | | | | | |

DB 79 QOSNSWP 85

RESULT 12

KVMSL7

IG kappa chain precursor V region (L7) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999
C:Accession: A01925
R:Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding s
A:Reference number: A93259; MUID:81220975
A:Accession: A01925
A:Molecule type: DNA
A:Residues: 1-115 <PEC>
A:Cross-references: GB:V01564; GB:J00574; NID:g51718; PIDN:CAA24884.1; PID:g758153
A:Note: the sequence was determined from the germline gene
A:Note: there appear to be two possible splice junctions at the 3' end of the intron;
C:Genetics:
A:Introns: 17/1

Query Match 100.0%; Score 55; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 |||||
 DB 101 QQSNSWPHT 109

RESULT 3

B45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J.; Virol, J.; 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human IgG1 heavy chain variable domain (Mab 33) - mouse (fragment)
 A:Reference number: A45722; MUID:93100833
 A:Accession: B45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 52; DB 2; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.015;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 |||||
 DB 89 QQSNSWPHT 97

RESULT 4

PL0267
 Ig kappa chain V region (anti-DNA, DPL2VK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0267
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation of the V region
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0267
 A:Molecule type: mRNA
 A:Residues: 1-106 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-106/Region: framework 4

Query Match 89.1%; Score 49; DB 2; Length 106;
 Best Local Similarity 88.9%; Pred. No. 0.051;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 |||||
 DB 89 QQSNSWPHT 97

RESULT 5

PH1081
 Ig light chain V region (clone 165.6) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
 C:Accession: PH1081
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective hypermutation of the V region
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1081
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-67 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 85.5%; Score 47; DB 2; Length 67;
 Best Local Similarity 88.9%; Pred. No. 0.072;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 |||||
 DB 58 QQSNSWPHT 66

RESULT 6

PH1080
 Ig light chain V region (clone 165.60) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
 C:Accession: PH1080
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective hypermutation of the V region
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1080
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-69 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 85.5%; Score 47; DB 2; Length 69;
 Best Local Similarity 88.9%; Pred. No. 0.074;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
 |||||
 DB 60 QQSNSWPHT 68

RESULT 7

S26346
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26346
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <STA>
 A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:28 ; Search time 130.08 Seconds
(without alignments)
4.698 Million cell updates/sec

Title: US-09-016-061-86

Perfect score: 55

Sequence: 1 QQNSNWPHT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	107	2 A45722	anti-glycoprotein
2	55	100.0	123	2 S35479	Ig kappa chain pre
3	52	94.5	107	2 B45722	anti-glycoprotein
4	49	89.1	106	2 P40267	Ig kappa chain v r
5	47	85.5	67	2 P1081	Ig light chain v r
6	47	85.5	69	2 P1080	Ig light chain v r
7	46	83.6	102	2 S26346	Ig kappa chain v r
8	44	80.0	104	2 B43413	Ig kappa chain v r
9	44	80.0	108	2 C30502	Ig kappa chain v r
10	44	80.0	138	2 A36471	Ig kappa chain pre
11	42	76.4	87	2 P1082	Ig light chain v r
12	42	76.4	115	1 KVMSL7	Ig kappa chain pre
13	42	76.4	128	2 PNO445	Ig kappa chain pre
14	40	72.7	128	2 S40343	Ig kappa chain v r
15	40	72.7	613	4 C40201	artifact-warning s
16	38	69.1	91	2 S37527	Ig kappa chain v r
17	38	69.1	242	2 H64824	arginine transport
18	38	69.1	278	2 S60619	homeotic protein c
19	36	65.5	86	2 C28195	Ig kappa chain v r
20	36	65.5	96	2 JC5945	regulatory protein
21	36	65.5	107	2 C45722	anti-glycoprotein
22	36	65.5	108	1 K1HULY	Ig kappa chain v r
23	36	65.5	109	1 K3HUPM	Ig kappa chain v r
24	36	65.5	118	2 S59461	hypothetical prote
25	36	65.5	226	1 KCUP	brachyurin (EC 3.4
26	36	65.5	400	1 JC1428	ketol-acid reducto
27	36	65.5	640	2 T26820	hypothetical prote
28	36	65.5	1185	2 A42404	collagen adhesin -
29	36	65.5	1581	2 T30832	pentafunctional en

genome polyprotein
Ig kappa chain v r
Ig kappa chain - h
hypothetical prote
probable alanine r
transcription acti
Ig kappa chain v r
Ig kappa chain v r
anti-DNA autoantib
Ig kappa chain - h
transposase (clone
glycoprotein gp82/
Ig kappa chain NIG
NADH dehydrogenase
trypanothione redu
gag polyprotein -

ALIGNMENTS

RESULT 1

A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C:Species: Mus musculus (house mouse))
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 55; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQNSNWPHT 9
Db 89 QQNSNWPHT 97
|||||

RESULT 2

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wiser, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-References: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 11
| | | | |
DB 46 LLIKYASQSI 56

Search completed: March 28, 2001, 07:01:58
Job time: 1337 sec

;; MEDIUM TYPE: Floppy disk
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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/487,200
;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 62:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-487-200-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQIS 11
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Db 46 LLIKYASQIS 56

RESULT 14
US-08-487-200-63
; Sequence 63, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200

;; FILING DATE: 7-JUN-1995
;; CLASSIFICATION: 424
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;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-487-200-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQIS 11
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Db 46 LLIKYASQIS 56

RESULT 15
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:

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; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLIRYSQSIS 11
Db 46 LLIRYSQSIS 56

RESULT 12
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
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; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLIRYSQSIS 11
Db 46 LLIRYSQSIS 56

RESULT 13
US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
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Query Match 87.8%; Score 43; DB 1; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.12;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 Db 46 LLIKYASQSIS 56

RESULT 9
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 ; Sequence 87, Application US/08477728
 ; Patent No. 5585089
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
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 APPLICATION NUMBER: US/08/477,728
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/534,278
 FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 87:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-477-728-87

Query Match 87.8%; Score 43; DB 1; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.12;
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QY 1 LLIRYSQSIS 11
 Db 46 LLIKYASQSIS 56

RESULT 10
 US-08-474-040-62
 ; Sequence 62, Application US/08474040
 ; Patent No. 5693761
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301

COMPUTER READABLE FORM:
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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
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 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-474-040-62

Query Match 87.8%; Score 43; DB 1; Length 107;
 Best Local Similarity 81.8%; Pred. No. 0.12;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
 Db 46 LLIKYASQSIS 56

RESULT 11
 US-08-474-040-63
 ; Sequence 63, Application US/08474040
 ; Patent No. 5693761
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung

; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 7
US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 8
US-08-477-728-63
; Sequence 63, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
|||:|:||||
Db 46 LLIKVASQSIS 56

RESULT 5
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 87.8%; Score 43; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSIS 11
|||:|:||||
Db 46 LLIKVASQSIS 56

RESULT 6
US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975

US-08-737-560A-9

Query Match 87.8%; Score 43; DB 2; Length 96;
Best Local Similarity 81.8%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSQSIS 11
Db 46 LLIKYASQSIS 56

RESULT 2

US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 100 amino acids
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-463-19

Query Match 87.8%; Score 43; DB 1; Length 100;
Best Local Similarity 81.8%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSQSIS 11
Db 46 LLIKYASQSIS 56

RESULT 3

US-08-326-362-4
; Sequence 4, Application US/08326362
; Patent No. 5730981

GENERAL INFORMATION:

APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,362
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DE P 42 08 795.3
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:

NAME: Einaudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 02481-1276-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-326-362-4

Query Match 87.8%; Score 43; DB 1; Length 106;
Best Local Similarity 81.8%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSQSIS 11
Db 46 LLIRYSSESIS 56

RESULT 4

US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:57 ; Search time 113.49 Seconds
(without alignments)
1.740 Million cell updates/sec

Title: US-09-016-061-84

Perfect score: 49

Sequence: 1 LLIRYSSQIS11

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*

2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*

3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*

4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	43	87.8	96	2	US-08-737-560A-9
2	43	87.8	100	1	US-08-436-463-19
3	43	87.8	106	1	US-08-326-362-4
4	43	87.8	107	1	US-07-634-278-62
5	43	87.8	107	1	US-07-634-278-63
6	43	87.8	107	1	US-07-634-278-87
7	43	87.8	107	1	US-08-477-728-62
8	43	87.8	107	1	US-08-477-728-63
9	43	87.8	107	1	US-08-477-728-87
10	43	87.8	107	1	US-08-474-040-62
11	43	87.8	107	1	US-08-474-040-63
12	43	87.8	107	1	US-08-474-040-87
13	43	87.8	107	1	US-08-487-200-62
14	43	87.8	107	1	US-08-487-200-63
15	43	87.8	107	1	US-08-487-200-87
16	43	87.8	107	1	US-08-436-463-20
17	43	87.8	107	1	US-08-107-669D-1
18	43	87.8	107	1	US-08-472-788A-1
19	43	87.8	107	2	US-08-477-531B-1
20	43	87.8	107	2	US-08-082-842A-1
21	43	87.8	108	2	US-08-737-560A-11
22	43	87.8	109	1	US-07-942-245-4
23	43	87.8	127	1	US-07-634-278-83
24	43	87.8	127	1	US-08-477-728-83
25	43	87.8	127	1	US-08-474-040-83
26	43	87.8	127	1	US-08-487-200-83
27	43	87.8	127	1	US-08-436-463-4
28	43	87.8	127	1	US-08-436-463-18

29 41 83.7 103 1 US-08-436-463-21 Sequence 21, Appl
30 40 81.6 106 2 US-08-800-198-4 Sequence 4, Appl
31 40 81.6 106 3 US-09-296-595-4 Sequence 4, Appl
32 40 81.6 107 2 US-08-232-081B-9 Sequence 9, Appl
33 40 81.6 107 2 US-08-232-081B-40 Sequence 40, Appl
34 40 81.6 107 2 US-08-476-176B-4 Sequence 4, Appl
35 40 81.6 107 3 US-08-127-721A-4 Sequence 4, Appl
36 40 81.6 107 3 US-08-485-246A-4 Sequence 6, Appl
37 40 81.6 127 2 US-08-476-176B-6 Sequence 8, Appl
38 40 81.6 127 2 US-08-476-176B-8 Sequence 10, Appl
39 40 81.6 127 2 US-08-476-176B-10 Sequence 6, Appl
40 40 81.6 127 3 US-08-127-721A-6 Sequence 8, Appl
41 40 81.6 127 3 US-08-127-721A-8 Sequence 10, Appl
42 40 81.6 127 3 US-08-127-721A-10 Sequence 6, Appl
43 40 81.6 127 3 US-08-485-246A-6 Sequence 8, Appl
44 40 81.6 127 3 US-08-485-246A-8 Sequence 10, Appl
45 40 81.6 127 3 US-08-485-246A-10

ALIGNMENTS

RESULT 1
US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuill
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuill
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; CITY: Kwanak-gu
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: VK23.32'CL

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:29 ; Search time 130.08 Seconds
(without alignments)
4.698 Million cell updates/sec

Title: US-09-016-061-88

Perfect score: 54

Sequence: 1 QOSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 6790655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	90.7	107	2 A45722	anti-glycoprotein
2	49	90.7	123	2 S35479	Ig kappa chain - h
3	46	85.2	107	2 B45722	anti-glycoprotein
4	43	79.6	106	2 PL0267	Ig kappa chain pre
5	41	75.9	67	2 PH1081	Ig light chain v r
6	41	75.9	69	2 PH1080	Ig light chain v r
7	40	74.1	102	2 S26346	Ig kappa chain v r
8	38	70.4	104	2 B43413	Ig kappa chain v r
9	38	70.4	108	2 C30502	Ig kappa chain v r
10	38	70.4	138	2 A28471	Ig kappa chain pre
11	38	70.4	235	1 SQMS	parotid secretory
12	37	68.5	433	2 B82965	hypothetical prote
13	37	68.5	739	2 S47772	biotin sulfoxide r
14	36	66.7	87	2 PH1082	Ig light chain v r
15	36	66.7	100	2 S63860	hypothetical prote
16	36	66.7	115	1 KVMSL7	Ig kappa chain pre
17	36	66.7	128	2 PN0445	Ig kappa chain pre
18	36	66.7	323	2 T46671	probable aromatase
19	35	64.8	170	2 C82480	hypothetical prote
20	35	64.8	235	2 B42337	parotid secretory
21	35	64.8	400	1 JCI428	ketol-acid reducto
22	35	64.8	484	2 B82165	glycogen synthase
23	35	64.8	731	2 A83536	conserved hypothet
24	35	64.8	770	2 S76095	hypothetical prote
25	35	64.8	774	1 JQ0550	1,4-alpha-glucan b
26	35	64.8	4845	2 T31067	BIR repeat contain
27	34	63.0	96	2 JC5945	regulatory protein
28	34	63.0	97	2 D82789	hypothetical prote
29	34	63.0	118	2 S40374	Ig kappa chain - h

30	34	63.0	122	2 S40338	Ig kappa chain - h
31	34	63.0	128	2 S40343	Ig kappa chain v-j
32	34	63.0	133	2 S23230	Ig kappa chain pre
33	34	63.0	254	2 S30957	gene 12 protein -
34	34	63.0	448	2 T17290	hypothetical prote
35	34	63.0	452	1 WZBE4	gene 4 protein - h
36	34	63.0	608	2 T53269	prolactin receptor
37	34	63.0	613	4 C40201	artifect-warnin s
38	34	63.0	640	2 T26820	hypothetical prote
39	34	63.0	815	2 H64949	biotin sulfoxide r
40	34	63.0	817	2 A47716	dolichyl-phosphate
41	34	63.0	848	2 C64841	trimethylamine-N-o
42	34	63.0	1045	2 T16275	hypothetical prote
43	34	63.0	1189	1 JC2366	protein-tyrosine-p
44	34	63.0	1918	2 S43719	lactase (EC 3.2.1.
45	34	63.0	1920	2 S43720	lactase (EC 3.2.1.

ALIGNMENTS

RESULT 1
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C)
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. NO. 0.061;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QOSTSWPHT 9
Db 89 QOSTSWPHT 97
RESULT 2
S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

```

Query Match      90.7%; Score 49; DB 2; Length 123;
Best Local Similarity 88.9%; Pred. No. 0.071;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
   ||| |||||
Db 101 QQSNSWPHT 109

RESULT 3
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: B45722; MUID:93100833
A:Accession: B45722
A>Status: preliminary: not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 46; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
   ||: |||||
Db 89 QOTNSWPHT 97

RESULT 4
PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match      79.6%; Score 43; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.68;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
   ||| |||||
Db 89 QQSNSWPHT 97

RESULT 5
PHI081
Ig light chain V region (clone 165.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PHI081
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PHI081
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-67 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match      75.9%; Score 41; DB 2; Length 67;
Best Local Similarity 77.8%; Pred. No. 0.94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
   ||| |||||
Db 58 QQSNSWPHT 66

RESULT 6
PHI080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PHI080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PHI080
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match      75.9%; Score 41; DB 2; Length 69;
Best Local Similarity 77.8%; Pred. No. 0.97;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
   ||| |||||
Db 60 QQSNSWPHT 68

RESULT 7
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421
A:Accession: S26346
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PTDN:CAA41921.1; PID:g1334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

```

?

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 102;
 Best Local Similarity 66.7%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 |||:||||

DB 87 QQSNSWPT 95

RESULT 8

Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B43413
 R:Tomiya, Y.; Brojer, E.; Ruggieri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 38; DB 2; Length 104;
 Best Local Similarity 77.8%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 |||:||||

DB 86 QQSNSWPT 94

RESULT 9

Ig kappa chain V region (D444) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
 C:Accession: C30502
 R:Eilat, D.; Webster, D.M.; Rees, A.R.
 J. Immunol. 141, 1745-1753, 1988
 A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m/c
 A:Reference number: A30502; MUID:88315787
 A:Accession: C30502
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <EIL>
 A:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 38; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 5.2;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 |||:||||

DB 89 QQTNSWPT 97

RESULT 10

A26471
 Ig kappa chain precursor V region (MAK33) - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C:Accession: A26471
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
 A:Reference number: A91572; MUID:87248058
 A:Accession: A26471
 A:Molecule type: mRNA
 A:Residues: 1-138 <BUC>
 A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 70.4%; Score 38; DB 2; Length 138;
 Best Local Similarity 77.8%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
 |||:||||

DB 109 QQSNSWPT 117

RESULT 11

SOMS
 parotid secretory protein precursor - mouse
 N:Alternate names: PSP
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
 C:Accession: A23031; I53236
 R:Madsen, H.O.; Hjorth, J.P.
 Nucleic Acids Res. 13, 1-13, 1985
 A:Title: Molecular cloning of mouse PSP mRNA.
 A:Reference number: A23031; MUID:85215456
 A:Accession: A23031
 A:Molecule type: mRNA
 A:Residues: 1-235 <MAD>
 A:Cross-references: GB:X01697; NID:g53810; PIDN:CAA25846.1; PID:g758163
 R:Poulsen, K.; Jakobsen, B.K.; Mikkelsen, B.M.; Harmark, K.; Nielsen, J.T.; Hjorth, J
 EMBO J. 5, 1891-1896, 1986
 A:Title: Coordination of murine parotid secretory protein and salivary amylase expres
 A:Reference number: I53236; MUID:87004556
 A:Accession: I53236
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: DNA
 A:Residues: 1-87 <RES>
 A:Cross-references: GB:M26807; NID:g200556; PIDN:AAA40009.1; PID:g554264
 C:Comment: PSP is the most abundant protein in the parotid gland. Its function is not
 C:Genetics:
 A:Gene: PSP
 A:Map position: 2
 A:Introns: 41/1
 A:Note: list of introns may be incomplete
 C:Superfamily: parotid secretory protein
 C:Keywords: parotid gland; saliva
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-235/Product: parotid secretory protein #status predicted <MAT>

Query Match 70.4%; Score 38; DB 1; Length 235;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSTSWP 7
 ||:||||

DB 54 QQATSWP 60

RESULT 12

B82965

hypothetical protein PA5456 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
 C:Accession: B82965
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: B82965
 A:Accession: B82965
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-433 <STO>
 A:Cross-references: GB:AE004958; GB:AE004091; NID:g9951776; PIDN:AAG08841.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA5456

Query Match 68.5%; Score 37; DB 2; Length 433;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSTSWP 8

Db 346 EATAMP 353
 :::|::|

RESULT 13

S47772
 biotin sulfoxide reductase (BC 1-...-1) - Escherichia coli
 C:Species: Escherichia coli
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S47772; J0071; A65154

R:Plunkett, G.
 submitted to the EMBL Data Library, March 1994

A:Reference number: S47666
 A:Accession: S47772
 A:Molecule type: DNA
 A:Residues: 1-739 <PLU>
 A:Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18528.1; PID:g466689
 R:Pierston, D.E.; Campbell, A.
 J. Bacteriol. 172, 2194-2198, 1990
 A:Title: Cloning and nucleotide sequence of bscC, the structural gene for biotin sulfoxi
 A:Reference number: J0071; MUID:90202748
 A:Accession: J00071
 A:Molecule type: DNA
 A:Residues: 1-544, 'AFLPRAGD', 554-557, 'OR', 561-708, 'MAVRVIRRHGKNTVRN' <PIE>
 A:Cross-references: GB:M34827; NID:g145435; PIDN:AA23522.1; PID:g145436
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617
 A:Accession: A65154
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-739 <BLAT>
 A:Cross-references: GB:AE000432; GB:U00096; NID:g2367241; PIDN:AAC76575.1; PID:g1789973;
 A:Experimental source: strain K-12, substrain MG1655
 C:Comment: This enzyme may serve as a scavenger, allowing the cell to utilize biotin sul
 C:Genetics:
 A:Gene: bscC
 A:Map position: 79 min
 C:Superfamily: trimethylamine-N-oxide reductase
 C:Keywords: ATP; molybdenum; P-loop; oxidoreductase
 F:486-493/Region: nucleotide-binding motif A (P-loop)

Query Match 68.5%; Score 37; DB 2; Length 739;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWP 7
 ::|::|::|

Db 129 QOSTSWP 135

RESULT 14

PH1082
 Ig light chain V region (clone 165.54) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1082
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1082
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-87 <TIL>
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:6-80/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 36; DB 2; Length 87;
 Best Local Similarity 85.7%; Pred. No. 9.3;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWP 7

Db 79 QOSTSWP 85
 ::|::|::|

RESULT 15

S69860
 hypothetical protein YML116w-a - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
 C:Accession: S69860
 R:Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, May 1995

A:Reference number: S53954
 A:Accession: S69860
 A:Molecule type: DNA
 A:Residues: 1-100 <SKE>
 A:Cross-references: EMBL:249210; GSPDB:GN00013; MIPS:YML116w-a
 C:Genetics:
 A:Gene: MIPS:YML116w-a
 A:Map position: 13L
 C:Superfamily: Saccharomyces hypothetical protein YML116w-a

Query Match 66.7%; Score 36; DB 2; Length 100;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9

Db 22 QDLTSWPNT 30
 ::|::|::|

Search completed: March 28, 2001, 07:04:31
 Job time: 1089 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:11 ; Search time 72.95 Seconds
(without alignments)
3.941 Million cell updates/sec

Title: us-09-016-061-88

Perfect score: 54

Sequence: 1 QQSTSWPHT 9

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	70.4	235	1 PSP_MOUSE	P07743 mus musculus
2	37	68.5	777	1 BISC_ECOLI	P20099 escherichia
3	36	66.7	115	1 KV5I_MOUSE	P01642 mus musculus
4	35	64.8	400	1 ILV5_NEUCR	P38674 neurospora
5	35	64.8	734	1 GLGB_AGRU	P52979 agrobacteri
6	35	64.8	770	1 GLGB_SINY3	P52981 synechocyst
7	35	64.8	773	1 GLGB_SINP7	P16954 synechococc
8	34	63.0	96	1 CTC1_ACILW	Q33947 acinetobact
9	34	63.0	178	1 ATPQ_DROME	Q24251 drosophila
10	34	63.0	254	1 VG12_BPML5	Q05328 mycobacteri
11	34	63.0	452	1 IE63_VZVD	P09269 varicella-z
12	34	63.0	608	1 PRUR_MOUSE	Q08501 mus musculus
13	34	63.0	809	1 B1S2_ECOLI	P46923 escherichia
14	34	63.0	817	1 PMT1_YEAST	P33775 saccharomyc
15	34	63.0	848	1 TORA_ECOLI	P33225 escherichia
16	34	63.0	1189	1 PTNE_MOUSE	Q62130 mus musculus
17	34	63.0	1926	1 LPH_RABIT	P09849 oryctolagus
18	33	61.1	591	1 LAC1_CRYPA	Q03966 cryptoneutr
19	33	61.1	605	1 VP40_VZVD	P09286 varicella-z
20	33	61.1	668	1 MTMW_METWO	Q59647 methanobact
21	33	61.1	765	1 YF63_MYCTU	Q10768 mycobacteri
22	33	61.1	780	1 NH48_CAEEL	Q94407 caenorhabdi
23	33	61.1	810	1 IL4R_MOUSE	P16382 mus musculus
24	33	61.1	862	1 PCGV_MACNE	Q28858 macaca neme
25	33	61.1	1417	1 BLM_HUMAN	P54132 homo sapien
26	33	61.1	1517	1 YD22_SCHPO	Q10250 schizosacch
27	33	61.1	3396	1 PCGV_HUMAN	P13611 homo sapien
28	32	59.3	105	1 RNF1_GIBBA	P16411 gibberella
29	32	59.3	105	1 RNF2_GIBBA	P16412 gibberella
30	32	59.3	106	1 RNF1_GIBFU	P10282 gibberella
31	32	59.3	175	1 VPG_BWVVF	P09511 beet wester
32	32	59.3	175	1 VPG_BWVVG	P09512 beet wester
33	32	59.3	179	1 RIML_ECOLI	P13857 escherichia

34 32 59.3 211 1 UL45_HSVMB P22652 marek's dis
35 32 59.3 211 1 UL45_HSVMM P22653 marek's dis
36 32 59.3 232 1 KLK_PIG P00752 sus scrofa
37 32 59.3 242 1 ARTP_ECOLI P30858 escherichia
38 32 59.3 261 1 KLK3_MOUSE P00756 mus musculus
39 32 59.3 272 1 OX40_MOUSE P47741 mus musculus
40 32 59.3 335 1 XYNB_STRLI P26515 streptomyce
41 32 59.3 336 1 CH12_ORYSA P25765 oryza sativ
42 32 59.3 348 1 NU2M_MYXGL O21078 myxine glut
43 32 59.3 367 1 YC36_HAEIN P44132 haemophilus
44 32 59.3 492 1 TYTR_TRYCR P28593 trypanosoma
45 32 59.3 513 1 BMP6_HUMAN P22004 homo sapien

ALIGNMENTS

RESULT 1

PSP_MOUSE STANDARD; PRT; 235 AA.
ID PSP_MOUSE
AC P07743;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PAROTID SECRETORY PROTEIN PRECURSOR (PSP).

GN PSP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PAROTID GLAND;

RX MEDLINE; 85215456.

RA Madsen H.O., Hjorth J.P.;

RT "Molecular cloning of mouse PSP mRNA.";

RL Nucleic Acids Res. 13:1-13(1985).

RN [2]

RP SEQUENCE OF 1-87 FROM N.A.

RC STRAIN=C3H; TISSUE=SPLEEN;

RX MEDLINE; 87004356.

RA Poulsen K., Jakobsen B.K., Mikkelsen B.M., Harmark K.,

RA Nielsen J.T., Hjorth J.P.;

RT "Coordination of murine parotid secretory protein and salivary

amylase expression.";

RL EMBO J. 5:1891-1896(1986).

CC -1- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.

CC ITS FUNCTION IS NOT KNOWN; HOWEVER, ITS PRODUCTION IS COORDINATED

CC WITH THAT OF SALIVARY AMYLASE.

CC -----

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CC -----

CC EMBL; X01697; CAA25846.1; -

DR EMBL; M26807; AAA40009.1; -

DR EMBL; M26806; AAA40009.1; JOINED.

DR EMBL; M26806; AAA40009.1; JOINED.

DR PIR; A23031; SQMS.

DR MGD; MGI:97787; PSP.

KW Parotid gland; signal.

FT SIGNAL 1 20

FT CHAIN 21 235

SQ SEQUENCE 235 AA; 24753 MW; 23311BAE1E6E2EF3 CRC64;

POTENTIAL.

PAROTID SECRETORY PROTEIN.

Query Match 70.4%; Score 38; DB 1; Length 235;

Best Local Similarity 85.7%; Pred. No. 4;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSTSWP 7


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Db 486 EESTSWP 492
:::|||||
RESULT 7
GLGB_SYPN7 STANDARD; PRT; 773 AA.
AC PL6954;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
DE ENZYME).
GN GLGB.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90323609.
RA Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.;
RT "Nucleotide sequence of the Synecococcus sp. PCC7942 branching
RL enzyme gene (glgB): expression in Bacillus subtilis.";
Gene 89:77-84(1990).
CC -!- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
CC -!- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS
CC APPROXIMATELY 35 DEGREES CELSIUS.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
-----
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-----
DR EMBL; M31544; AAB39038.1; -
DR PIR; JQ0550; JQ0550.
DR INTERPRO; IPR000461; -
DR PFAM; PF00128; alpha-amylase; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT INIT-MET 0
FT ACT_SITE 439 439 BY SIMILARITY.
FT ACT_SITE 492 492 BY SIMILARITY.
FT ACT_SITE 560 560 BY SIMILARITY.
SQ SEQUENCE 773 AA; 89063 MW; 52BAAL7CA337BF57 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 773;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSTSWP 7
:::|||||
Db 492 EESTSWP 498
RESULT 8
CTCL_ACILW STANDARD; PRT; 96 AA.
AC O33947;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MUCONOLACTONE DELTA-ISOMERASE 1 (EC 5.3.3.4) (MIASE 1).
GN CATC3.
OS Acinetobacter lwofii.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99168769.
RA Caggese C., Ragone G., Perrini B., Moschetti R., De Pinto V.,
RA Caizzi R., Barsanti P.;
RT "Identification of nuclear genes encoding mitochondrial proteins:
RT isolation of a collection of D. melanogaster cDNAs homologous to
RL sequences in the Human Gene Index database.";
Mol. Gen. Genet. 261:64-70(1999).
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC
CC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC IT HAS NO APPARENT BACTERIAL HOMOLOG AND ITS EXACT FUNCTION IS
CC UNKNOWN.
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(0) SEEMS TO

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CC      * HAVE NINE SUBUNITS: A, B, C, D, E, F, G, F6 AND 8 (OR A6L).
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X99667; CAA67981.1; -.
DR      FLYBASE: FBgn0016120; ATPsyn-d.
KW      Hydrogen ion transport; CF(0); Mitochondrion.
SQ      SEQUENCE 178 AA; 20228 MW; 199B43BEBA8E02B9 CRC64;

Query Match      63.0%; Score 34; DB 1; Length 178;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 TSWPHT 9
Db 152 TPWPH 157

RESULT 10
VG12_BPML5      STANDARD; PRT; 254 AA.
AC Q05328;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE GENE 12 PROTEIN (GP12).
GN 12.
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -----
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CC -----
DR      EMBL: Z18946; CAA79388.1; -.
DR      PIR: S30957; S30957.
SQ      SEQUENCE 254 AA; 28847 MW; 8627B76D26E42360 CRC64;

Query Match      63.0%; Score 34; DB 1; Length 254;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QSTSWPH 8
Db 234 QGFSWPH 240

RESULT 11
IE63_VZVD
ID IE63_VZVD      STANDARD; PRT; 452 AA.
AC P09269;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)

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DE      TRANSCRIPTIONAL REGULATOR IE63 HOMOLOG.
GN 4.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsRNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86306657.
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC HSV-2 UL54, EBV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC -----
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CC -----
DR      EMBL: X04370; CAA27887.1; -.
DR      PIR: D27212; WZBE4.
KW Transcription regulation.
SQ      SEQUENCE 452 AA; 51543 MW; 42926E471E380B4 CRC64;

Query Match      63.0%; Score 34; DB 1; Length 452;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOSTSWP 7
Db 242 KONTSWP 248

RESULT 12
PRLR_MOUSE
ID PRLR_MOUSE      STANDARD; PRT; 608 AA.
AC Q08501; Q62099; P15213; P15212;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=C3H; TISSUE=MAMMARY GLAND;
RX MEDLINE: 94085788.
RA Moore R.C., Oka T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
RT long-form prolactin receptor.";
RL Gene 134:263-265(1993).
RN [2]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE: 93307149.
RA Clarke D.L., Linzer D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
RT mouse ovary.";
RL Endocrinology 133:224-232(1993).
RN [3]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA Sasaki M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=BALB/C; TISSUE=MAMMARY GLAND;
RA Edery M., Pezet A., Nandi S., Kelly P.A.;

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RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
 RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
 RX MEDLINE; 89261824.
 RA Davis J.A., Linzer D.I.H.;
 RT "Expression of multiple forms of the prolactin receptor in mouse
 liver.";
 RL Mol. Endocrinol. 3:674-680(1989).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN, AS WELL AS BACTERIAL LACTOGEN I AND II.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
 CC (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
 CC GENE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; L13593; AAC37641.1; -;
 CC EMBL; L14811; AAA02686.1; -;
 CC EMBL; D10214; BAA01066.1; -;
 CC EMBL; X73372; CAA51789.1; -;
 CC EMBL; M22959; AAA39977.1; -;
 CC EMBL; M22958; AAA39976.1; -;
 CC PIR; JT0671; JT0671.
 CC HSP; P16471; Ibp3.
 CC MGD; MGI:97763; PRLR.
 CC INTERPRO; IPR000950; -;
 CC INTERPRO; IPR001777; -;
 CC INTERPRO; IPR002465; -;
 CC PFAM; PF00041; fn3; 2.
 CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 608
 FT DOMAIN 20 229
 FT TRANSEM 230 253
 FT DOMAIN 254 608
 FT DOMAIN 20 117
 FT DOMAIN 119 222
 FT DISULFID 31 41
 FT DISULFID 70 81
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 127 127
 FT VARSPLIC 281 292
 FT VARSPLIC 293 608
 FT VARSPLIC 281 303
 FT VARSPLIC 304 608
 FT CONFLICT 558 558
 FT CONFLICT 558 558
 SQ SEQUENCE 608 AA; 68240 MW; B8CE202B2EFC9FC6 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 608;
 Best Local Similarity 71.4%; Pred. No. 57;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSTSWP 7

t :|:|:|

Db 474 KONTSWP 480

RESULT 13
 BISZ_ECOLI
 ID BISZ_ECOLI STANDARD; PRT; 809 AA.
 AC P46923; P76292; P97187;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE BIORIN SULFOXIDE REDUCTASE 2 (EC 1.-.-.-) (BDS REDUCTASE 2) (BSO
 DE REDUCTASE 2).
 DE BISZ.
 GN Escherichia coli.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC [1]
 RN RP SEQUENCE FROM N.A.
 GN STRAIN=K12 / ACC5;
 RX MEDLINE; 97077292.
 RA del Campillo-Campbell A., Campbell A.M.;
 RT "Alternative gene for biotin sulfoxide reduction in Escherichia coli
 RT K-12.";
 RL J. Mol. Evol. 42:85-90(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 GN STRAIN=K12 / MGI655;
 RX MEDLINE; 97428617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 GN STRAIN=K12;
 RX MEDLINE; 97251358.
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Silvasundaram S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 CC -1- FUNCTION: THIS ENZYME MAY SERVE AS A SCAVENGER, ALLOWING THE CELL
 CC TO UTILIZE BIOTIN SULFOXIDE AS A BIOTIN SOURCE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: REDUCES A SPONTANEOUS OXIDATION PRODUCT OF
 CC BIOTIN, D-BIOTIN D-SULFOXIDE (BSO OR BDS), BACK TO BIOTIN.
 CC -1- COFACTOR: MOLYBDENUM (MOLYBDOTERIN) (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOTERIN-CONTAINING
 CC OXIDOREDUCTASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; U38839; AAC44131.1; -;
 CC EMBL; AE000281; AAC74942.1; ALT_INIT.
 CC EMBL; D90829; BAA15682.1; -;
 CC EMBL; D90830; BAA15689.1; -;
 CC HSP; Q57366; ICYT.
 CC ECOGENE; EGI3276; BISZ.
 CC INTERPRO; IPR001467; -;
 CC PFAM; PF01568; Molybdop_binding; 1.
 CC PFAM; PF00384; molybdopterin; 1.
 CC PROSITE; PS00551; MOLYBDOTERIN_PROK_1; FALSE_NEG.
 CC PROSITE; PS00490; MOLYBDOTERIN_PROK_2; 1.
 CC PROSITE; PS00932; MOLYBDOTERIN_PROK_3; 1.
 KW Oxidoreductase; Molybdenum.

FT CONFLICT 76 76 A -> T (IN REF. 1).
 FT CONFLICT 291 292 HD -> TI (IN REF. 1).
 FT CONFLICT 299 304 YTTGVP -> TLPGIR (IN REF. 1).
 FT CONFLICT 406 409 EMSA -> DFIGP (IN REF. 1).
 FT CONFLICT 801 803 AFD -> GFG (IN REF. 1).
 SQ SEQUENCE 809 AA; 88964 MW; 44A84F6302531D09 CRC64;

 Query Match 63.0%; Score 34; DB 1; Length 809;
 Best Local Similarity 71.4%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 QOSTSWP 7
 Db 195 EQOSTSWP 201

 RESULT 14
 ID PMT1_YEAST STANDARD; PRT; 817 AA.
 AC P33775;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOsylTRANSFERASE 1
 DE (EC 2.4.1.109).
 GN PMT1 OR YDL095W OR D2390.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE; 93376764.
 RX Strahl-Bolsinger S., Immervoll T., Deutzmann R., Tanner W.;
 RT "PMT1, the gene for a key enzyme of protein O-glycosylation in
 RT Saccharomycetes cerevisiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8164-8168(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / FV1679;
 RX MEDLINE; 97082507.
 RA Boskovic J., Saiz J.E., Soler-Mira A., Garcia-Cantalejo J.M.,
 RA Ballesta J.P.G., Jimenez A., Remacha M.;
 RT "The sequence of a 16,691 bp segment of Saccharomycetes cerevisiae
 RT chromosome IV identifies the DUN1, PMT1, PMT5, SRP14 and DPR1 genes,
 RT and five new open reading frames.";
 RL Yeast 12:1377-1384(1996).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE; 97076135.
 RA Gaentzsch M., Tanner W.;
 RT "The PMT gene family: protein O-glycosylation in Saccharomycetes
 RT cerevisiae is vital.";
 RL EMBO J. 15:5752-5759(1996).
 CC -!- FUNCTION: TRANSFERS MANNOSE FROM DOL-P-MANNOSE TO SER OR THR
 CC RESIDUES ON PROTEINS. SEEMS TO BE ACTIVE ON CHITINASE.
 CC -!- CATALYTIC ACTIVITY: DOLICHYL PHOSPHATE D-MANNOSE + PROTEIN -
 CC DOLICHYL PHOSPHATE + O-D-MANNOSYL-PROTEIN.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
 CC RETICULUM.
 CC -!- SIMILARITY: BELONGS TO THE FUNGAL PMT FAMILY.
 CC
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 CC
 DR EMBL; L19169; AAA02928.1; -;
 DR EMBL; X95644; CAA64917.1; -;

DR EMBL; Z74144; CAA98663.1; -;
 DR PIR; A47716; A47716.
 DR SGD; S000223; PMT1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Endoplasmic reticulum; Multigene family.
 FT DOMAIN 1 50 CYTOPLASMIC (POTENTIAL).
 FT TRANSHEM 51 71 POTENTIAL.
 FT DOMAIN 72 133 LUMENAL (POTENTIAL).
 FT TRANSHEM 134 154 POTENTIAL.
 FT DOMAIN 155 179 CYTOPLASMIC (POTENTIAL).
 FT TRANSHEM 180 200 POTENTIAL.
 FT DOMAIN 201 234 LUMENAL (POTENTIAL).
 FT TRANSHEM 235 259 POTENTIAL.
 FT DOMAIN 260 273 CYTOPLASMIC (POTENTIAL).
 FT TRANSHEM 274 291 POTENTIAL.
 FT DOMAIN 292 584 LUMENAL, CATALYTIC (POTENTIAL).
 FT TRANSHEM 585 605 POTENTIAL.
 FT DOMAIN 606 685 CYTOPLASMIC (POTENTIAL).
 FT TRANSHEM 686 710 POTENTIAL.
 FT DOMAIN 711 817 LUMENAL (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 743 743 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 817 AA; 92675 MW; 6309BBA71BAD8D21 CRC64;

 Query Match 63.0%; Score 34; DB 1; Length 817;
 Best Local Similarity 75.0%; Pred. No. 78;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 QOSTSWP 8
 Db 359 QOSTLYPH 366

 RESULT 15
 ID TORA_ECOLI STANDARD; PRT; 848 AA.
 AC P33225; P78227;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TRIMETHYLAMINE-N-OXIDE REDUCTASE PRECURSOR (EC 1.6.6.9) (TMAO
 DE REDUCTASE) (TRIMETHYLAMINE OXIDASE).
 GN TORA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 40-46.
 RC STRAIN-K12;
 RX MEDLINE; 94293785.
 RA Mejean V., Lobbi-Nivol C., Lepelletier M., Giordano G., Chippaux M.,
 RA Pascal M.-C.;
 RT "TMAO anaerobic respiration in Escherichia coli: involvement of the
 RT tor operon.";
 RL Mol. Microbiol. 11:1169-1179(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE; 97061202.
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

Job time: 149 sec

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RT Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RN SEQUENCE OF 767-848 FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 94134695.
RY Ueguchi C., Kakeda M., Yamada H., Mizuno T.;
RT "An analogue of the DnaJ molecular chaperone in Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1054-1058(1994).
CC -1- FUNCTION: REDUCES TRIMETHYLAMINE-N-OXIDE (TMAO) INTO
CC TRIMETHYLAMINE; AN ANAEROBIC REACTION COUPLED TO ENERGY-YIELDING
CC REACTIONS.
CC -1- CATALYTIC ACTIVITY: NADH + TRIMETHYLAMINE-N-OXIDE = NAD(+) +
CC TRIMETHYLAMINE + H(2)O.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X73888; CAA52095.1; -;
CC EMBL; AE002021; AAC74082.1; -;
CC EMBL; D90736; BAA36139.1; -;
CC EMBL; D90737; BAA35764.1; -;
CC EMBL; D16500; -; NOT_ANNOTATED_CDS.
CC PIR; S34222; S34222.
CC HSSP; Q57366; 1CXT.
CC ECGENE; EG11814; TORA.
CC INTERPRO; IPR001467; -;
CC PFAM; PF01568; Molybdop_binding; 1.
CC PFAM; PF00384; molybdopterin; 1.
CC PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
CC PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
CC PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
CC Oxidoreductase; NAD; Molybdenum; Periplasmic; Signal.
KW SIGNAL
FT SIGNAL 1 39
FT CHAIN 40 848 TRIMETHYLAMINE-N-OXIDE REDUCTASE.
FT CONFLICT 173 173 L -> R (IN REF. 1).
FT CONFLICT 176 176 A -> R (IN REF. 1).
FT CONFLICT 256 256 A -> R (IN REF. 1).
FT CONFLICT 258 258 V -> S (IN REF. 1).
FT CONFLICT 281 281 R -> G (IN REF. 1).
FT CONFLICT 325 325 Q -> E (IN REF. 1).
FT CONFLICT 348 348 T -> S (IN REF. 1).
FT CONFLICT 503 504 KL -> NV (IN REF. 1).
FT CONFLICT 713 714 QQ -> HE (IN REF. 1).
FT CONFLICT 751 751 L -> M (IN REF. 1).
FT CONFLICT 781 781 P -> L (IN REF. 1 AND 3).
SQ SEQUENCE 848 AA; 94456 MW; 59DDACB00B1843E7 CRC64;

Query Match 63.08; Score 34; DB 1; Length 848;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 210 EQOTSWP 216

Search completed: March 28, 2001, 07:35:12

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:21 ; Search time 443.95 Seconds
(without alignments)
2.376 Million cell updates/sec

Title: US-09-016-061-88

Perfect score: 54

Sequence: 1 QQSTSWPHT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	81.5	1194	Q9VSI2	Q9vsi2 drosophila
2	43	79.6	1109	Q9VVB9	Q9vcb9 drosophila
3	37	68.5	551	Q9K6S3	Q9k6s3 bacillus ha
4	37	68.5	2556	Q9VXP7	Q9vxp7 drosophila
5	36	66.7	296	13 Q93312	Q93312 brachydanio
6	36	66.7	297	13 Q73779	Q73779 brachydanio
7	36	66.7	323	2 Q54490	Q54490 streptomyce
8	36	66.7	419	10 Q9SY03	Q9sy03 arabidopsi
9	35	64.8	170	2 Q9KMR2	Q9kmr2 vibrio chol
10	35	64.8	235	11 Q63471	Q63471 rattus norv
11	35	64.8	315	13 Q9YGU0	Q9ygu0 brachydanio
12	35	64.8	327	13 Q9YH10	Q9yhb6 cyprinid ca
13	35	64.8	484	2 Q9KRB6	Q9krb6 vibrio chol
14	35	64.8	1109	10 Q9ZVX6	Q9zvx6 arabidopsi
15	35	64.8	1313	5 Q9NE22	Q9ne22 leishmania
16	35	64.8	4829	4 Q9NR09	Q9nr09 homo sapien
17	35	64.8	4845	11 Q88738	Q88738 mus musculu
18	34	63.0	94	2 Q9XCE0	Q9xce0 mycobacteri
19	34	63.0	96	2 Q9Z9Y5	Q9z9y5 frateuria s

20	34	63.0	97	2 Q9PES1	Q9pfs1 xylella fas
21	34	63.0	178	5 Q9VE03	Q9ve03 drosophila
22	34	63.0	448	4 Q9UFP1	Q9ufp1 homo sapien
23	34	63.0	522	13 Q9VXC4	Q9vgx4 brachydanio
24	34	63.0	596	4 Q00185	Q00185 homo sapien
25	34	63.0	640	5 Q9XWZ6	Q9xwz6 caenorhabdi
26	34	63.0	734	5 Q9V706	Q9v7q6 drosophila
27	34	63.0	746	2 Q44289	Q44289 anabaena sp
28	34	63.0	849	11 Q9JLJ8	Q9jlj8 mus musculu
29	34	63.0	1045	5 Q20047	Q20047 caenorhabdi
30	34	63.0	1059	5 Q9VNP5	Q9vnp5 drosophila
31	34	63.0	1402	10 Q9SL14	Q9sl14 arabidopsi
32	34	63.0	1919	6 Q29518	Q29518 oryctolagus
33	34	63.0	1920	6 Q29519	Q29519 oryctolagus
34	33.5	62.0	411	4 Q75876	Q75876 homo sapien
35	33	61.1	74	6 Q9N068	Q9n068 macaca fasc
36	33	61.1	160	4 Q9N7S8	Q9nts8 homo sapien
37	33	61.1	255	2 Q9SZA3	Q9s2a3 streptomyce
38	33	61.1	267	6 Q02764	Q02764 oryctolagus
39	33	61.1	387	5 Q39907	Q39907 gonyaulax p
40	33	61.1	413	10 Q9M9E4	Q9m9e4 arabidopsi
41	33	61.1	486	10 Q9M9U1	Q9m9u1 arabidopsi
42	33	61.1	491	5 Q76269	Q76269 leishmania
43	33	61.1	491	5 Q76343	Q76343 leishmania
44	33	61.1	500	10 Q9SHG3	Q9shg3 arabidopsi
45	33	61.1	523	12 P89903	P89903 chimpanzee

ALIGNMENTS

RESULT 1

Q9VSI2 PRELIMINARY; PRT: 1194 AA.

AC Q9VSI2; AC Q9VSI2; DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE C67112 PROTEIN.

GN C67112.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pelegyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; Pubmed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,

RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos A.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Bahilke C., Davenport L.B., Davies P.,

RA de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003555; AAF50437.1; -;
DR FLYBASE; FBgn0035879; CG7112.
DR INTERPRO; IPR001095; -;
DR PFAM; PF00566; TBC; 1;
SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 81.5%; Score 44; DB 5; Length 1194;
Best Local Similarity 77.8%; Pred. No. 6.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 461 QOQSSSWPYT 469
|||||:|

RESULT 2
Q9VTB9
ID Q9VTB9 PRELIMINARY; PRT; 1109 AA.
AC Q9VTB9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG7958 PROTEIN.
GN CG7958.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brothstein P., Brotler P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003547; AAF50133.1; -;
DR FLYBASE; FBgn0036103; CG7958.
SQ SEQUENCE 1109 AA; 116491 MW; 4FD726183EE642AC CRC64;

Query Match 79.8%; Score 43; DB 5; Length 1109;
Best Local Similarity 66.7%; Pred. No. 8.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 591 QMNTNWPHT 599
|:|:|:|

RESULT 3
Q9K6S3
ID Q9K6S3 PRELIMINARY; PRT; 551 AA.
AC Q9K6S3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE BH3653 PROTEIN.
GN BH3653.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RA Takami H., Nakasone K., Takaki Y.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP001519; BAB07372.1; -;
SQ SEQUENCE 551 AA; 62089 MW; A437311B88B9C1F60 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 551;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 524 EQQSTSWKYT 532
:|||||:

RESULT 4
Q9VXP7
ID Q9VXP7 PRELIMINARY; PRT; 2556 AA.
AC Q9VXP7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CG8473 PROTEIN.
GN CG8473.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berland B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jajaeli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaverl J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003500; AAF48511.1; -;
 DR FLYBASE; FBgn0030689; CG8473.
 DR INTERPRO; IPR001617; -;
 DR INTERPRO; IPR001680; -;
 DR INTERPRO; IPR002557; -;
 DR PFAM; PF00005; ABC_tran; 2.
 DR PFAM; PF00400; WD40; 2.
 DR PFAM; PF01607; Chitin_bind_2; 2.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 SQ SEQUENCE 2556 AA; 290937 MW; 82612D442484D8CD CRC64;

Query Match 68.5%; Score 37; DB 5; Length 2556;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 STSWPHT 9
 : | | | | |
 Db 1652 NTKWPHT 1658
 PRELIMINARY; PRT; 296 AA.

RESULT 5
 ID O93312 PRELIMINARY; PRT; 296 AA.
 AC O93312;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE FORKHEAD-5.
 GN FKH5.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RP SEQUENCE FROM N.A.
 RN Grinblat Y., Gamse J., Patel M., Sive H.;
 RT "Determination of the zebrafish forebrain: induction and patterning.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF052851; AAC25103.1; -;
 DR HSSP; Q63245; 2HFH.
 DR INTERPRO; IPR001766; -;
 DR PFAM; PF00250; Fork_head; 1.
 DR PRINTS; PR00053; FORKHEAD.
 DR PROSITE; PS00657; FORK_HEAD_1; 1.
 DR PROSITE; PS00658; FORK_HEAD_2; UNKNOWN_1.
 DR PROSITE; PS00039; FORK_HEAD_3; 1.
 SQ SEQUENCE 296 AA; 33066 MW; 5909FB9552C3F61C CRC64;

Query Match 66.7%; Score 36; DB 13; Length 296;
 Best Local Similarity 62.5%; Pred. No. 44;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPH 8
 : | | | | |
 Db 196 QLTTAMPH 203

RESULT 6
 ID O73779 PRELIMINARY; PRT; 297 AA.
 AC O73779;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE FORK HEAD DOMAIN PROTEIN FKD3.
 GN MAR OR FKD3.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RP SEQUENCE FROM N.A.
 RN Odenthal J., Nuesslein-Volhard C.;
 RL Dev. Genes Evol. 0:0-0(1998).
 DR EMBL; AF052246; AAC06363.1; -;
 DR HSSP; Q63245; 2HFH.
 DR ZFIN; ZDB-GENE-980526-563; mar.
 DR INTERPRO; IPR001766; -;
 DR PFAM; PF00250; Fork_head; 1.
 DR PRINTS; PR00053; FORKHEAD.
 DR PROSITE; PS00657; FORK_HEAD_1; 1.
 DR PROSITE; PS00658; FORK_HEAD_2; UNKNOWN_1.
 DR PROSITE; PS00039; FORK_HEAD_3; 1.
 SQ SEQUENCE 297 AA; 32945 MW; 8E06934453255836 CRC64;

Query Match 66.7%; Score 36; DB 13; Length 297;
 Best Local Similarity 62.5%; Pred. No. 44;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPH 8
 : | | | | |
 Db 191 QLTTAMPH 198

RESULT 7
 ID Q54490 PRELIMINARY; PRT; 323 AA.
 AC Q54490;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE SNOE (AROMATASE).
 GN SNOE.
 OS Streptomyces nogalater.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=38314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27451;
 RA Ylihonko K.P.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27451;
 RA Ylihonko K., Tuukkanen J., Jussila S., Cong L., Mantsala P.;
 RT "A gene cluster involved in nogalamycin biosynthesis from Streptomyces
 RT nogalater: sequence analysis and complementation of early-block
 RT mutations in the anthracycline pathway.";
 RL Mol. Gen. Genet. 251:113-120(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27451;
 RX MEDLINE=96349102; PubMed=8760909;
 RA Ylihonko K., Hakala J., Kunnari T., Mantsala P.;
 RT "Production of hybrid anthracycline antibiotics by heterologous
 RT expression of Streptomyces nogalater nogalamycin biosynthesis genes.";
 RL Microbiology 142:1965-1972(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27451;
 RX MEDLINE=98007868; PubMed=9349712;
 RA Torkkell S., Ylihonko K., Hakala J., Skurnik M., Mantsala P.;
 RT "Characterization of Streptomyces nogalater genes encoding enzymes
 RT involved in glycosylation steps in nogalamycin biosynthesis.";
 RL Mol. Gen. Genet. 256:203-209(1997).
 DR EMBL: AJ224512; CAA12012.1;
 SQ SEQUENCE 323 AA; 35864 MW; ABF4C42324C0254E CRC64;

Query Match 66.7%; Score 36; DB 2; Length 323;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 TSWPHT 9
 Db 34 TSWPHT 39
 | | | | |
 | | | | |

RESULT 8
 Q9SY03 PRELIMINARY; PRT; 419 AA.
 AC Q9SY03;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 46.0 KDA PROTEIN.
 GN T5J8.6 OR AT4G02760.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA de la Bastide M., Gnoj L., Habermann K., Huang E.N., Gottesman T.,
 RA Kaplan N., Lodhi M., Jensen K., Hameed A., Schutz K., Martienssen R.,
 RA Dedhia N., Parnell L.D., McCombie W.R.;
 RT "Arabidopsis thaliana BAC T5J8 from chromosome IV, short arm.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
 RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
 RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004044; AAD15350.1;
 DR EMBL: AL161495; CAB77761.1;
 KW Hypothetical protein.
 SQ SEQUENCE 419 AA; 45950 MW; D1EDE76771AA0A29 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 419;
 Best Local Similarity 85.7%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QOSTSWP 7
 Db 112 QNSTSWP 118
 | | | | |
 | | | | |

RESULT 9
 Q9KMR2 PRELIMINARY; PRT; 170 AA.
 ID Q9KMR2;
 AC Q9KMR2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL PROTEIN VCA0258.
 GN VCA0258.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL: AE004366; AAF96169.1;
 DR TIGR: VCA0258;
 KW Hypothetical protein.
 SQ SEQUENCE 170 AA; 19430 MW; 9D70B2D1141851A9 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 TSWPH 8
 Db 56 TSWPH 60
 | | | | |
 | | | | |

RESULT 10
 Q63471 PRELIMINARY; PRT; 235 AA.
 ID Q63471;
 AC Q63471;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

```

DE PAROTID SECRETORY PROTEIN PRECURSOR.
GN PSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92129360; PubMed=1370829;
RA Mirzels L., Ball W.D.;
RT "Neonatal rat submandibular gland protein SMG-A and parotid secretory
RT protein are alternatively regulated members of a salivary protein
RT multigene family.";
RL J. Biol. Chem. 267:2679-2687(1992).
DR EMBL; M83209; AAC06334.1; -.
KW SIGNAL.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 235 PAROTID SECRETORY PROTEIN.
SQ SEQUENCE 235 AA; 24529 MW; 0B36EC779025986E CRC64;

Query Match 64.8%; Score 35; DB 11; Length 235;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSTSWP 7
Db 54 QOATWTP 60

RESULT 11
Q9YGU0
ID Q9YGU0 PRELIMINARY; PRT; 315 AA.
AC Q9YGU0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HOMEBOX PROTEIN.
GN HOXA11A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasboridae; Danio.
ON NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RT "Zebrafish hox clusters and vertebrate genome evolution.";
RL Science 282:1711-1714(1998).
DR EMBL; AF071240; AAD15934.1; -.
DR HSSP; P02834; 1BBI.
DR INTERPRO; IPR001356; -.
DR PFAM; PF00046; homeobox; 1.
DR PRINTS; PF00024; HOMEBOX.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 315 AA; 36239 MW; 51F50C709B345CC5 CRC64;

Query Match 64.8%; Score 35; DB 13; Length 315;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 STSWPH 8
Db 71 STKWPH 76

RESULT 12
Q9YH10
ID Q9YH10 PRELIMINARY; PRT; 327 AA.
AC Q9YH10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CTH1 PROTEIN.
GN CTH1.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
ON NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX Stevens C.J.M., Schipper H., Samallo J., Stroband H.W.J.,
RA Tekronnie G.;
RT "Blastomeres and cells with mesodermal fates of carp embryos
RT express cth1, a member of the Tis11 family of primary response
RT genes.";
RL Int. J. Dev. Biol. 42:181-188(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Stevens C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Stroband H.W.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y10163; CAA71245.2; -.
DR INTERPRO; IPR000571; -.
DR PFAM; PF00642; zf-CCCH; 4.
SQ SEQUENCE 327 AA; 36216 MW; 87D775113164DA21 CRC64;

Query Match 64.8%; Score 35; DB 13; Length 327;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TSWPH 8
Db 221 TSWPH 225

RESULT 13
Q9KRB6
ID Q9KRB6 PRELIMINARY; PRT; 484 AA.
AC Q9KRB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE GLYCOCEN SYNTHASE.
GN VC1726.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
ON NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EL TOR N16961 / SEROTYPE O1;
RC MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004250; AAF94876.1; -.
DR TIGR; VC1726; -.
SQ SEQUENCE 484 AA; 55066 MW; 776D1D3E6BCC0920 CRC64;

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Query Match 64.8%; Score 35; DB 2; Length 484;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TSWPHT 9
| | | | |
DB 65 THWPHT 70

RESULT 14
Q9NE22 PRELIMINARY; PRT; 1109 AA.

AC Q9NE22; PRT; 1109 AA.
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE TMV RESISTANCE PROTEIN.
GN F12A24.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Rensing C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC005167; AAC64218.1; -
DR INTERPRO: IPR000157; -
DR INTERPRO: IPR000767; -
DR INTERPRO: IPR001611; -
DR INTERPRO: IPR001617; -
DR INTERPRO: IPR002182; -
DR PFAM: PF00560; LRR: 3.
DR PFAM: PF00931; NB-ARC: 2.
DR PFAM: PF01582; TIR: 1.
DR PRINTS: PRO0364; DISEASERISIT.
SQ SEQUENCE 1109 AA; 125679 MW; 865678FBC55DE694 CRC64;

Query Match 64.8%; Score 35; DB 10; Length 1109;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
| | | | |
DB 900 QOHSWEHT 908

RESULT 15
Q9NE22 PRELIMINARY; PRT; 1313 AA.

AC Q9NE22; PRT; 1313 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 140.2 KDA PROTEIN.
GN L232.07.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;
RA Beck A., Klages S., Reinhardt R., Ivens A.C., Quail M.,
RA Rajagream M.A., Barrell B.G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL354553; CAB89634.1; -
KW Hypothetical protein.
SQ SEQUENCE 1313 AA; 140187 MW; 2BA3034A75AD23AC CRC64;

Query Match 64.8%; Score 35; DB 5; Length 1313;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QOSTSWPHT 9
| | | | |
DB 1218 QDTLWPHS 1225

Search completed: March 28, 2001, 07:53:24
Job time: 517 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:53 ; Search time 154.19 Seconds
(without alignments)
1.996 Million cell updates/sec

Title: us-09-016-061-88

Perfect score: 54

Sequence: 1 QOSTSWPHT 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT:*
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- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	9	19 W76034	LM609 grafted anti
2	49	90.7	9	19 W76033	LM609 grafted anti
3	49	90.7	9	20 W06372	Murine monoclonal
4	49	90.7	107	13 R25729	Humanised VL regio
5	49	90.7	109	20 Y06388	Humanised LM609 an
6	49	90.7	109	20 Y06380	Murine monoclonal
7	49	90.7	109	20 Y06382	Humanised LM609 an
8	49	90.7	127	15 R54033	Sequence of mouse
9	47	87.0	9	19 W76013	LM609 grafted anti
10	47	87.0	107	19 W76006	LM609 grafted anti
11	47	87.0	107	19 W76002	Vitaxin antibody 1
12	47	87.0	107	19 W76004	LM609 antibody lig

13	43	79.6	107	14 R38601	HYH light chain.
14	43	79.6	107	19 W58482	Murine HYH antibody
15	43	79.6	108	12 R15438	Light chain variab
16	43	79.6	109	15 R52033	Light chain variab
17	43	79.6	143	18 W19580	Mouse anti-idiotyp
18	43	79.6	240	12 R15443	Single chain Fv fr
19	40	74.1	105	20 W87456	JK gene product.
20	40	74.1	105	20 W87458	Humanised anti-alp
21	40	74.1	107	20 W84098	Humanised anti-alp
22	40	74.1	108	20 W84094	Murine vitronectin
23	40	74.1	112	20 W84100	Vitronectin alpha-
24	39	72.2	9	14 R37604	hIL2R Ab L chain v
25	39	72.2	9	19 W76036	LM609 grafted anti
26	39	72.2	107	14 R37612	hIL2R Ab L chain v
27	39	72.2	107	14 R37610	B-B10 MAb L chain
28	38	70.4	9	19 W44180	Monoclonal antibody
29	38	70.4	9	20 Y26992	CDR3 domain reshap
30	38	70.4	106	19 W71241	Light chain variab
31	38	70.4	107	15 R50190	Light chain variab
32	38	70.4	107	18 W28531	Humanised CA2 ligh
33	38	70.4	107	19 W40820	Light chain variab
34	38	70.4	107	20 Y26979	Light chain variab
35	38	70.4	107	20 Y23243	Light chain variab
36	38	70.4	107	21 Y70604	Vkappa region of h
37	38	70.4	127	15 R50187	Light chain variab
38	38	70.4	127	15 R50191	Light chain variab
39	38	70.4	127	15 R50192	Light chain variab
40	38	70.4	127	19 W44176	Monoclonal antibody
41	38	70.4	127	20 Y26980	Light chain variab
42	38	70.4	127	20 Y26981	Light chain variab
43	38	70.4	127	20 Y26982	Light chain variab
44	38	70.4	240	19 W71243	scFv comprising he
45	38	70.4	245	21 Y70605	scFv fragment of h

ALIGNMENTS

RESULT 1

W76034
ID W76034 standard; Protein; 9 AA.

XX W76034;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR3 protein fragment #3.

DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; anglogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 9705-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49871.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 54; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 |||||
 Db 1 qgstswpht 9

RESULT 2

ID W76033 standard; Protein; 9 AA.

XX W76033;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR3 protein fragment #2.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49870.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 9 AA;

Query Match 90.7%; Score 49; DB 19; Length 9;

Best Local Similarity 88.9%; Pred. No. 2.1e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9

||| |||||

Db 1 qgstswpht 9

RESULT 3

ID Y06372 standard; Peptide; 9 AA.

XX Y06372;

AC Y06372;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VL CDR3.

KW Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX Mus musculus.

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 45; 55pp; English.

XX This sequence represents complementarity determining region 3
 CC (LCDR3) of the light chain of murine monoclonal antibody LM609.
 CC LM609 is directed to integrin alpha-v beta-3. It selectively
 CC promotes apoptosis of vascular cells stimulated to undergo
 CC angiogenesis, making it a tool for cancer diagnosis and therapy.

CC The invention provides humanised antibodies, especially humanised
 CC mouse antibody such as LM609 is grafted onto a human light chain,
 CC and a heavy chain CDR from a mouse antibody is grafted onto a human
 CC antibody heavy chain to produce libraries from which a humanised
 CC murine antibody having the desired specificity is selected. By
 CC preserving the original CDR sequences such as the HCDR3 and LCDR3
 CC sequences of LM609, the humanisation strategy ensures epitope
 CC conservation.

XX Sequence 9 AA;

Query Match 90.7%; Score 49; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QOSTSWPHT 9
| | | | | | | |
Db 1 qgsnswpht 9

RESULT 4

R25729 ID R25729 standard; Protein; 107 AA.

AC XX

DT 13-JAN-1993 (first entry)

Humanised VL region of the mouse CMV5 antibody.

Murine; immunoglobulin; CDR: non immunogenic; cytomegalovirus;
gH; light chain; variable region; framework; human; Wol.

OS Mus musculus.

Key	Location/Qualifiers
Region	24..34
Region	/note= "CDR"
Region	50..56
Region	/note= "CDR"
Region	89..97
Region	/note= "CDR"
Misc-difference	49
	/note= "mutated residue"

XX WO9211018-A.

XX 09-JUL-1992.

XX 19-DEC-1991; 91WO-US09711.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coellingh KL, Landolfi NF, Queen CL, Schneider WP;

XX WPI; 1992-249842/30.

XX New immunoglobulin(9) having murine CDRs in human framework
regions - have lower antigenicity; useful for treating e.g. HSV,
CMV, T-cell disorders, myeloid disorders and auto-immune
conditions

XX Claim 40; Fig 27A; 141pp; English.

XX The sequence shows the humanised mature light chain variable
region of the mouse CMV5 antibody. Murine CDRs were used
in a human Wol framework to produce a pure humanised immunoglobulin
(Ig) which is capable of binding to the gH glycoprotein of
cytomegalovirus. The Ig is non immunogenic, due to the human
framework, and has a strong affinity for its predetermined
antigen. They can be produced in large quantities via recombinant
DNA and monoclonal antibody technology. The humanised Igs may be
used alone or in combination with chemotherapeutic agents such as
non-steroidal anti-inflammatory drugs or immunosuppressants.
See also R25721-32.

XX Sequence 107 AA;

Query Match 90.7%; Score 49; DB 13; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QOSTSWPHT 9
| | | | | | | |
Db 89 qgsnswpht 97

RESULT 5

Y06388 ID Y06388 standard; Protein; 109 AA.

XX Y06388;

XX 06-SEP-1999 (first entry)

XX Humanised LM609 antibody VL domain.

XX Humanised antibody; antibody humanisation; antibody engineering;
LM609; monoclonal antibody; complementarity determining region;
CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
cancer; therapy; diagnosis.

OS Homo sapiens.
OS Synthetic.

Key	Location/Qualifiers
Peptide	1..2
Region	/note= "vector-encoded residues"
Region	24..34
Region	/note= "CDR1"
Region	50..56
Region	/note= "CDR2"
Region	89..97
Region	/note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52; 55pp; English.

XX This sequence represents the light chain variable region of a
humanised LM609 antibody. LM609 is directed to human integrin
alpha-v beta-3. It selectively promotes apoptosis of vascular
cells that have been stimulated to undergo angiogenesis, making it
a tool for cancer diagnosis and therapy. The invention provides
humanised antibodies, especially humanised LM609. In such humanized
antibodies, a light chain CDR from a mouse antibody such as LM609 is
grafted onto a human light chain, and a heavy chain CDR from a mouse
antibody is grafted onto a human antibody heavy chain to produce
libraries from which a humanised murine antibody having the desired
specificity is selected. By preserving the original CDR sequences
such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
humanisation strategy ensures epitope conservation.

XX Sequence 109 AA;

Query Match	90.7%;	Score 49;	DB 20;	Length 105;
Best Local Similarity	88.9%;	Pred. No. 0.061;		
Matches	8;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

Qy 1 QOSTSWPHT 9
 III IIIII
 Db 89 qqnswpht 97

RESULT 8

R54093 R54093 standard; Protein; 127 AA.

XX AC R54093;

XX DT 29-DEC-1994 (first entry)

XX DE Sequence of mouse V-kappa showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.

XX KW Feline herpes virus: FHV-1; monoclonal antibody; CDR;

XX KW complementarity determining region.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT Region /label= leader

FT FT 21..43

FT FT /label= FR1

FT FT 44..54

FT FT /label= CDR1

FT FT 55..70

FT FT /label= FR2

FT FT 71..76

FT FT /label= CDR2

FT FT 77..108

FT FT /label= FR3

FT FT 109..117

FT FT /label= CDR3

FT FT 118..127

FT FT /label= FR4

XX PN W09412661-A.

XX PD 09-JUN-1994.

XX PF 25-NOV-1993; 93WO-JP01724.

XX PR 28-NOV-1992; 92JP-0341255.

XX PA (KAGA) CEMO SERO THERAPEUTIC RES INST.

XX PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

XX DR WPI; 1994-200288/24.

XX DR N-PSDB; Q64167.

XX PT Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.

XX PS Disclosure; Page 18-19; 53pp; Japanese.

XX CC The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.

XX SQ Sequence 127 AA;

Query Match 90.7%; Score 49; DB 15; Length 127;
 Best Local Similarity 88.9%; Pred. No. 0.072;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
 III IIIII
 Db 109 qqnswpht 117

RESULT 9

W76013 W76013 standard; Protein; 9 AA.

XX AC W76013;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR3 protein fragment #1.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49850.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 9 AA;

Query Match 87.0%; Score 47; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
 III IIIII
 Db 1 qqsgswpht 9

```

XX AC W76002;
XX DT 02-NOV-1998 (first entry)
XX DE Vitaxin antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2..
XX XX
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX PT WPI: 1998-437472/37.
XX DR N-PSDB; V49821.
XX XX
XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX SQ Claim 1; Fig lb; 129pp; English.
XX XX
CC This sequence represents the vitaxin antibody variable light chain
CC region. Vitaxin and the antibody LM609 bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
CC ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
XX SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 QQTSWPEHT 9
   III IIIIII
Db 89 qqgsgwpht 97

RESULT 12
W76004 ID W76004 standard; Protein; 107 AA.
XX AC
XX DE W76004;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

```

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

OS WO9833919-A2.

PN 06-AUG-1998.

PD 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; W76004.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 46; Fig 2b; 129pp; English.

XX This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;

Best Local Similarity 88.9%; Pred. No. 0.14;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9

Db 89 qgsgswpht 97

RESULT 13

R38601
 ID R38601 standard; peptide: 107 AA.

XX R38601;

AC 28-OCT-1993 (first entry)

DT HYH light chain.

DE Antibody; variable domain; light; L; heavy; H; consensus;
 KW affinity; antigen; immunogenicity; humanisation; framework.

XX Homo sapiens.

OS WO9311794-A.

XX 24-JUN-1993.

XX 14-DEC-1992; 92WO-US10906.

XX

PR 13-DEC-1991; 91US-0808464.

XX (XOMA) XOMA CORP.

PA Fishwild DM, Kohn FR, Little RG, Studnicka GM;

PI WPI; 1993-213827/26.

XX Antibodies prepn. used for treatment of auto-immune diseases - by

PT replacement of critical residues to reduce immunogenicity but

PT retain binding affinity, etc.

XX Disclosure; Page 84; 160pp; English.

XX The amino acid sequences of the light and heavy chains of the
 CC variable domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex]
 CC (R38601 and R38608, respectively), MCPC [IgA Fab MCP603-phosphocholine
 CC complex] (R38602-03 and R38609-10, respectively), NEWM [Ig Fab' NEW]
 CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
 CC R38612, respectively) may be used to determine an alignment from which
 CC appropriate changes may be made.

CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.

XX Sequence 107 AA;

Query Match 79.6%; Score 43; DB 14; Length 107;

Best Local Similarity 77.8%; Pred. No. 0.72;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9

Db 89 qgsgswpht 97

RESULT 14

W58482

ID W58482 standard; protein: 107 AA.

XX W58482;

AC 18-AUG-1998 (first entry)

DT Murine HYH antibody light chain variable domain.

DE Humanised; human; mouse; CD5: anti-CD5 antibody; immunoglobulin;
 KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
 KW autoimmune disease; rheumatoid arthritis; type I diabetes.

XX Mus sp.

XX US5770196-A.

XX 23-JUN-1998.

XX 07-JUN-1995; 95US-0472788.

XX 23-JUN-1993; 93US-0082842.

PR 13-DEC-1991; 91US-0808464.

PR 14-DEC-1992; 92WO-US10906.

PR 07-JUN-1995; 95US-0472788.

XX (XOMA) XOMA CORP.

XX Studnicka GM;

XX WPI; 1998-376744/32.

XX

PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
 XX with humanised variable regions
 PS Disclosure; Column 43-44; 77pp; English.

XX A method has been developed of depleting CD5+ cells in an animal. The
 CC method comprises administering a cytotoxic protein containing a modified
 CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
 CC molecule or an immunoconjugate or fusion protein containing an anti-CD5
 CC Ig molecule, and where the modified Ig variable domain comprises at
 CC least one of (a) a modified light chain variable region (see W58478 or
 CC W58480), and (b) a modified heavy chain variable region (see W58479 or
 CC W58481), where W58478 and W58479 are humanised forms of the H65 light
 CC and heavy chain variable domains with low risk amino acid substitutions
 CC (i.e. low risk of reducing antigen-binding specificity.) and W58480 and
 CC W58481 are humanised forms of the H65 light and heavy chain variable
 CC domains with moderate risk amino acid substitutions and are present in
 CC humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
 CC treating autoimmune diseases, especially systemic lupus erythematosus,
 CC rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
 CC represents the murine HYH antibody light chain variable domain.

XX Sequence 107 AA;

Query Match 79.6%; Score 43; DB 19; Length 107;
 Best Local Similarity 77.8%; Pred. No. 0.72;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
 Db 89 qgsnswpyt 97
 ||| |||:|

RESULT 15

R15438
 ID R15438 standard; Protein; 108 AA.

XX AC R15438;

XX DT 25-FEB-1992 (first entry)

XX Light chain variable region of MAb 1A6.

XX HRV; ICAM-1; antigen-binding fragment; inflammation;
 KW auto-immune disease.

XX OS Homo sapiens.

XX PN EP459577-A.

XX PD 04-DEC-1991.

XX PF 25-MAY-1991; 91EP-0201243.

XX PR 01-JUN-1990; 90US-0532001.

XX PA (MERI) MERCK & CO INC.

XX PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;

XX WPI; 1991-355850/49.

XX Microbially expressed portions of monoclonal antibody - can block
 PT attachment of rhinovirus ligands to inter-cellular adhesion
 PT molecule (ICAM-1)

XX Claim 1; Page 19; 28pp; English.

XX Thk3 is one of six antibody fragments from MAB's specific for domain
 CC 1 of ICAM-1. MAB 1A6 also specifically blocks the major group of
 CC human rhinovirus from binding to and infecting HeLa cells. The
 CC peptide fragments can be used to treat or prevent rhinovirus

CC infection. See R15437-R15443.

XX

SQ Sequence 108 AA;

Query Match 79.6%; Score 43; DB 12; Length 108;
 Best Local Similarity 77.8%; Pred. No. 0.72;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9

Db 89 qgsnswpyt 97

||| |||:|

Search completed: March 28, 2001, 06:59:53
 Job time: 1389 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:58 ; Search time 113.49 Seconds
(without alignments)
1.424 Million cell updates/sec

Title: US-09-016-061-88

Perfect score: 54

Sequence: 1 QOSTSWPHT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgnl_7/ptodata/1/1aa/PCTUS_COMB.pep.*

5: /cgnl_7/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	90.7	100	1	US-08-436-463-19
2	49	90.7	107	1	US-07-634-278-62
3	49	90.7	107	1	US-07-634-278-63
4	49	90.7	107	1	US-07-634-278-87
5	49	90.7	107	1	US-08-477-728-62
6	49	90.7	107	1	US-08-477-728-63
7	49	90.7	107	1	US-08-477-728-87
8	49	90.7	107	1	US-08-474-040-62
9	49	90.7	107	1	US-08-474-040-63
10	49	90.7	107	1	US-08-474-040-87
11	49	90.7	107	1	US-08-487-200-62
12	49	90.7	107	1	US-08-487-200-63
13	49	90.7	107	1	US-08-487-200-87
14	49	90.7	127	1	US-07-634-278-83
15	49	90.7	127	1	US-08-477-728-83
16	49	90.7	127	1	US-08-474-040-83
17	49	90.7	127	1	US-08-487-200-83
18	49	90.7	127	1	US-08-436-463-4
19	43	79.6	107	1	US-08-436-463-20
20	43	79.6	107	1	US-08-107-669D-1
21	43	79.6	107	1	US-08-472-788A-1
22	43	79.6	107	2	US-08-477-531B-1
23	43	79.6	107	2	US-08-082-842A-1
24	43	79.6	109	1	US-07-942-245-4
25	43	79.6	143	2	US-08-653-402B-8
26	39	72.2	9	2	US-08-232-081B-6
27	39	72.2	107	2	US-08-232-081B-9
28	39	72.2	107	2	US-08-232-081B-40

29 38 70.4 9 2 US-08-476-176B-55 Sequence 55, Appl
30 38 70.4 9 3 US-08-127-721A-55 Sequence 55, Appl
31 38 70.4 9 3 US-08-485-246A-55 Sequence 55, Appl
32 38 70.4 13 1 US-08-221-580-7 Sequence 7, Appl
33 38 70.4 13 4 PCT-US95-04018-69 Sequence 69, Appl
34 38 70.4 103 1 US-08-436-463-21 Sequence 21, Appl
35 38 70.4 106 2 US-08-800-198-4 Sequence 4, Appl
36 38 70.4 106 3 US-09-296-595-4 Sequence 4, Appl
37 38 70.4 107 1 US-08-192-102-3 Sequence 3, Appl
38 38 70.4 107 1 US-08-324-799-3 Sequence 3, Appl
39 38 70.4 107 2 US-08-192-861A-3 Sequence 3, Appl
40 38 70.4 107 2 US-08-476-176B-4 Sequence 4, Appl
41 38 70.4 107 3 US-08-127-721A-4 Sequence 4, Appl
42 38 70.4 107 3 US-08-485-246A-4 Sequence 4, Appl
43 38 70.4 127 1 US-08-436-463-18 Sequence 18, Appl
44 38 70.4 127 2 US-08-476-176B-6 Sequence 6, Appl
45 38 70.4 127 2 US-08-476-176B-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-19

Query Match 90.7%; Score 49; DB 1; Length 100;
Best Local Similarity 88.9%; Pred. No. 0.082;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 III IIIII
 Db 89 QQSNSWPHT 97

RESULT 2

US-07-634-278-62
 ; Sequence 62, Application US/07634278
 ; Patent No. 5530101
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/634,278
 ; FILING DATE: 19-DEC-1990
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 62:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-634-278-62

Query Match 90.7%; Score 49; DB 1; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.088;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 III IIIII
 Db 89 QQSNSWPHT 97

RESULT 3

US-07-634-278-63
 ; Sequence 63, Application US/07634278

; Patent No. 5530101
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/634,278
 ; FILING DATE: 19-DEC-1990
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 63:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-634-278-63

Query Match 90.7%; Score 49; DB 1; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.088;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
 III IIIII
 Db 89 QQSNSWPHT 97

RESULT 4

US-07-634-278-87
 ; Sequence 87, Application US/07634278
 ; Patent No. 5530101
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 89 QQNSWPHT 97

RESULT 5
US-08-477-728-62
Sequence 62, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 89 QQNSWPHT 97

RESULT 6
US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQSNWPHT 97

RESULT 7
US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:

; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQSNWPHT 97

RESULT 8
US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen E.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSTSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 9
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSTSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 10
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSTSWPHT 9

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Db      89 QOQNSWPHT 97
      111 111111
RESULT 11
US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-62

Query Match      90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1 QOQTSWPHT 9
      111 111111
Db      89 QOQNSWPHT 97
      111 111111
RESULT 13
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
US-08-487-200-63

Query Match      90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1 QOQTSWPHT 9
      111 111111
Db      89 QOQNSWPHT 97
      111 111111
RESULT 12
US-08-487-200-63
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SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 9
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 10
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9

```
Db      89 QQSNSWPHT 97
      111 111111
RESULT 11
US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-62

Query Match      90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QQSTSWPHT 9
      111 111111
Db      89 QQSNSWPHT 97
      111 111111
RESULT 13
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-63

Query Match      90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QQSTSWPHT 9
      111 111111
Db      89 QQSNSWPHT 97
      111 111111
RESULT 12
US-08-487-200-63
```

APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 90.7%; Score 49; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 89 QOQNSWPHT 97

RESULT 14
US-07-634-278-83
Sequence 83, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-83

Query Match 90.7%; Score 49; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 109 QOQNSWPHT 117

RESULT 15
US-08-477-728-83
Sequence 83, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-83

Query Match 90.7%; Score 49; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPHT 9
Db 109 QQNSWPHT 117

Search completed: March 28, 2001, 07:01:58
Job time: 1337 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:31 ; Search time 130.08 Seconds
(without alignments)
4.698 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QSGSWPLT 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR66:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	88.2	104	2 B43413	Ig kappa chain V r
2	45	88.2	138	2 A26471	Ig kappa chain pre
3	40	78.4	106	2 P0267	Ig kappa chain V r
4	40	78.4	106	2 PC4282	Ig kappa chain (an
5	40	78.4	107	2 C45722	anti-glycoprotein
6	39	76.5	67	2 PH1081	Ig light chain V r
7	39	76.5	69	2 PH1080	Ig light chain V r
8	39	76.5	553	2 T15220	hypothetical prote
9	38	74.5	107	2 A45722	anti-glycoprotein
10	38	74.5	123	2 S35479	Ig kappa chain pre
11	37	72.5	102	2 S26346	Ig kappa chain V r
12	37	72.5	128	2 PNO445	Ig kappa chain pre
13	37	72.5	144	2 P10106	Ig kappa chain pre
14	37	72.5	154	2 T17816	hypothetical prote
15	37	72.5	642	2 H69466	conserved hypotet
16	37	72.5	764	2 T48446	hypothetical prote
17	36	70.6	87	2 PH1082	Ig light chain V r
18	36	70.6	91	2 S37525	Ig kappa chain V r
19	36	70.6	108	2 C30502	Ig kappa chain V r
20	36	70.6	115	1 KVM5L7	Ig kappa chain pre
21	36	70.6	117	2 S40362	Ig kappa chain - h
22	36	70.6	169	2 D65126	probable general s
23	36	70.6	204	2 T32062	hypothetical prote
24	36	70.6	275	2 D70737	hypothetical prote
25	36	70.6	543	2 T06523	cytochrome P450 mo
26	36	70.6	1221	2 E83327	conserved hypotet
27	35	68.6	100	2 G81749	hypothetical prote
28	35	68.6	107	2 B45722	anti-glycoprotein
29	35	68.6	235	1 SQMS	parotid secretory

30 35 68.6 317 2 B82084 probable cobalamin
31 35 68.6 365 1 SAVLWE large surface anti
32 35 68.6 366 1 SAVLBD large surface anti
33 35 68.6 366 1 SAVLWD large surface anti
34 35 68.6 499 2 A27198 cellulase (EC 3.2.
35 35 68.6 508 2 A26874 cellulase (EC 3.2.
36 35 68.6 939 2 H71532 valine--trna ligas
37 35 68.6 939 2 H81686 valyl--trna synthet
38 35 68.6 940 2 B72120 valine--trna ligas
39 34 66.7 91 2 S37511 Ig kappa chain V r
40 34 66.7 96 2 JC5945 regulatory protein
41 34 66.7 125 2 S40344 Ig kappa chain V-J
42 34 66.7 146 2 G65008 hypochetrical prote
43 34 66.7 219 2 H75621 GDEF family prote
44 34 66.7 250 2 B83008 histidine utilizat
45 34 66.7 259 2 G75400 probable oxidoredu

ALIGNMENTS

RESULT 1
B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.;
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci
A:Reference number: A43413; MUID:92388177
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 45; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9
DB 86 QSGSWPLT 94

RESULT 2
A26471
Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M16162; NID:gl96893; PIDN:AAA38823.1; PID:gl96894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 88.2%; Score 45; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 0.54;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||| |||||
 Db 109 QOQNSWPLT 117

RESULT 3

PL0267
 Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0267
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0267
 A:Molecule type: mRNA
 A:Residues: 1-106 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-106/Region: framework 4

Query Match 78.4%; Score 40; DB 2; Length 106;
 Best Local Similarity 77.8%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||| |||||
 Db 89 QOQNSWPYT 97

RESULT 4

PC4282
 Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
 C:Accession: PC4282; PC4284
 R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
 Biochem. Biophys. Res. Commun. 232, 101-106, 1997
 A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltration
 A:Reference number: PC4279; MUID:97236289
 A:Accession: PC4282
 A:Molecule type: protein
 A:Residues: 1-106 <SU2>
 A:Note: E-42
 A:Accession: PC4284
 A:Molecule type: protein
 A:Residues: 1-106 <SU2>
 A:Note: E-56

C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 40; DB 2; Length 106;
 Best Local Similarity 77.8%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||| |||||
 Db 87 QORASWPLT 95

RESULT 5

C45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: C45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: C45722
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 40; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 3.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||| |||||
 Db 89 QOSHNNWPLT 97

RESULT 6

PHI081
 Ig light chain V region (clone 165.6) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
 C:Accession: PHI081
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PHI081
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-67 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 76.5%; Score 39; DB 2; Length 67;
 Best Local Similarity 77.8%; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 ||| |||||
 Db 58 QOQNSWPQT 66

RESULT 7

PHI080
 Ig light chain V region (clone 165.60) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
 C:Accession: PHI080
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PHI080
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-69 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 76.5%; Score 39; DB 2; Length 69;
 Best Local Similarity 77.8%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| ||| |
 Db 60 QQNSWPQT 68

RESULT 8

T15220

hypothetical protein F57C9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15220

R:Giesel, C.; Kramer, J.; Gibson, A.

submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid F57C9.

A:Reference number: Z18309

A:Accession: T15220

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-553 <GEI>

A:Cross-references: EMBL:AF003142; NID:g2088743; PIDN:AAB54191.1; GSPDB:GN

A:Experimental source: strain Bristol N2; clone F57C9

C:Genetics:

A:Gene: CESP:F57C9.8

A:Map position: 1

A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match 76.5%; Score 39; DB 2; Length 553;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 |:||||| :
 Db 373 QRSGSWPFS 381

RESULT 9

A45722

anti-glycoprotein II monoclonal antibody light-chain variable domain (Mab 5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: A45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J.; Virol, 67, 489-496, 1993

A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu

A:Reference number: A45722; MUID:93100833

A:Accession: A45722

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-107 <STM>

A:Note: sequence extracted from NCBI backbone (NCBIP:120589)

C:Superfamily: immunoglobulin V region; Immunoglobulin homology

C:Keywords: glycoprotein

F:16-90/Domain: Immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 107;
 Best Local Similarity 77.8%; Pred. No. 6.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| ||| |
 Db 89 QQNSWPHT 97

RESULT 10

S35479

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0445

R:Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polym

A:Reference number: PN0444; MUID:93138402

A:Accession: PN0445

A:Molecule type: mRNA

A:Residues: 1-128 <KAL>

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from

A:Reference number: S35479; MUID:92375706

A:Accession: S35479

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <YAK>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F:18-102/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 123;
 Best Local Similarity 77.8%; Pred. No. 7.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| ||| |
 Db 101 QQNSWPHT 109

RESULT 11

S26346

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26346

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421

A:Accession: S26346

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-102 <STA>

A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:gl334075

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 102;
 Best Local Similarity 66.7%; Pred. No. 9.7;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| :||| |
 Db 87 QQNTWPYT 95

RESULT 12

PN0445

Ig kappa chain precursor V-I region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0445

R:Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polym

A:Reference number: PN0444; MUID:93138402

A:Accession: PN0445

A:Molecule type: mRNA

A:Residues: 1-128 <KAL>

A:Cross-references: GB:L02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-10/Domain: signal sequence #status predicted <SIG>

F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>

F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 128;

Best Local Similarity 66.7%; Pred. No. 12;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

||| |||

Db 99 QQTNSWPTT 107

RESULT 13

PL0106

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PL0106

R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec

A:Reference number: PL0106; MUID:89235583

A:Accession: PL0106

A:Molecule type: mRNA

A:Residues: 1-144 <SL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 144;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

||| |||

Db 109 QQRSNWPLT 117

RESULT 14

TI7816

hypothetical protein a317L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: TI7816

R:Graves, W.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: TI7816

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-154 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96685.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: a317L

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 154;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPL 8

||| |||

Db 33 QQTSGSWPV 40

RESULT 15

H69466

conserved hypothetical protein AFL737 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999

C:Accession: H69466

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343

A:Accession: H69466

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-642 <KLE>

A:Cross-references: GB:AE000983; GB:AE000782; NID:g2689306; PIDN:AAB89512.1; PID:g264

C:Superfamily: conserved hypothetical protein yyal

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 642;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCSWPLT 9

||| |||

Db 101 SCSWPLT 107

Search completed: March 28, 2001, 07:04:32

Job time: 1070 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:12 ; Search time 72.95 Seconds
(without alignments)
3.941 Million cell updates/sec

Title: us-09-016-061-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	40	78.4	745	1 CUL2_HUMAN	Q13617 homo sapien
2	36	70.6	115	1 KV51_MOUSE	P01642 mus musculus
3	36	70.6	169	1 GSPH_ECOLI	P41443 escherichia
4	36	70.6	543	1 C821_PEA	Q43068 pisum sativ
5	35	68.6	235	1 PSP_MOUSE	P07743 mus musculus
6	35	68.6	365	1 VMSA_HPBDC	P30029 duck hepati
7	35	68.6	366	1 VMSA_HPBDB	P17194 duck hepati
8	35	68.6	499	1 GUN1_BACSU	P07983 bacillus su
9	35	68.6	499	1 SVV_CHLTR	O84304 chlamydia t
10	35	68.6	939	1 SVV_CHLTPN	Q92987 chlamydia p
11	35	68.6	92	1 CATC_RHOOP	P95609 rhodococcus
12	34	66.7	92	1 CTC1_ACILW	O33947 acinetobact
13	34	66.7	146	1 YFDK_ECOLI	P77656 escherichia
14	34	66.7	470	1 IE83_HSVB	P28939 equine herp
15	34	66.7	470	1 IE83_HSVK	Q05906 equine herp
16	34	66.7	470	1 IE83_HSVK	Q05906 equine herp
17	34	66.7	540	1 NUSA_MYCPN	P75591 mycoplasma
18	34	66.7	777	1 BISC_ECOLI	P20099 escherichia
19	34	66.7	1456	1 RRPO_PVX	P09395 potato viru
20	34	66.7	1456	1 RRPO_PVXCP	P22591 potato viru
21	34	66.7	1456	1 RRPO_PVXHB	P07630 potato viru
22	34	66.7	1456	1 RRPO_PVX3	P17779 potato viru
23	34	66.7	2329	1 YS89_CAEEL	Q09624 caenorhabdi
24	33	64.7	226	1 NUKN_NEUCR	O47950 neurospora
25	33	64.7	251	1 BIOC_ECOLI	P12999 escherichia
26	33	64.7	300	1 GP40_HUMAN	O14842 homo sapien
27	33	64.7	468	1 NIFB_KLEPN	P10390 klebsiella
28	33	64.7	516	1 Y4NW_RHISN	P55585 rhizobium s
29	33	64.7	517	1 LADI_HUMAN	O00515 homo sapien
30	33	64.7	796	1 PTPA_RAT	Q03348 rattus norv
31	33	64.7	802	1 PTPA_HUMAN	P18433 homo sapien
32	33	64.7	829	1 PTPA_MOUSE	P18052 mus musculus
33	33	64.7	3329	1 BRC2_MOUSE	P97929 mus musculus

34 33 64.7 3418 1 BRC2_HUMAN P51587 homo sapien
35 32 62.7 302 1 CYSO_ECOLI P21156 escherichia
36 32 62.7 336 1 CHI2_ORYSA P25765 oryza sativ
37 32 62.7 402 1 OPDE_PSAE Q01602 pseudomonas
38 32 62.7 471 1 STCH_HUMAN P48723 homo sapien
39 32 62.7 474 1 P2X2_CAVPO O70397 cavia porce
40 32 62.7 492 1 TYTR_TRYCR P28593 trypanosoma
41 32 62.7 528 1 HEXA_MOUSE P29416 mus musculus
42 32 62.7 529 1 HEXA_HUMAN P06865 homo sapien
43 32 62.7 575 1 MIS_BOVIN P03972 bos taurus
44 32 62.7 621 1 TRA_STRLI P22409 streptomyce
45 32 62.7 630 1 Y4BJ_RHISN P55377 rhizobium s

ALIGNMENTS

RESULT 1
ID CUL2_HUMAN STANDARD; PRT; 745 AA.
AC Q13617; O00200;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CULLIN HOMOLOG 2 (CUL-2).
GN CUL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE: 97225922.
RA Pause A., Lee S., Worrel R., Chen D.Y.T., Burgess W.H.,
RA Linehan W.M., Klausner R.D.;
RT "The von Hippel-Lindau tumor-suppressor gene product forms a stable
RT complex with human CUL-2, a member of the Cdc53 family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:2156-2161(1997).
RN [2]
RP SEQUENCE OF 95-745 FROM N.A.
RX MEDLINE: 96279828.
RA Kipreos E.T., Lander L.E., Wing J.P., He W.W., Hedgecock E.M.;
RT "cul-1 is required for cell cycle exit in C. elegans and identifies a
RT novel gene family.";
RL Cell 85:829-839(1996).
CC -1- FUNCTION: FORMS A STABLE COMPLEX WITH THE VHL TUMOR SUPPRESSOR.
CC -1- SIMILARITY: BELONGS TO THE CULLIN FAMILY.
CC -----
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CC -----
CC EMBL: U83410; AAC51190.1; -;
DR EMBL: U58088; AAC50545.1; -;
DR MIM: 603135; -;
DR INTERPRO: IPR001373; -;
DR PRAM: PF00888; Cullin; 1.
DR PROSITE: PS01256; CULLIN_1; 1.
DR PROSITE: PSS0069; CULLIN_2; 1.
FT CONFLICT 95 98. SKGA -> IRHE (IN REF. 2).
FT CONFLICT 109 109 S -> N (IN REF. 2).
FT CONFLICT 681 681 Q -> H (IN REF. 2).
SQ SEQUENCE 745 AA; 86956 MW; A39475AE379C9005 CRC64;

Query Match 78.4%; Score:40; DB 1; Length 745;
Best Local Similarity 75.0%; Pred.No. 7.8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2 QSGSWPLT 9
Db 513 QAGAWPLT 520

RESULT 2
KVSI_MOUSE
ID KVSI_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81220975.
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -1- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PIR; A01925; KVM5L7.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWP 7
Db 109 QQSNSWP 115

RESULT 3
GSPH_ECOLI
ID GSPH_ECOLI STANDARD; PRT; 169 AA.
AC P41443;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE GENERAL SECRETION PATHWAY PROTEIN H PRECURSOR (PROTEIN
DE TRANSPORT PROTEIN HOFH).
GN HOFH OR HOPH.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
[2]
SEQUENCE OF 1-30 FROM N.A.
STRAIN-K12;
MEDLINE; 95204361.
RA Stojiljkovic I., Schoenherr R., Kusters J.G.;
RT "Identification of the hopG gene, a component of Escherichia coli
RT K-12 type II export system, and its conservation among different
RT pathogenic Escherichia coli and Shigella isolates.";
RL J. Bacteriol. 177:1892-1895(1995).
CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/XEXH/XCPU FAMILY.
CC
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CC
CC EMBL; U18997; AAA58126.1; -.
CC EMBL; AE000409; AAC76354.1; -.
CC EMBL; U20786; AAG69032.1; -.
CC ECOGENE; EG12887; HOFH.
CC INTERPRO: IPR001120; -.
CC INTERPRO: IPR002416; -.
CC PRINTS; PR00885; BCTERIALGSPH.
CC PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW TRANSPORT; Methylation.
FT PROPEP 1 6 BY SIMILARITY.
FT CHAIN 7 169 PUTATIVE GENERAL SECRETION PATHWAY
FT PROTEIN H.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 169 AA; 18565 MW; D42B1127FB81A09 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QSGSWPL 8
Db 154 QSGSWPL 159

RESULT 4
C82L_PEA
ID C82L_PEA STANDARD; PRT; 543 AA.
AC Q43068;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 82A1 (EC 1.14.-.-) (CYPLXXXII) (FRAGMENT).
GN CYP82A1 OR CYP82.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96417083.
RA Frank M.R., Deyneka J.M., Schuler M.A.;
RT "Cloning of wound-induced cytochrome P450 monooxygenases expressed in
RT pea.";
RL Plant Physiol. 110:1035-1046(1996).
CC -1- INDUCTION: BY WOUND.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC
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CC -----
 DR EMBL: U29333; AAC49188.1; -
 DR INTERPRO; IPR001128; -
 DR PFAM; PF00067; P450; 1.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Membrane; Heme.
 FT NON_TER 1
 FT BINDING 480 480 HEME (BY SIMILARITY).
 SQ SEQUENCE 543 AA; 62064 MW; C8C86A415317C56A CRC64;

Query Match 70.6%; Score 36; DB 1; Length 543;
 Best Local Similarity 100.08; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SGSWPL 8
 Db 39 SGSWPL 44

RESULT 5
 PSP_MOUSE
 ID PSP_MOUSE STANDARD; PRT; 235 AA.
 AC P07743;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PAROTID SECRETORY PROTEIN PRECURSOR (PSP).
 GN PSP.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=PAROTID GLAND;
 RX MEDLINE; 85215456.
 RA Madsen H.O., Hjorth J.P.;
 RT "Molecular cloning of mouse PSP mRNA."
 RL Nucleic Acids Res. 13:1-13(1985).
 RN [2]
 RP SEQUENCE OF 1-87 FROM N.A.
 RC STRAIN=C3H; TISSUE=SPLEEN;
 RX MEDLINE; 87004556.
 RA Poulsen K., Jakobsen B.K., Mikkelsen B.M., Harmark K.,
 RT Nielsen J.T., Hjorth J.P.;
 RT "Coordination of murine parotid secretory protein and salivary
 RT amylase expression."
 RL EMBO J. 5:1891-1896(1986).

CC ITS FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.
 CC WITH THAT OF SALIVARY AMYLASE.
 CC -----
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CC -----
 DR EMBL: X01697; CAA25846.1; -
 DR EMBL: M26807; AAA40009.1; -
 DR EMBL: M26806; AAA40009.1; JOINED.
 DR PIR; A23031; SQMS.
 DR MGD; MGI:97787; PSP.
 KW Parotid gland; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 235
 POTENTIAL.
 PAROTID SECRETORY PROTEIN.

SQ SEQUENCE 235 AA; 24753 MW; 23311BAE1E6E2EF3 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 235;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPL 8
 Db 54 QQATSWPL 61

RESULT 6
 VMSA_HPBDC
 ID VMSA_HPBDC STANDARD; PRT; 365 AA.
 AC P30029;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MAJOR SURFACE ANTIGEN PRECURSOR.
 GN S.

OS Duck hepatitis B virus (strain China) (DHBV).
 CC Viruses; Retroviruses; Hepadnaviridae; Avihepadnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91045091.
 RA Tong S., Mattes F., Teubner K., Blum H.E.;
 RT "Complete nucleotide sequence of a Chinese duck hepatitis B virus."
 RL Nucleic Acids Res. 18:6139-6139(1990).
 CC -----

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CC -----
 DR EMBL: M21953; AAA45746.1; -
 DR PIR; S12842; SAVLWE.
 DR INTERPRO; IPR000349; -
 DR PFAM; PF00695; VMSA; 2.
 KW Antigen.
 FT PROPEP 1 198
 FT CHAIN 199 365
 FT CARBOHYD 297 297
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 365 AA; 40511 MW; 67F3A4174CB7D884 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 365;
 Best Local Similarity 71.4%; Pred. No. 29;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
 Db 96 QQQGWMP 102

RESULT 7
 VMSA_HPBDC
 ID VMSA_HPBDC STANDARD; PRT; 366 AA.
 AC P17194;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE MAJOR SURFACE ANTIGEN PRECURSOR.
 GN S.

OS Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).
 CC Viruses; Retroviruses; Hepadnaviridae; Avihepadnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90085807.
 RA Uchida M., Esumi M., Shikata T.;

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RT "Molecular cloning and sequence analysis of duck hepatitis B virus
RL genomes of a new variant isolated from Shanghai ducks.";
Virology 173:600-606(1989).
-----
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-----
DR EMBL; M32990; AAA45755.1; ALT_INIT.
DR PIR; C33746; SAVLWD.
DR INTERPRO; IPR000349; -.
DR PFAM; PF00695; VMSA; 2.
KW Antigen.
FT PROPEP 1 199
FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 366 AA; 40897 MW; 5B72879A182EFF38 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 366;
Best Local Similarity 71.4%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
   |||
Db 96 QQQGAWP 102

RESULT 8
VMSA_HPBW STANDARD; PRT; 366 AA.
AC P17195;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE MAJOR SURFACE ANTIGEN PRECURSOR.
GN S.
OS Duck hepatitis B virus (white Shanghai duck isolate S31) (DHBV).
OC Viruses; Retroviridae; Hepadnaviridae; Avihepadnavirus.
RN [1]
RX MEDLINE; 90085807.
RA Uchida M., Esumi M., Shikata T.;
RT "Molecular cloning and sequence analysis of duck hepatitis B virus
RL genomes of a new variant isolated from Shanghai ducks.";
Virology 173:600-606(1989).
CC
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-----
DR EMBL; M32991; AAA45752.1; ALT_INIT.
DR PIR; D33746; SAVLWD.
DR INTERPRO; IPR000349; -.
DR PFAM; PF00695; VMSA; 2.
KW Antigen.
FT PROPEP 1 199
FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 366 AA; 40858 MW; CF60E78B7B2FCD52 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 366;

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Best Local Similarity 71.4%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
   |||
Db 96 QQQGAWP 102

RESULT 9
GUNL_BACSU STANDARD; PRT; 499 AA.
ID GUNL_BACSU STANDARD; PRT; 499 AA.
AC P07983;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOGLUCANASE PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE)
DE (CELLULOSE).
GN BGLC OR GLD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DLG;
RX MEDLINE; 87194581.
RA Robson L.M., Chambliss G.H.;
RT "Endo-beta-1,4-glucanase gene of Bacillus subtilis DLG.";
RL J. Bacteriol. 169:2017-2025(1987).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
CC LINKAGES IN CELLULOSE.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
CC HYDROLASES).
CC
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-----
DR EMBL; M16185; AAA22496.1; ALT_INIT.
DR PIR; A26874; A26874.
DR HSSP; Q06851; INBC.
DR INTERPRO; IPR001547; -.
DR INTERPRO; IPR001956; -.
DR PFAM; PF00942; CBD_3; 1.
DR PFAM; PF00150; cellulase; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 29
FT CHAIN 30 499 ENDOGLUCANASE.
FT ACT_SITE 169 169 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).
FT DOMAIN 350 499 CELLULOSE-BINDING (BY SIMILARITY).
SQ SEQUENCE 499 AA; 55187 MW; 339D04EE95A63EE1 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 499;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
   :| | | | |
Db 309 KTGQWPLT 316

RESULT 10
SYV_CHLTR
ID SYV_CHLTR STANDARD; PRT; 939 AA.
AC O84304;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VALRS).
 GN VALS OR CT302.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D/UN-3/CX;
 RX MEDLINE: 99000809.
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis."
 RL Science 282:754-759(1998).
 CC -!- SUBCELLULAR LOCATION: ATP + L-VALINE + TRNA(VAL) = AMP +
 CC PYROPHOSPHATE + L-VALYL-TRNA(VAL).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC
 DR EMBL: AE001302; AAC67895.1; -;
 DR INTERPRO: IPR001412; -;
 DR INTERPRO: IPR002300; -;
 DR PFAM: PF00133; trna-synt_1; 1.
 DR PRINTS: PR00986; TRNASYNTHAL.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 DR Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 47 57 "HIGH" REGION.
 FT BINDING 563 567 "KMSKS" REGION.
 FT BINDING 566 566 ATP (BY SIMILARITY).
 SQ SEQUENCE 939 AA; 107036 MW; CEB8449DC7BB9066 CRC64;

 Query Match 68.6%; Score 35; DB 1; Length 939;
 Best Local Similarity 85.7%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 3 SGSWPLT 9
 DB 459 SGLWPLT 465

 RESULT 11
 STV_CHLPN STANDARD; PRT; 940 AA.
 AC Q92987;
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VALRS).
 GN VALS OR CPN0094.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CWL029;
 RX MEDLINE: 99206606.
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
 RL Nat. Genet. 21:385-389(1999).
 CC -!- CATALYTIC ACTIVITY: ATP + L-VALINE + TRNA(VAL) = AMP +
 CC PYROPHOSPHATE + L-VALYL-TRNA(VAL).

CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC
 DR EMBL: AE001595; AAD18247.1; -;
 DR INTERPRO: IPR001412; -;
 DR INTERPRO: IPR002300; -;
 DR PFAM: PF00133; trna-synt_1; 1.
 DR PRINTS: PR00986; TRNASYNTHAL.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 DR Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 47 57 "HIGH" REGION.
 FT BINDING 564 568 "KMSKS" REGION.
 FT BINDING 567 567 ATP (BY SIMILARITY).
 SQ SEQUENCE 940 AA; 107111 MW; 28054683FB9D0404 CRC64;

 Query Match 68.6%; Score 35; DB 1; Length 940;
 Best Local Similarity 85.7%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 3 SGSWPLT 9
 DB 460 SGLWPLT 466

 RESULT 12
 CATC_RHOOP STANDARD; PRT; 92 AA.
 ID CATC_RHOOP
 AC P95609;
 DT 15-JUL-1999 (rel. 38, Created)
 DT 15-JUL-1999 (rel. 38, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE MUCONOLACTONE DELTA-ISOMERASE (EC 5.3.3.4) (MIASE).
 GN CATC.
 OS Rhodococcus opacus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
 RC STRAIN=ICP;
 RX MEDLINE: 97144521.
 RA Eulberg D., Golovleva L.A., Schloemann M.;
 RT "Characterization of catechol catabolic genes from Rhodococcus
 RT erythropolis ICP."
 RL J. Bacteriol. 179:370-381(1997).
 CC -!- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE =
 CC 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE
 CC -!- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
 CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
 CC -!- SUBUNIT: HOMODECAMER (BY SIMILARITY).
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 CC
 DR EMBL: X99622; CAA67935.1; -;
 DR Aromatic hydrocarbons catabolism; Isomerase.
 FT INIT_MET 0
 SQ SEQUENCE 92 AA; 10780 MW; 9CCE5A17DED4B153 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 92;
 Best Local Similarity 71.4%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWP 7
 I:|I|I|
 Db 35 QRSQKWP 41

RESULT 13

CTC1_ACILW STANDARD; PRT; 96 AA.
 AC O33947;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MUONOLACTONE DELTA-ISOMERASE 1 (EC 5.3.3.4) (MIASE 1).
 GN CATC1.
 OS Acinetobacter lwoffii.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 RP SEQUENCE FROM N.A.
 RC STRAIN-K24;
 RX MEDLINE: 97405925.
 RA Kim S.I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
 RA Park Y.K., Lee Y.N., Ha K.-S.;
 RT "Cloning and characterization of two catA genes in Acinetobacter
 RT lwoffii K24.";
 RL J. Bacteriol. 179:5226-5231(1997).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K24;
 RX MEDLINE: 98139907.
 RA Kim S.I., Leem S.-H., Choi J.-S., Ha K.-S.;
 RT "Organization and transcriptional characterization of the catI gene
 RT cluster in Acinetobacter lwoffii K24.";
 RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
 CC -!- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE =
 CC 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.
 CC -!- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
 CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
 CC -!- SUBUNIT: HOMODECAMER (BY SIMILARITY).
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 DR EMBL: U77658; AAC46227.1;
 KW Aromatic hydrocarbons catabolism; Isomerase.
 SQ SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;

Query Match 66.7%; Score 34; DB 1; Length 96;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWP 7
 I:|I|I|
 Db 35 QRSQKWP 41

RESULT 14

YFDK_ECOLI STANDARD; PRT; 146 AA.
 AC P77656;
 DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 16.4 KDA PROTEIN IN INTC-DSDC INTERGENIC REGION.
 GN YFDK.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE: 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE: 97349980.
 RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
 RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT analysis of its sequence features.";
 RL DNA Res. 4:91-113(1997).
 CC -!- SIMILARITY: STRONG, TO E.COLI YMFS.

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 CC or send an email to license@isb-sib.ch).
 DR EMBL: AE000324; AAC75413.1;
 DR EMBL: D90866; CAB22145.1;
 DR EMBL: D90865; CAB22143.1;
 DR EMBL: E014135; YFDK.
 KW Hypothetical protein.
 SQ SEQUENCE 146 AA; 16408 MW; 28F3CA711C5E9C79 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 146;
 Best Local Similarity 83.3%; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QOQSGSWP 7
 I:|I|I|I|
 Db 23 QOQSGSWP 28

RESULT 15

IE63_HSVEB STANDARD; PRT; 470 AA.
 AC P28939;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE TRANSCRIPTIONAL REGULATOR IE63 HOMOLOG.
 GN 5.
 OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
 OC Viruses; GSDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92295566.

```

RA   Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT   "The DNA sequence of equine herpesvirus-1.";
RL   Virolology 189:304-316(1992).
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC   HSV-2 UL54, EBV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M86664; AAB02440.1; -.
DR   PIR; F36795; WZBEA4.
KW   Transcription regulation.
SQ   SEQUENCE 470 AA; 51320 MW; 99AC5258EFB74B0E CRC64;

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Query Match 66.7%; Score 34; DB 1; Length 470;
 Best Local Similarity 71.4%; Pred. No. 57;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY   1 QSGSWP 7
DB   127 QSGSWP 133

```

Search completed: March 28, 2001, 07:35:14
 Job time: 151 sec

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: March 28, 2001, 07:53:24 ; Search time 443.95 Seconds
(without alignments)
2.376 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QSGSWPLT 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15:
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	80.4	153	13 Q9YH52	Q9YH52 gallus gall
2	40	78.4	745	4 Q9UNF9	Q9UNF9 homo sapien
3	40	78.4	1194	5 Q9VSI2	Q9VSI2 drosophila
4	39	76.5	553	5 Q01825	Q01825 caenorhabdi
5	38	74.5	265	5 Q9VX10	Q9VX10 drosophila
6	38	74.5	379	4 Q9NR38	Q9NR38 homo sapien
7	38	74.5	399	4 Q9NR37	Q9NR37 homo sapien
8	38	74.5	447	4 Q9UHD6	Q9UHD6 homo sapien
9	38	74.5	459	4 Q9Y638	Q9Y638 homo sapien
10	38	74.5	471	4 Q9UB19	Q9UB19 homo sapien
11	38	74.5	497	4 Q9UHD5	Q9UHD5 homo sapien
12	37	72.5	154	12 Q84631	Q84631 paramecium
13	37	72.5	642	1 Q28537	Q28537 archaeglob
14	37	72.5	737	5 Q9U9P1	Q9U9P1 drosophila
15	37	72.5	764	10 Q9L275	Q9L275 arabidopsis
16	37	72.5	781	5 Q9VRA2	Q9VRA2 drosophila
17	36	70.6	204	5 Q16703	Q16703 caenorhabdi
18	36	70.6	275	2 Q50711	Q50711 mycobacteri
19	36	70.6	396	2 Q9RDF1	Q9RDF1 streptomyce

20	36	70.6	613	5 Q9VHU1	Q9VHU1 drosophila
21	36	70.6	847	10 Q9SGW2	Q9SGW2 arabidopsis
22	36	70.6	1903	5 Q9USD6	Q9USD6 plautia sta
23	35	68.6	100	2 Q9PLT4	Q9PLT4 chlamydia m
24	35	68.6	123	4 Q9UKB9	Q9UKB9 homo sapien
25	35	68.6	317	2 Q9KPI7	Q9KPI7 vibrio chol
26	35	68.6	327	12 Q67852	Q67852 duck hepati
27	35	68.6	330	12 Q72885	Q72885 duck hepati
28	35	68.6	330	12 Q66405	Q66405 duck hepati
29	35	68.6	366	12 Q66404	Q66404 duck hepati
30	35	68.6	407	2 Q9R904	Q9R904 brachyspira
31	35	68.6	413	2 Q9R905	Q9R905 brachyspira
32	35	68.6	415	2 Q9ZH11	Q9ZH11 serpulina i
33	35	68.6	415	2 Q9R908	Q9R908 treponema h
34	35	68.6	415	2 Q9R902	Q9R902 serpulina i
35	35	68.6	416	2 Q9ZHJ3	Q9ZHJ3 brachyspira
36	35	68.6	418	2 Q9ZH16	Q9ZH16 brachyspira
37	35	68.6	420	2 Q9ZH17	Q9ZH17 serpulina s
38	35	68.6	420	2 Q9R907	Q9R907 treponema h
39	35	68.6	421	2 Q9ZH18	Q9ZH18 serpulina a
40	35	68.6	421	2 Q9R906	Q9R906 serpulina m
41	35	68.6	422	2 Q9R903	Q9R903 brachyspira
42	35	68.6	423	2 Q9ZHJ0	Q9ZHJ0 serpulina i
43	35	68.6	423	2 Q9ZHJ2	Q9ZHJ2 brachyspira
44	35	68.6	424	2 Q9ZH19	Q9ZH19 serpulina m
45	35	68.6	426	3 Q9UWV5	Q9UWV5 alternaria

ALIGNMENTS

RESULT 1
Q9YH52 ID Q9YH52 PRELIMINARY; PRT; 153 AA.
AC Q9YH52;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE HYPOTHETICAL 17.4 KDA PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H.B19;
RX MEDLINE=90077532; PubMed=2592020;
RA Kaufman J., Salomonsen J., Skjoldt K.;
RT "B-G CDNA clones have multiple small repeats and hybridize to both
RT chicken MHC regions.";
RL Immunogenetics 30:440-451(1989).
DR EMBL; M27666; AAA69840.1; -;
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17404 MW; 6D344F572FA7EE48 CRC64;

Query Match 80.4%; Score 41; DB 13; Length 153;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
Db 65 QSGHWPLT 72

RESULT 2
Q9UNF9 ID Q9UNF9 PRELIMINARY; PRT; 745 AA.
AC Q9UNF9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE CULLIN 2.
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX
RN
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99194561; PubMed=10092517;
RT Wada H., Yeh E.T., Kamitani T.;
RL Biochem. Biophys. Res. Commun. 257:100-105(1999).
DR EMBL; AF126404; AAD23581.1; -;
DR INTERPRO; IPR001373; -;
DR PFAM; PF00888; Cullin.1.
DR PROSITE; PS01256; CULLIN.1; 1.
DR PROSITE; PS50069; CULLIN_2; 1.
FT VARIANT 109 109 N -> S.
SQ SEQUENCE 745 AA; 86982 MW; 30647248F671AB0E CRC64;

Query Match 78.4%; Score 40; DB 4; Length 745;
Best Local Similarity 75.0%; Pred No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
 I:|||||
DB 513 QAGAWPLT 520

RESULT 3
Q9VS12 ID Q9VS12 PRELIMINARY; PRT: 1194 AA.
AC Q9VS12;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CG7112 PROTEIN.
GN CG7112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Prorygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RX
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Ruan K.H., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

DR PFAM: PF00620: RhoGAP: 1.
SQ SEQUENCE 553 AA; 60849 MW; A50EDF9C2F560139 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 553;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QOQSGSWPLT 9
I:|||||
Db 373 QRSQSWPFS 381

RESULT 5
O9VXLO PRELIMINARY; PRT; 265 AA.
ID Q9VXLO;
AC Q9VXLO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG12697 PROTEIN.
GN CG12697.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J.R., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spivey E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AE003500; AAF48549.1;
DR FLYBASE; FBgn0030715; CG12697.
SQ SEQUENCE 265 AA; 30472 MW; 892FEFBF7B2EE8D4 CRC64;

Query Match 74.5%; Score 38; DB 5; Length 265;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 SSGSWPLT 9
:|||||
Db 21 NGSWPLT 27

RESULT 6
Q9NR38 PRELIMINARY; PRT; 379 AA.
ID Q9NR38;
AC Q9NR38;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PURINOCEPTOR P2X2H.
GN P2X2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Chang T.K., Kosaka A.H., Oglesby I.B., Gevers J.R., Lachnit W.G.,
RA Ford A.P.D.W., Chang D.J.;
RT "Cloning and Molecular Characterization of Human P2X2 and Its Splice Variants";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260428; AAF74203.1;
SQ SEQUENCE 379 AA; 41254 MW; 8D1AA9A069D7F008 CRC64;

Query Match 74.5%; Score 38; DB 4; Length 379;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 SSGSWPLT 9
|||||
Db 296 SSGSWPT 302

RESULT 7
Q9NR37 PRELIMINARY; PRT; 399 AA.
ID Q9NR37;
AC Q9NR37;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PURINOCEPTOR P2X2I.
GN P2X2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Chang T.K., Kosaka A.H., Oglesby I.B., Gevers J.R., Lachnit W.G.,
RA Ford A.P.D.W., Chang D.J.;
RT "Cloning and Molecular Characterization of Human P2X2 and Its Splice Variants";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260429; AAF74204.1;
SQ SEQUENCE 399 AA; 43726 MW; 8B55562C9BAEAE5E CRC64;

Query Match 74.5%; Score 38; DB 4; Length 399;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 316 SGSWPVT 322

RESULT 8
 Q9UHD6 PRELIMINARY; PRT; 447 AA.

AC Q9UHD6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE P2X2C RECEPTOR.
 GN P2X2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PITUITARY;
 RA Lynch K.J., Touma E., Niforatos W., Kage K.L., Burgard E.C.,
 RA van Biesen T., Kowaluk E.A., Jarvis M.F.,
 RT "Molecular and Functional Characterization of Human P2X(2)
 RT Receptors.";
 RL Mol. Pharmacol. 56:1171-1181(1999).
 DR EMBL; AF190824; AAF19172.1; -;
 DR INTERPRO; IPR001429; -;
 DR INTERPRO; IPR003045; -;
 DR PFAM; PF00864; P2X_receptor; 1.
 DR PRINTS; PRO1307; P2XRECEPTOR.
 DR PRINTS; PRO1309; P2X2RECEPTOR.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 447 AA; 49266 MW; BAF5513A27314DID CRC64;

Query Match 74.5%; Score 38; DB 4; Length 447;
 Best Local Similarity 85.7%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 364 SGSWPVT 370

RESULT 9
 Q9Y638 PRELIMINARY; PRT; 459 AA.

AC Q9Y638;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE P2X2A RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA McMahon R.A., Egan T.M., Hurley P.T., Nelson A., Rogers M., Martin F.,
 RT "Cloning of the human P2X2 receptor cDNA and multiple splice
 RT variants.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
 DR EMBL; AF109387; AAD42947.1; -;
 DR INTERPRO; IPR001429; -;
 DR PFAM; PF00864; P2X_receptor; 1.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 KW Receptor;; Ionic channel; Transmembrane; Ion transport.

SQ SEQUENCE 459 AA; 50655 MW; 21E3B4513E6A1F46 CRC64;

Query Match 74.5%; Score 38; DB 4; Length 459;
 Best Local Similarity 85.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 376 SGSWPVT 382

RESULT 10
 Q9UBL9 PRELIMINARY; PRT; 471 AA.

AC Q9UBL9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE P2X2A RECEPTOR (PURINOCEPTOR P2X2A).
 GN P2X2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lynch K.J., Touma E., Niforatos W., Kage K.L., Burgard E.C.,
 RA van Biesen T., Kowaluk E.A., Jarvis M.F.,
 RT "Molecular and Functional Characterization of Human P2X(2)
 RT Receptors.";
 RL Mol. Pharmacol. 56:1171-1181(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RA Chang T.K., Kosaka A.H., Oglesby I.B., Gever J.R., Lachnit W.G.,
 RA Ford A.P.D.W., Chang D.J.,
 RT "Cloning and Molecular Characterization of Human P2X2 and Its Splice
 RT Variants.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF190826; AAF19174.1; -;
 DR EMBL; AF190822; AAF19170.1; -;
 DR EMBL; AF260426; AAF74201.1; -;
 DR INTERPRO; IPR001429; -;
 DR INTERPRO; IPR003045; -;
 DR PFAM; PF00864; P2X_receptor; 1.
 DR PRINTS; PRO1307; P2XRECEPTOR.
 DR PRINTS; PRO1309; P2X2RECEPTOR.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 471 AA; 51754 MW; 84CD61DA136EF420 CRC64;

Query Match 74.5%; Score 38; DB 4; Length 471;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 388 SGSWPVT 394

RESULT 11
 Q9UHD5 PRELIMINARY; PRT; 497 AA.

AC Q9UHD5;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE P2X2D RECEPTOR.
 GN P2X2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PIUITARY;
 RA Lynch K.J., Touma E., Niforatos W., Kage K.L., Burgard E.C.,
 RA van Biesen T., Kowaluk E.A., Jarvis M.F.;
 RT "Molecular and Functional Characterization of Human P2X(2)
 RT Receptors.";
 RL Mol. Pharmacol. 56:1171-1181(1999).
 DR EMBL; AF190825; AAF19173.1; -;
 DR INTERPRO; IPR001429; -;
 DR INTERPRO; IPR003045; -;
 DR PFAM; PF00864; P2X_receptor; 1.
 DR PRINTS; PR01307; P2XRECEPTOR.
 DR PRINTS; PR01309; P2X2RECEPTOR.
 DR PROSITE; PS01212; P2X_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 497 AA; 54513 MW; FC4007F5BDD46E0E CRC64;

Query Match 74.5%; Score 38; DB 4; Length 497;
 Best Local Similarity 85.7%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSGSWPLT 9
 |||||:
 Db 414 GSGSWPVT 420

RESULT 12
 Q84631
 ID Q84631 PRELIMINARY; PRT; 154 AA.
 AC Q84631;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE GENOME, PARTIAL SEQUENCE.
 GN A317L.
 OS Paramyxium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9513167; PubMed=7831789;
 RA Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 45 kb of DNA located at the left end of the chlorella
 RT virus PBCV-1 genome.";
 RL Virology 206:339-352(1995).
 DR EMBL; U42580; AAC96685.1; -;
 SQ SEQUENCE 154 AA; 18564 MW; 7B45EE2E7F518E15 CRC64;

Query Match 72.5%; Score 37; DB 12; Length 154;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWPL 8
 | |||||:
 Db 33 QTSGSWPV 40

RESULT 13
 O28537
 ID O28537 PRELIMINARY; PRT; 642 AA.
 AC O28537;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN AF1737.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;

OC Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE000983; AAB89512.1; -;
 DR TIGR; AF1737; -;
 KW Hypothetical protein.
 SQ SEQUENCE 642 AA; 74057 MW; 3E680BA624D747B5 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 642;
 Best Local Similarity 85.7%; Pred. No. 85;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GSGSWPLT 9
 || |||||
 Db 101 GSGWPLT 107

RESULT 14
 Q9U9P1
 ID Q9U9P1 PRELIMINARY; PRT; 737 AA.
 AC Q9U9P1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MAROON-LIKE PROTEIN.
 GN MAL.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON S;
 RA Primus J., Arcangeli L., Finnerty V.;
 RT "The maroon-like gene in Drosophila encodes a putative sulfatase.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162681; AAD50777.1; -;
 SQ SEQUENCE 737 AA; 83139 MW; 76DFEE077E3F06D4 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 737;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSWPLT 9
 |||||
 Db 533 GSWPLT 538

RESULT 15
 Q9LZ75
 ID Q9LZ75 PRELIMINARY; PRT; 764 AA.
 AC Q9LZ75;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 GN HYPOTHETICAL 86.3 KDA PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarroel R., Gielens J., Van Montagu M., Bancroft I., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL162875; CAB85556.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 764 AA; 86299 MW; AFE0E482FF091CB8 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 764;
 Best Local Similarity 62.5%; Pred. No. 1e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9
 Db 112 ESGAWPVT 119

Search completed: March 28, 2001, 07:53:27
 Job time: 520 sec

GenCore version 4.5.
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:53 ; Search time 154.19 Seconds
(without alignments)
1.996 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QQSGSWPLT 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36.*

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2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
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4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
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13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT.*
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21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	19 W76035	LM609 grafted anti
2	45	88.2	9	14 R37604	hIL2R Ab L chain V
3	45	88.2	9	19 W76036	LM609 grafted anti
4	45	88.2	107	14 R37612	hIL2R Ab L chain V
5	45	88.2	107	14 R37610	B-B10 MAb L chain
6	44	86.3	9	19 W76013	LM609 grafted anti
7	44	86.3	107	19 W76006	LM609 grafted anti
8	44	86.3	107	19 W76002	Vitaxin antibody 1
9	44	86.3	107	19 W76004	LM609 antibody lig
10	42	82.4	127	21 Y32405	Mouse anti-verotox
11	42	82.4	127	21 Y32407	Mouse anti-verotox
12	41	80.4	105	20 W87456	Jk gene product.

13	41	80.4	105	20 W87458	Humanised anti-alp
14	41	80.4	107	20 W84098	Humanised anti-alp
15	41	80.4	108	20 W84094	Murine vitronectin
16	41	80.4	112	20 W84100	Vitronectin alpha-
17	40	78.4	107	14 R38601	HYH light chain.
18	40	78.4	107	19 W58482	Murine HYH antibody
19	40	78.4	108	12 R15438	Light chain variab
20	40	78.4	109	15 R52033	Light chain variab
21	40	78.4	143	18 W19580	Mouse anti-idiotyp
22	40	78.4	240	12 R15443	Single chain Fv fr
23	39	76.5	9	19 W44180	Monoclonal antibod
24	39	76.5	9	20 Y26992	CDR3 domain reshap
25	39	76.5	106	19 W1241	Light chain variab
26	39	76.5	107	15 R50190	Light chain variab
27	39	76.5	107	18 W28531	Humanised cA2 ligh
28	39	76.5	107	19 W40820	Light chain variab
29	39	76.5	107	20 Y26979	Light chain variab
30	39	76.5	107	20 Y23243	Light chain variab
31	39	76.5	107	21 Y70604	Vkappa region of h
32	39	76.5	127	15 R50187	Light chain variab
33	39	76.5	127	15 R50191	Light chain variab
34	39	76.5	127	15 R50192	Light chain variab
35	39	76.5	127	19 W44176	Monoclonal antibod
36	39	76.5	127	20 Y26980	Light chain variab
37	39	76.5	127	20 Y26981	Light chain variab
38	39	76.5	127	20 Y26982	Light chain variab
39	39	76.5	240	19 W71243	Light chain variab
40	39	76.5	245	21 Y70605	scFv comprising he
41	38	74.5	9	19 W76033	scFv fragment of h
42	38	74.5	9	20 Y06372	LM609 grafted anti
43	38	74.5	107	13 R25729	Murine monoclonal
44	38	74.5	109	20 Y06388	Humanised VL regio
45	38	74.5	109	20 Y06380	Humanised LM609 an
					Murine monoclonal

ALIGNMENTS

RESULT 1
W76035
ID W76035 standard; Protein; 9 AA.
XX
W76035;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-L region CDR3 protein fragment #4.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
N-PSDB; V49872.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PS angiogenesis or restenosis
 XS Claim 62; Page 44; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 9 AA;

Query Match: 100.0%; Score 51; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
 DB 1 ||||| ||||| 9

RESULT 2
 ID R37604 standard; peptide; 9 AA.
 XX
 AC R37604;
 XX
 DT 13-OCT-1993 (first entry)
 XX
 DE hIL2R Ab L chain V region CDR3.
 XX
 KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid.
 XX
 OS Mus musculus.
 XX
 PN WO9311238-A.
 XX
 PD 10-JUN-1993.
 XX
 PF 03-DEC-1992; 92WO-JP01583.
 XX
 PR 06-DEC-1991; 91JP-0323319.
 XX
 PA (BIOT) BIOTEST PHARMA GMBH.
 PA (UNNO-) INNOTHERAPIE LAB.
 PA (SUMO) SUMITOMO PHARM CO LTD.
 XX
 XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;
 XX WPI; 1993-197057/24.
 XX
 XX Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor
 XX
 PS Claim 1; Page 43; 62pp; English.
 XX
 CC The sequences given in R37599-604 represent the complementarity-
 CC determining regions (CDRs) of a humanised antibody (Ab) which binds
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). These

CC CDRs were derived from the murine anti-human IL-2 receptor monoclonal
 CC Ab (MAB) B-B10 (see also Q43242-43). This MAB is antagonistic to the
 CC binding of IL-2 to the IL-2 receptor on human T-cells. It also
 CC inhibits the human mixed lymphocyte reaction. The CDNA encoding the
 CC variable (V) region of the B-B10 Ab was cloned by PCR and sequenced
 CC (see also Q43226-32 and Q43233-36). A human Ab with high levels of
 CC amino acid sequence homology to the murine sequence was selected and
 CC the framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10 V
 CC region (see also Q43244-45). The DNA sequence coding this humanised
 CC B-B10 was synthesised and a plasmid expressing humanised B-B10 was
 CC constructed.
 XX
 SQ Sequence 9 AA;

Query Match: 88.2%; Score 45; DB 14; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
 DB 1 ||||| ||||| 9

RESULT 3
 ID W76036 standard; Protein; 9 AA.
 XX
 AC W76036;

DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-L region CDR3 protein fragment #5.

XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.

OS Mus sp.
 PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 1998-437472/37.

DR N-PSDB; V49873.

XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 44; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 9 AA;

Query Match 88.2%; Score 45; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
 IIIIIII I
 Db 1 qqsgswpqt 9

RESULT 4
 R37612
 ID R37612 standard; Protein; 107 AA.
 XX
 AC R37612;

DT 13-OCT-1993 (first entry)
 XX
 DE hIL2R Ab L chain V region..

XX Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid; heavy; H; light; L.

XX Mus musculus/Homo sapiens.

XX WO9311238-A.

XX 10-JUN-1993.

XX 03-DEC-1992; 92WO-JP01583.

XX 06-DEC-1991; 91JP-0323319.

XX (BIOT) BIOTEST PHARMA GMBH.

XX (INNO-) INNOTHERAPIE LAB.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;

XX WPI: 1993-197057/24.

XX N-PSDB; Q43245.

XX Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor

XX Claim 2; Fig 5; 62pp; English.

XX The sequences given in R37611-12 represent the heavy (H) and light (L)
 CC chain variable (V) regions of a humanised antibody (Ab) which binds
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). The
 CC complementarity-determining regions (CDRs) of these V regions were
 CC derived from the murine anti-human IL-2 receptor monoclonal Ab (MAB)
 CC B-B10 (see also R37599-04). This MAB is antagonistic to the binding
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
 CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.

XX Sequence 107 AA;

Query Match 88.2%; Score 45; DB 14; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.35;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
 IIIIIII I
 Db 89 qqsgswpqt 97

RESULT 5
 R37610
 ID R37610 standard; Protein; 107 AA.
 XX
 AC R37610;

DT 13-OCT-1993 (first entry)
 XX
 DE B-B10 MAb L chain V region.

XX Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid; heavy; H; light; L.

XX Mus musculus.

XX WO9311238-A.

XX 10-JUN-1993.

XX 03-DEC-1992; 92WO-JP01583.

XX 06-DEC-1991; 91JP-0323319.

XX (BIOT) BIOTEST PHARMA GMBH.

XX (INNO-) INNOTHERAPIE LAB.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;

XX WPI: 1993-197057/24.

XX N-PSDB; Q43243.

XX Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor

XX Disclosure; Fig 2; 62pp; English.

XX The sequences given in R37609-10 represent the heavy (H) and light (L)
 CC chain variable (V) regions of the murine anti-human IL-2 receptor
 CC monoclonal antibody (MAB) B-B10, respectively. This MAB was used in
 CC the construction of a humanised antibody (Ab) which binds specifically
 CC to human interleukin (IL)-2 receptor (hIL2R). The complementarity
 CC determining regions (CDRs) for the hIL2R MAB were derived from B-B10
 CC (see also R37599-04). The hIL2R MAB is antagonistic to the binding
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
 CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.

XX Sequence 107 AA;

Query Match 88.2%; Score 45; DB 14; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.35;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 III IIIII
 Db 89 qdsswpl 97

RESULT 6

ID W76013 standard; Protein; 9 AA.
 XX W76013;
 XX 02-NOV-1998 (first entry)
 DT
 XX LM609 grafted antibody V-L region CDR3 protein fragment #1.
 DE
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.

XX W09833919-A2.
 XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 DR N-PSDB; V49850.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 9 AA;

Query Match 86.3%; Score 44; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.1e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
 IIIII I
 Db 1 qdsgswpl 9

RESULT 7

ID W76006 standard; Protein; 107 AA.
 XX W76006;
 AC
 XX 02-NOV-1998 (first entry)
 DT
 XX LM609 grafted antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX Key Location/Qualifiers
 FT Misc-difference 49
 FT /label= Arg, Met

XX W09833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49843.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 19; Fig 7; 129pp; English.

XX This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.52;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9

Db 89 qdsgswpl 97

RESULT 8

ID W76002 standard; Protein; 107 AA.

XX AC W76002;
 XX DT 02-NOV-1998 (first entry)
 XX DE Vitaxin antibody light chain variable region protein fragment.
 XX DE
 XX DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 XX DR N-PSDB; V49821.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PS Claim 1; Fig 1b; 129pp; English.
 XX This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.52;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
 ||||| |
 Db 89 qqsgswpht 97

RESULT 9
 W76004
 ID W76004 standard; Protein; 107 AA.
 XX AC W76004;
 XX DT 02-NOV-1998 (first entry)
 XX DE LM609 antibody light chain variable region protein fragment.
 XX DE
 XX DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW LM609; integrin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 XX DR N-PSDB; W76004.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX PS Claim 46; Fig 2b; 129pp; English.
 XX This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3
 CC and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.52;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
 ||||| |
 Db 89 qqsgswpht 97

RESULT 10
 Y32405
 ID Y32405 standard; Protein; 127 AA.
 XX AC Y32405;
 XX DT 13-MAR-2000 (first entry)
 XX DE Mouse anti-verotoxin II antibody VTml-1 light chain variable region.
 XX DE
 KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
 KW monoclonal antibody; light chain; mouse; humanised antibody;
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
 KW HUS; therapy.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /note= "signal peptide"
 FT 21..127

FT Region /note= "mature protein"
 FT 44..54
 FT /note= "complementarity determining region 1"
 FT 70..76
 FT /note= "complementarity determining region 2"
 FT 109..117
 FT /note= "complementarity determining region 3"
 FT Misc-difference 62
 FT /note= "encoded by GAG"

XX WO9959629-A1.

PN 25-NOV-1999.

XX 19-MAY-1999; 99WO-US11179.

XX 20-MAY-1998; 98US-0086570.

XX (TEIJ) TEIJIN LTD.

PA (PROT-) PROTEIN DESIGN LABS INC.

XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;

XX WPI; 2000-086580/07.

DR N-PSDB; Y35242.

XX Humanized antibody binding to verotoxin II used for treating Verotoxin
 producing E. coli -

PS Claim 5; Fig 1b; 59pp; English.

XX This sequence represents the light chain variable region of murine
 monoclonal antibody Vtm1-1 (MuVtm1-1), an antibody that specifically
 binds to the B subunit of verotoxin II (VT2). The invention relates
 to humanised antibodies against VT2 that are capable of neutralizing
 VT2 and/or VT2 variants. The humanised antibody is a humanized form
 of MuVtm1-1 comprising the complementarity determining regions of
 MuVtm1-1 and the heavy and light chain variable region frameworks
 from the human GF4 antibody heavy and light chain frameworks.
 provided that at least 1 position selected from L49, H29, H30, H49
 and H98 is occupied by the amino acid at the equivalent position of
 the MuVtm1-1 antibody heavy or light chain variable region framework.
 CC Such humanized antibodies (see Y32406-07) have an affinity for VT2
 CC that is 3-, 5 or 10-times that of MuVtm1-1. They are used for
 CC treating a patient suffering from, or at risk of, the toxic effects
 CC from VT2 (claimed), especially for treating verotoxin producing
 CC Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome
 CC (HUS).

XX Sequence 127 AA;

Query Match 82.4%; Score 42; DB 21; Length 127;
 Best Local Similarity 88.9%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

DB 109 qqsyswplt 117

RESULT 11

Y32407
 ID Y32407 standard; Protein; 127 AA.

XX Y32407;

XX 13-MAR-2000 (first entry)

XX Moué-anti-verotoxin II antibody Vtm1-1 humanised VL region.

DE Verotoxin II; VT2; shiga-like toxin; Vtm1-1; MuVtm1-1;

KW monoclonal antibody; light chain; mouse; humanised antibody; human;

KW

KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
 KW HUS; therapy.

XX Homo sapiens.

OS Synthetic.

XX Key

FT Location/Qualifiers

FT Peptide

FT /note= "signal peptide"

FT Protein

FT /note= "mature protein"

FT 44..54

FT /note= "complementarity determining region 1"

FT 70..76

FT /note= "complementarity determining region 2"

FT 109..117

FT /note= "complementarity determining region 3"

XX WO9959629-A1.

PN 25-NOV-1999.

XX 19-MAY-1999; 99WO-US11179.

XX 20-MAY-1998; 98US-0086570.

XX (TEIJ) TEIJIN LTD.

PA (PROT-) PROTEIN DESIGN LABS INC.

XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;

XX WPI; 2000-086580/07.

DR N-PSDB; Y35244.

XX Humanized antibody binding to verotoxin II used for treating Verotoxin
 producing E. coli -

PS Claim 12; Fig 2b; 59pp; English.

XX This sequence represents a humanised light chain variable region of
 murine monoclonal antibody Vtm1-1 (MuVtm1-1), an antibody that
 specifically binds to the B subunit of verotoxin II (VT2). The
 invention relates to humanised antibodies against VT2 that are capable
 of neutralizing VT2 and/or VT2 variants. The humanised antibody is a
 humanized form of MuVtm1-1 comprising the complementarity determining
 regions of MuVtm1-1 and the heavy and light chain variable region
 frameworks from the human GF4 antibody heavy and light chain
 frameworks, provided that at least 1 position selected from L49, H29,
 H30, H49 and H98 is occupied by the amino acid at the equivalent
 position of the MuVtm1-1 antibody heavy or light chain variable region
 framework. Such humanized antibodies have an affinity for VT2 that is
 3-, 5 or 10-times that of MuVtm1-1. They are used for treating a
 patient suffering from, or at risk of, the toxic effects from VT2
 (claimed), especially for treating verotoxin producing Escherichia
 coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).

XX Sequence 127 AA;

Query Match 82.4%; Score 42; DB 21; Length 127;
 Best Local Similarity 88.9%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

DB 109 qqsyswplt 117

RESULT 12

ID W87456

XX W87456 standard; Protein; 105 AA.

AC W87456;

XX 15-MAR-1999 (first entry)
 DT Jk gene product.
 XX
 DE Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angio genesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI; Jk protein.
 XX Mus sp.
 OS
 XX WO9840488-A1.
 PN 17-SEP-1998.
 PD 12-MAR-1998; 98WO-US04987.
 PF 12-MAR-1997; 97US-0039609.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Johnson KO, Jonak ZL, Taylor AH;
 PI WPI; 1999-034590/03.
 DR N-PSDB; V71803.
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 PT
 PS Example 14; Page 66; 97pp; English.
 XX This polypeptide is encoded by a Jk synthetic gene segment (see
 CC V71803). It was utilising in novel D12H2LCREI humanised light chain
 CC variable region (see W87458), which comprises a human REI framework
 CC and complementarity determining regions from the anti-human alpha-v
 CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
 CC and angiogenic associated diseases.
 XX
 SQ Sequence 105 AA;
 Query Match 80.4%; Score 41; DB 20; Length 105;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQSGSWPLT 9
 III III I
 Db 89 qqsnswpft 97
 RESULT 13
 W87458
 ID W87458 standard; Protein; 105 AA.
 XX
 AC W87458;
 XX
 DT 15-MAR-1999 (first entry)
 XX Humanised anti-alpha-v beta-3 MAB D12H2LCREI VL.
 DE
 XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angio genesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW

KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9840488-A1.
 PN 17-SEP-1998.
 PD 12-MAR-1998; 98WO-US04987.
 PF 12-MAR-1997; 97US-0039609.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Johnson KO, Jonak ZL, Taylor AH;
 PI WPI; 1999-034590/03.
 DR N-PSDB; V71803.
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 PT
 PS Example 14; Page 68-69; 97pp; English.
 XX This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2LCREI. It is based on a synthetic
 CC humanised kappa chain based on a modified human REI kappa
 CC framework and complementarity determining regions from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see W84094). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer, is
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.
 XX
 SQ Sequence 105 AA;
 Query Match 80.4%; Score 41; DB 20; Length 105;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQSGSWPLT 9
 III III I
 Db 89 qqsnswpft 97
 RESULT 14
 W84098
 ID W84098 standard; Protein; 107 AA.
 XX
 AC W84098;
 XX
 DT 15-MAR-1999 (first entry)
 XX Humanised anti-alpha-v beta-3 MAB D12H2LCREI 1-0 VL.
 DE
 XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angio genesis; diabetic retinopathy; inflammation;
 KW

KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2HC-10.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Region 24..34

FT /label= CDR1

FT Region 50..56

FT /label= CDR2

FT Region 89..97

FT /label= CDR3

XX WO9840488-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX WPI: 1999-034590/03.

XX N-PSDB; V71800.

XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX Claim 2; Page 61-62; 97pp; English.

XX This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
 CC (see W84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions (CDRs) from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see W84093). 3 Murine framework residues (1, 49 and 60)
 CC are retained. The humanised light chain can be expressed in host
 CC cells using nucleic acid molecules (see V71800) of the invention.
 CC Humanised D12 VH is also provided (see W84097)). The humanised
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
 CC angiogenic-related disorders, such as angiogenesis associated
 CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
 CC inflammatory disorders, macular degeneration, rheumatoid arthritis
 CC and cancer, e.g. solid tumour metastasis, and diseases where bone
 CC resorption is associated with pathology such as osteoporosis,
 CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.

XX Sequence 107 AA;

Query Match 80.4%; Score 41; DB 20; Length 107;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPILT 9

Db 89 qqsnswpft 97

RESULT 15

W84094

ID

XX

AC

XX

XX

DT

XX

DE

XX

KW

KW

KW

KW

KW

KW

XX

OS

XX

FH

FT

FT

FT

FT

FT

XX

XX

PN

XX

XX

PD

XX

PF

XX

XX

PR

XX

XX

PA

XX

PI

XX

DR

XX

XX

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

XX

Sequence 108 AA;

108 AA;

Sequence 108 AA;

Sequence 108 AA;

Sequence 108 AA;

Sequence 108 AA;

Query Match 80.4%; Score 41; DB 20; Length 108;
Best Local Similarity 77.8%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
 | | | | | | |
Db 89 qqsnswpft 97

Search completed: March 28, 2001, 06:59:53
Job time: 1389 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:58 ; Search time 113.49 Seconds
(without alignments)
1.424 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QOQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgnl_/ptodata/1/iaa/5A_COMB.pep.*
2: /cgnl_/ptodata/1/iaa/5B_COMB.pep.*
3: /cgnl_/ptodata/1/iaa/6_COMB.pep.*
4: /cgnl_/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgnl_/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	45	88.2	9	2	US-08-232-081B-6
2	45	88.2	103	1	US-08-436-463-21
3	45	88.2	107	2	US-08-232-081B-9
4	45	88.2	107	2	US-08-232-081B-40
5	45	88.2	127	1	US-08-436-463-18
6	40	78.4	107	1	US-08-436-463-20
7	40	78.4	107	1	US-08-107-669D-1
8	40	78.4	107	1	US-08-472-788A-1
9	40	78.4	107	2	US-08-477-531B-1
10	40	78.4	107	2	US-08-082-842A-1
11	40	78.4	109	1	US-07-942-245-4
12	40	78.4	143	2	US-08-653-402B-8
13	39	76.5	9	2	US-08-476-176B-55
14	39	76.5	9	3	US-08-127-721A-55
15	39	76.5	9	3	US-08-485-246A-55
16	39	76.5	13	1	US-08-221-580-7
17	39	76.5	13	4	PCT-US95-04018-69
18	39	76.5	106	2	US-08-800-198-4
19	39	76.5	106	3	US-09-296-595-4
20	39	76.5	107	1	US-08-192-102-3
21	39	76.5	107	1	US-08-324-799-3
22	39	76.5	107	2	US-08-192-861A-3
23	39	76.5	107	2	US-08-476-176B-4
24	39	76.5	107	3	US-08-127-721A-4
25	39	76.5	107	3	US-08-485-246A-4
26	39	76.5	127	2	US-08-476-176B-6
27	39	76.5	127	2	US-08-476-176B-8
28	39	76.5	127	2	US-08-476-176B-10

29	39	76.5	127	3	US-08-127-721A-6	Sequence 6, Appli
30	39	76.5	127	3	US-08-127-721A-8	Sequence 8, Appli
31	39	76.5	127	3	US-08-127-721A-10	Sequence 10, Appl
32	39	76.5	127	3	US-08-485-246A-6	Sequence 6, Appli
33	39	76.5	127	3	US-08-485-246A-8	Sequence 8, Appli
34	39	76.5	127	3	US-08-485-246A-10	Sequence 10, Appl
35	39	76.5	240	2	US-08-800-198-8	Sequence 8, Appli
36	39	76.5	240	3	US-09-296-595-8	Sequence 8, Appli
37	38	74.5	100	1	US-08-436-463-19	Sequence 19, Appl
38	38	74.5	107	1	US-07-634-278-62	Sequence 62, Appl
39	38	74.5	107	1	US-07-634-278-63	Sequence 63, Appl
40	38	74.5	107	1	US-07-634-278-87	Sequence 87, Appl
41	38	74.5	107	1	US-08-477-728-62	Sequence 62, Appl
42	38	74.5	107	1	US-08-477-728-63	Sequence 63, Appl
43	38	74.5	107	1	US-08-477-728-87	Sequence 87, Appl
44	38	74.5	107	1	US-08-474-040-62	Sequence 62, Appl
45	38	74.5	107	1	US-08-474-040-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-08-232-081B-6
; Sequence 6, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-232-081B-6

Query Match 88.2%; Score 45; DB 2; Length 9;
Best Local Similarity 88.9%; Pred No. 1.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QOQSGSWPLT 9
||| |||||
Db 1 QOQSSSWPLT 9

```

RESULT 2
US-08-436-463-21
: Sequence 21, Application US/08436463
: Patent No. 5760185
: GENERAL INFORMATION:
: APPLICANT: KIMACHI, Kazuhiko
: APPLICANT: MAEDA, Hiroaki
: APPLICANT: NISHIYAMA, Kiyoto
: APPLICANT: TOKIYOSHI, Sachio
: TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
: TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NETMARK, P.L.L.C.
: STREET: 419 Seventh Street, N.W., Suite 400
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,463
: FILING DATE: 26-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 341255/1992
: FILING DATE: 28-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: YUN, Allen C.
: REGISTRATION NUMBER: 37,971
: REFERENCE/DOCKET NUMBER: KIMACHI-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 103 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-436-463-21

Query Match 88.2%; Score 45; DB 1; Length 103;
Best Local Similarity 88.9%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 86 QQNSWPLT 94

RESULT 3
US-08-232-081B-9
: Sequence 9, Application US/08232081B
: Patent No. 5886152
: GENERAL INFORMATION:
: APPLICANT: NAKATANI, TOMOYUKI
: APPLICANT: GOMI, HIDEYUKI
: APPLICANT: WIJDENES, JOHN
: APPLICANT: NOGUCHI, HIROSHI
: TITLE OF INVENTION: HUMANIZED B-B10
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
: STREET: PO BOX 747
: CITY: FALLS CHURCH
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,081B
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: SVENSSON, LEONARD R
: REGISTRATION NUMBER: 30,330
: REFERENCE/DOCKET NUMBER: 20-3484
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: STREET: PO BOX 747

```

```

: CITY: FALLS CHURCH
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,081B
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: SVENSSON, LEONARD R
: REGISTRATION NUMBER: 30,330
: REFERENCE/DOCKET NUMBER: 20-3484
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 107 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-232-081B-9

Query Match 88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 4
US-08-232-081B-40
: Sequence 40, Application US/08232081B
: Patent No. 5886152
: GENERAL INFORMATION:
: APPLICANT: NAKATANI, TOMOYUKI
: APPLICANT: GOMI, HIDEYUKI
: APPLICANT: WIJDENES, JOHN
: APPLICANT: NOGUCHI, HIROSHI
: TITLE OF INVENTION: HUMANIZED B-B10
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
: STREET: PO BOX 747
: CITY: FALLS CHURCH
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,081B
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: SVENSSON, LEONARD R
: REGISTRATION NUMBER: 30,330
: REFERENCE/DOCKET NUMBER: 20-3484
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: STREET: PO BOX 747

```

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-081B-40

Query Match 88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 5
US-08-436-463-18
; Sequence 18, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-18

Query Match 88.2%; Score 45; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 109 QQSNWPLT 117

RESULT 6
US-08-436-463-20
; Sequence 20, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-20

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSNWPLT 97

RESULT 7
US-08-107-669D-1
; Sequence 1, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America

```
;
;
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-107-669D-1.

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSNWPYT 97

RESULT 8
US-08-472-788A-1
; Sequence 1, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
```

```
;
;
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-788A-1

Query Match 78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSNWPYT 97

RESULT 9
US-08-477-531B-1
; Sequence 1, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-477-531B-1

Query Match 78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| ||| |

Db 89 QOQSNWPYT 97

RESULT 10

US-08-082-842A-1
; Sequence 1, Application US/08082842A
; Patent No. 5869619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| ||| |

Db 89 QOQSNWPYT 97

RESULT 11

US-07-942-245-4
; Sequence 4, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:

; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-07-942-245-4

Query Match 78.4%; Score 40; DB 1; Length 109;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| ||| |

Db 89 QOQSNWPYT 97

RESULT 12

US-08-653-402B-8
; Sequence 8, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabeth
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B

; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-402B-8

Query Match 78.4%; Score 40; DB 2; Length 143;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
||| ||| |
Db 109 QQSNWPT 117

RESULT 13
US-08-476-176B-55
; Sequence 55, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-176B-55

Query Match 76.5%; Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
||| ||| |
Db 1 QQSDSWPT 9

RESULT 14
US-08-127-721A-55
; Sequence 55, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-127-721A-55

Query Match 76.5%; Score 39; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
||| ||| |
Db 1 QQSDSWPT 9

RESULT 15
US-08-485-246A-55
; Sequence 55, Application US/08485246A
; Patent No. 6072035

GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127.721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952.802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-246A-55

Query Match 76.5%; Score 39; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 QOQSGSWPLT 9
| | | | |
Db 1 QOQSDSWPTT 9

Search completed: March 28, 2001, 07:01:58
Job time: 1337 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:32 ; Search time 130.08 Seconds
(without alignments)
4.698 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QOQSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	88.5	67	PH1081	Ig light chain V r
2	46	88.5	69	PH1080	Ig light chain V r
3	41	78.8	107	A45722	anti-glycoprotein
4	41	78.8	123	S35479	Ig kappa chain pre
5	40	76.9	106	PI0267	Ig kappa chain V r
6	39	75.0	104	B43413	Ig kappa chain V r
7	39	75.0	108	C30502	Ig kappa chain V r
8	39	75.0	138	A26471	Ig kappa chain pre
9	38	73.1	107	B45722	anti-glycoprotein
10	38	73.1	553	T15220	hypothetical prote
11	37	71.2	102	S26346	Ig kappa chain V r
12	37	71.2	128	PH0445	Ig kappa chain pre
13	36	69.2	87	PH1082	Ig light chain V r
14	36	69.2	115	KVMSL7	Ig kappa chain pre
15	36	69.2	154	T17816	hypothetical prote
16	36	69.2	331	T48867	hypothetical prote
17	36	69.2	1456	1 WMMGPV	RNA-directed RNA p
18	36	69.2	1456	J02294	hypothetical 165.1
19	36	69.2	1456	S14005	hypothetical prote
20	35	67.3	365	1 SAVLWE	large surface anti
21	35	67.3	366	1 SAVLBD	large surface anti
22	35	67.3	366	1 SAVLWD	large surface anti
23	35	67.3	366	A37374	Fc gamma (IgG) rec
24	35	67.3	470	1 W2BEA4	transcription acti
25	35	67.3	470	1 B42746	transcription acti
26	35	67.3	618	2 T49177	hypothetical prote
27	35	67.3	753	2 JC2099	glutenin, high mol
28	35	67.3	789	2 A30843	glutenin high mole
29	35	67.3	791	2 JN0690	glutenin, high-mol

30 35 67.3 815 2 B30843 glutenin high mole
31 35 67.3 815 2 JN0689 glutenin, high-mol
32 35 67.3 830 2 S15720 glutenin high mole
33 34 65.4 96 2 JC5945 regulatory protein
34 34 65.4 106 2 PC4282 Ig kappa chain (an
35 34 65.4 107 2 C45722 anti-glycoprotein
36 34 65.4 146 2 G65008 hypothetical prote
37 34 65.4 179 1 XXECPL ribosomal-protein-
38 34 65.4 199 2 B49055 major histocompati
39 34 65.4 215 2 T16383 hypothetical prote
40 34 65.4 219 2 H75621 GGNF family prote
41 34 65.4 231 1 HLCBRL class II histocomp
42 34 65.4 250 2 B83008 histidine utilizat
43 34 65.4 259 2 G75400 probable oxidoredu
44 34 65.4 263 2 A23659 spectrin beta chai
45 34 65.4 295 2 S77308 hypothetical prote

ALIGNMENTS

RESULT 1
PH1081
Ig light chain V region (clone 165.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1081
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1081
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-67 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 88.5%; Score 46; DB 2; Length 67;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
III IIIII
Db 58 QOQNSWPQT 66

RESULT 2
PH1080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 88.5%; Score 46; DB 2; Length 69;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9

Db 60 QQSGSWPQT 68
||| |||||

RESULT 3

A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human glycoprotein H
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| |||||

RESULT 4

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a mouse
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| |||||

RESULT 5

PL0267
Ig kappa chain V region (anti-DNA, DPL2VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 76.9%; Score 40; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| |||||

RESULT 6

B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B43413
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific binding to alpha 5 beta 1 integrin
A:Reference number: A43413; MUID:92388177
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 104;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
||| |||||

RESULT 7

C30502
Ig kappa chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: C30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787
A:Accession: C30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <EIL>

C:Cross-references: GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g197072
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
||: |||:|
Db 89 QQTNSWPRT 97

RESULT 8
A26471
Ig kappa chain precursor V region (NAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajisz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A:Reference number: A91572; MUID:87248058
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M16162; NID:gl96893; PIDN:AAA38823.1; PID:gl96894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 75.0%; Score 39; DB 2; Length 138;
Best Local Similarity 77.8%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
||| ||| |
Db 109 QOQNSWPLT 117

RESULT 9
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833
A:Accession: B45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A>Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
||: ||| |
Db 89 QQTNSWPHT 97

RESULT 10
T15220
hypoetical protein F57C9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15220
R:Geisel, C.; Kramer, J.; Gibson, A.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F57C9.
A:Reference number: Z18309
A:Accession: T15220
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-553 <GEI>
A:Cross-references: EMBL:AF003142; NID:g2088743; PID:g2088751; PIDN:AAB54191.1; GSPDB
A:Experimental source: strain Bristol N2; clone F57C9
C:Genetics:
A:Gene: CESP:F57C9.8
A:Map position: 1
A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match 73.1%; Score 38; DB 2; Length 553;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7
|: ||| |
Db 373 QRSQSWP 379

RESULT 11
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421
A:Accession: S26346
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:gl334075
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 37; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
||| :|| |
Db 87 QQSNTWPYT 95

RESULT 12
PN0445
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0445
R:Kaluzza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polym
A:Reference number: PN0444; MUID:93138402
A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>
A:Cross-references: GB:L02347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:1-10/Domain: signal sequence #status predicted <SIG>
 F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
 F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 37; DB 2; Length 128;
 Best Local Similarity 66.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9

||: ||| |
 Db 99 QQTNSWPTT 107

RESULT 13

PH1082

Ig light chain V region (clone 165.54) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PH1082

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1082

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-87 <TII>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:6-80/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 87;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7

||| |||

Db 79 QQSNSWP 85

RESULT 14

KVMSL7

Ig kappa chain precursor V region (L7) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999

C:Accession: A01925

R:Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.

Nature 291, 668-670, 1981

A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequ

A:Reference number: A93259; MUID:81220975

A:Accession: A01925

A:Molecule type: DNA

A:Residues: 1-115 <PEC>

A:Cross-references: GB:V01564; GB:J00574; NID:g51718; PIDN:CAR24884.1; PID:g758153

A:Note: the sequence was determined from the germline gene

A:Note: there appear to be two possible splice junctions at the 3' end of the intron; th

C:Genetics:

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

F:43-108/Disulfide bonds: #status predicted

Query Match 69.2%; Score 36; DB 1; Length 115;

Best Local Similarity 85.7%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7

||| |||

Db 109 QQSNSWP 115

RESULT 15

TI7816

hypothetical protein a317L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: TI7816

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: TI7816

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-154 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96685.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: a317L

Query Match 69.2%; Score 36; DB 2; Length 154;

Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7

||| |||

Db 33 QTSWSWP 39

Search completed: March 28, 2001, 07:04:33

Job time: 1071 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:14 ; Search time 72.95 seconds
(without alignments)
3.941 Million cell updates/sec

Title: US-09-016-061-92
Perfect score: 52
Sequence: 1 QQSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	36	69.2	92	1 CATC_RHOOP
2	36	69.2	115	1 KV51_MOUSE
3	36	69.2	1456	1 RPO_PVX
4	36	69.2	1456	1 RPO_PVXCP
5	36	69.2	1456	1 RPO_PVXHB
6	36	69.2	1456	1 RPO_PVX3
7	35	67.3	365	1 -VMSA-HPBDC
8	35	67.3	366	1 FCN_RAT
9	35	67.3	366	1 VMSA-HPBDB
10	35	67.3	366	1 VMSA-HPBDW
11	35	67.3	470	1 IE63_HSVB
12	35	67.3	470	1 IE63_HSVK
13	34	65.4	96	1 CTCI_ACILW
14	34	65.4	146	1 YFDK_ECOLI
15	34	65.4	179	1 RIML_ECOLI
16	34	65.4	231	1 HB2L_CHICK
17	34	65.4	318	1 GBLP_DROME
18	34	65.4	318	1 PEK7_MOUSE
19	34	65.4	323	1 PEK7_HUMAN
20	34	65.4	491	1 TYTR_CRIFA
21	34	65.4	492	1 TYTR_TRYBB
22	34	65.4	492	1 TYTR_TRYCO
23	34	65.4	745	1 CUL2_HUMAN
24	34	65.4	1335	1 RPO_FAMV
25	33	63.5	353	1 LEU3_BACFR
26	33	63.5	360	1 VG47_BPMU
27	33	63.5	436	1 VU10_HSV6U
28	33	63.5	443	1 XJJ1_ECOLI
29	33	63.5	468	1 NIFB_KLEPN
30	33	63.5	528	1 HEXA_MOUSE
31	33	63.5	529	1 HEXA_HUMAN
32	33	63.5	658	1 EGN1_HUMAN
33	33	63.5	855	1 ENV_FIVT2

34	33	63.5	1435	1 NOS1_RABIT	O19132 oryctolagus
35	33	63.5	3329	1 BRC2_MOUSE	P97929 mus musculus
36	33	63.5	3418	1 BRC2_HUMAN	P51587 homo sapien
37	32	61.5	109	1 KV3B_HUMAN	P01620 homo sapien
38	32	61.5	169	1 GSPH_ECOLI	P41443 escherichia
39	32	61.5	276	1 RCEL_RHOP	O83005 rhodospseudo
40	32	61.5	336	1 CH12_ORYSA	P25765 oryza sativ
41	32	61.5	365	1 FCGN_MOUSE	Q61559 mus musculus
42	32	61.5	402	1 OPDE_PSEAE	Q01602 pseudomonas
43	32	61.5	473	1 XYL_A_CLOS	P48790 clostridium
44	32	61.5	492	1 TYTR_TRYCR	P28593 trypanosoma
45	32	61.5	510	1 NOAL_HUMAN	P51513 homo sapien

ALIGNMENTS

RESULT 1					
CATC_RHOOP					
ID	CATC_RHOOP	STANDARD;	PRT;	92 AA.	
AC	P95609;				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	MUCONOLACTONE DELTA-ISOMERASE (EC 5.3.3.4) (MIASE).				
GN	CATC.				
OS	Rhodococcus opacus.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.				
RC	STRAIN=ICP;				
RX	MEDLINE; 97114521.				
RA	Eulberg D., Golovleva L.A., Schloemann M.;				
RT	"Characterization of catechol catabolic genes from Rhodococcus				
RT	erythropolis ICP.";				
RL	J. Bacteriol. 179:370-381(1997).				
CC	-1- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE =				
CC	3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.				
CC	-1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-				
CC	AND ACETYL-COA IN THE BETA-KETOADIPE PATHWAY.				
CC	-1- SUBUNIT: HOMODECAMER (BY SIMILARITY).				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; X99622; CAA67935.1; ..				
KW	Aromatic hydrocarbons catabolism; Isomerase.				
FT	INIT_MET 0				
FT	SEQUENCE 92 AA; 10780 MW; 9CCE5A17DED4B153 CRC64;				

Query Match 69.2%; Score 36; DB 1; Length 92;
Best Local Similarity 62.5%; Pred. No. 6.1;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQ 8
Db 35 QRSQKWE 42

RESULT 2					
KV51_MOUSE					
ID	KV51_MOUSE	STANDARD;	PRT;	115 AA.	
AC	P01642;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				

DE IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81220975.
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS AT
THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
LACKING RESIDUES 17-19.
DR PIR; A01925; KVM5L7.
DR INTERPRO: IPR003006;
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 69.2%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWP 7
DB 109 QOSGSWP 115

RESULT 3
RRPO_PVX ID RRPO_PVX STANDARD; PRT; 1456 AA.
AC P09395;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (165 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
OS Potato virus X (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89083520.
RA Skryabin K.G., Kraev A.S., Morozov S.Y., Rozanov M.N., Chernov B.K.,
RA Lukashova L.I., Atabekov J.G.;
RT "The nucleotide sequence of potato virus X RNA.";
RL Nucleic Acids Res. 16:10929-10930(1988).
CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
CC -----
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CC -----
CC EMBL; M72416; AAA47167.1;
DR EMBL; X05198; CAA28826.1;
DR INTERPRO: IPR000506;
DR PFAM; PF01443; Viral_helicase; 1.

KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase.
FT NP_BIND 735 742 ATP (POTENTIAL).
SQ SEQUENCE 1456 AA; 165406 MW; F09FDF47E298988C CRC64;

Query Match 69.2%; Score 36; DB 1; Length 1456;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWP 8
DB 1361 QOSGSWP 1368

RESULT 4
RRPO_PVX ID RRPO_PVX STANDARD; PRT; 1456 AA.
AC P22591;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (165 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
OS Potato virus X (strain CP) (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90364772.
RA Orman B.E., Celnik R.M., Mandel A.M., Torres H.N., Mentaberry A.N.;
RT "Complete cDNA sequence of a South American isolate of potato virus
X.";
RL Virus Res. 16:293-306(1990).
CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
CC -----
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CC -----
CC EMBL; M31541; AAA47178.1;
DR EMBL; X55802; CAA39324.1;
DR PIR; S14005; S14005.
DR INTERPRO: IPR000606;
DR PFAM; PF01443; Viral_helicase; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase.
FT NP_BIND 735 742 POTENTIAL.
SQ SEQUENCE 1456 AA; 165301 MW; 489BA57EA070BD2E CRC64;

Query Match 69.2%; Score 36; DB 1; Length 1456;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWP 8
DB 1361 QOSGSWP 1368

RESULT 5
RRPO_PVX ID RRPO_PVX STANDARD; PRT; 1456 AA.
AC Q07630;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (165 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].

OS Potato virus X (strain HB) (PVX).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94015010.
 RA Querci M., van der Vlugt R., Goldbach R., Salazar L.F.;
 RT "RNA sequence of potato virus X strain HB.";
 RL J. Gen. Virol. 74:2251-2255(1993)
 CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
 CC POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
 CC -----
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 CC -----
 DR EMBL; X72214; CAA51012.1; -.
 DR INTERPRO; IPR000606; -.
 DR PFAM; PF01443; Viral_helicase1; 1.
 KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
 KW Transferase.
 FT NP_BIND 735 742 ATP (POTENTIAL).
 SQ SEQUENCE 1456 AA; 165138 MW; 10730A1EADA4FAB4 CRC64;
 Query Match 69.2%; Score 36; DB 1; Length 1456;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWPQ 8
 Db 1361 QKGSWPE 1368
 RESULT 6
 RRPO_PVXX3
 ID RRPO_PVXX3 STANDARD; PRT; 1456 AA.
 AC P17779;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE RNA REPLICATION PROTEIN (165 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
 DE DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
 OS Potato virus X (strain X3) (PVX).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 8829944.
 RA Huismann M.J., Linthorst H.J.M., Bol J.F., Cornelissen B.J.C.;
 RT "The complete nucleotide sequence of potato virus X and its
 RT homologues at the amino acid level with various plus-stranded RNA
 RT viruses";
 RL J. Gen. Virol. 69:1789-1798(1988).
 CC -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
 CC POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
 CC -----
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 CC -----
 DR EMBL; D00344; BAA00249.1; -.
 DR PIR; JA0102; WNWGPV.
 DR INTERPRO; IPR000606; -.
 DR PFAM; PF01443; Viral_helicase1; 1.
 KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
 KW Transferase.

FT NP_BIND 735 742 ATP (POTENTIAL).
 SQ SEQUENCE 1456 AA; 165605 MW; E06E3FF2AB48E97B CRC64;
 Query Match 69.2%; Score 36; DB 1; Length 1456;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWPQ 8
 Db 1361 QKGSWPE 1368
 RESULT 7
 VMSA_HPBDC
 ID VMSA_HPBDC STANDARD; PRT; 365 AA.
 AC P30029;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-JUL-1999 (Rel. 38, Last annotation update)
 DE MAJOR SURFACE ANTIGEN PRECURSOR.
 GN S.
 OS Duck hepatitis B virus (strain China) (DHBV).
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91045091.
 RA Tong S., Mattes F., Teubner K., Blum H.E.;
 RT "Complete nucleotide sequence of a Chinese duck hepatitis B virus";
 RL Nucleic Acids Res. 18:6139-6139(1990).
 CC -----
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 CC -----
 DR EMBL; M21953; AAA45746.1; -.
 DR PIR; S12842; SAVLWE.
 DR INTERPRO; IPR000349; -.
 DR PFAM; PF00695; VMSA; 2.
 KW Antigen.
 FT PROPEP 1 198
 FT CHAIN 199 365 MAJOR SURFACE ANTIGEN
 FT CARBOHYD 297 297 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 365 AA; 40511 MW; 67F3A4174CB7D884 CRC64;
 Query Match 67.3%; Score 35; DB 1; Length 365;
 Best Local Similarity 71.4%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQGSWP 7
 Db 96 QQQGWAP 102
 RESULT 8
 FCGN_RAT
 ID FCGN_RAT STANDARD; PRT; 366 AA.
 AC P13599;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE IGG RECEPTOR FCN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC
 DE RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN).
 GN FCGRT OR FCRN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-WTSTAR;
 RX MEDLINE; 89097257.
 RA Simister N.E., Mostov K.E.;
 FT "An Fc receptor structurally related to MHC class I antigens.";
 RL Nature 337:184-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EPIITHELIUM;
 RX MEDLINE; 90315866.
 RA Simister N.E., Mostov K.E.;
 FT "Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RL major histocompatibility complex class I antigen homolog.";
 RN Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 95059482.
 RA Burmeister W.P., Huber A.H., Bjorkman P.J.;
 FT "Crystal structure of the complex of rat neonatal Fc receptor with
 RL Fc.";
 RN Nature 372:379-383(1994).
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 98154319.
 RA Vaughn D.E., Bjorkman P.J.;
 FT "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RL receptor";
 RN Structure 6:63-73(1998).
 CC -!- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCERN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCERN INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -!- SUBUNIT: FCERN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
 CC LIKE HETERODIMER.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -!- SIMILARITY: STRONG, TO MHC CLASS I ANTIGENS.
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 CC -----
 DR EMBL; X14323; CAA32503.1; -;
 DR EMBL; M35495; AAA41611.1; -;
 DR PIR; S02117; S02117.
 DR PIR; A37374; A37374.
 DR PDB; 1FRT; 14-FEB-95.
 DR PDB; 3FRU; 10-JUN-98.
 DR INTERPRO; IPR000495; -;
 DR INTERPRO; IPR001039; -;
 DR INTERPRO; IPR001220; -;
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00129; MHC_I; 1.
 DR PFAM; PF00047; Ig; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 366 IGG RECEPTOR FCERN LARGE SUBUNIT P51.
 FT DOMAIN 23 111 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 112 201 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 202 291 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 292 298 CONNECTING PEPTIDE.
 FT TRANSMEM 299 322 POTENTIAL.
 FT DOMAIN 323 366 CYTOPLASMIC (POTENTIAL).

FT DISULFID 120 183 BY SIMILARITY.
 FT DISULFID 222 276 BY SIMILARITY.
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40168 MW; 8A8BF2873A698BB5 CRC64;
 Query Match 67.3%; Score 35; DB 1; Length 366;
 Best Local Similarity 71.4%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SGSSWPT 9
 DB 152 SGENPET 158
 II II:1
 RESULT 9
 VMSA_HPBDB STANDARD; PRT; 366 AA.
 ID VMSA_HPBDB STANDARD; PRT; 366 AA.
 AC P17194;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE MAJOR SURFACE ANTIGEN PRECURSOR.
 GN S.
 OS Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90085807.
 RA Uchida M., Esumi M., Shikata T.;
 RT "Molecular cloning and sequence analysis of duck hepatitis B virus
 RL genomes of a new variant isolated from Shanghai ducks.";
 RL Virology 173:600-606(1989).
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 CC -----
 DR EMBL; M32990; AAA45755.1; ALT_INIT.
 DR PIR; C33746; SAVLBD.
 DR INTERPRO; IPR000349; -;
 DR PFAM; PF00695; VMSA; 2.
 KW Antigen.
 FT PROPEP 1 199 MAJOR SURFACE ANTIGEN.
 FT CHAIN 200 366
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40897 MW; 5B72879A182EFF38 CRC64;
 Query Match 67.3%; Score 35; DB 1; Length 366;
 Best Local Similarity 71.4%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQSGSWP 7
 DB 96 QQQGWAP 102
 II II:1
 RESULT 10
 VMSA_HPBDB STANDARD; PRT; 366 AA.
 ID VMSA_HPBDB STANDARD; PRT; 366 AA.
 AC P17195;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)

MAJOR SURFACE ANTIGEN PRECURSOR.

S. Duck hepatitis B virus (white Shanghai duck isolate 931) (DHBV).
 Viruses; Retroviridae; Hepadnaviridae; Avihepadnavirus.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 90085807.
 RA Uchida M., Esumi M., Shikata T.;
 RT "Molecular cloning and sequence analysis of duck hepatitis B virus
 genomes of a new variant isolated from Shanghai ducks.";
 RL Virology 173:600-606(1989).
 CC -----
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 CC -----
 DR EMBL; M32991; AAA45752.1; ALT_INIT.
 DR PIR; D33746; SAVLWD.
 DR INTERPRO; IPR000349; -
 DR PFAM; PF00695; VMSA; 2.
 KW Antigen.
 FT PROPEP 1 199
 FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40958 MW; CF60E78B7B2FCD52 CRC64;
 CC -----
 Query Match 67.3%; Score 35; DB 1; Length 366;
 Best Local Similarity 71.4%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QOSGSWP 7
 Db 96 QOQGAWP 102
 CC -----
 RESULT 11
 ID IE63_HSVB STANDARD; PRT; 470 AA.
 AC P28939;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE TRANSCRIPTIONAL REGULATOR IE63 HOMOLOG.
 GN 5.
 OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92295566.
 RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
 RT "The DNA sequence of equine herpesvirus-1";
 RL Virology 189:304-316(1992).
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
 CC HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
 CC -----
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 CC -----
 DR EMBL; M86664; AAB02440.1;
 DR PIR; F36795; W2BEA4.
 KW Transcription regulation.

SQ SEQUENCE 470 AA; 51320 MW; 99AC5258EFB74B0E CRC64;
 Query Match 67.3%; Score 35; DB 1; Length 470;
 Best Local Similarity 62.5%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QOSGSWP 8
 Db 127 QSAGSWPK 134
 CC -----
 RESULT 12
 ID IE63_HSVK STANDARD; PRT; 470 AA.
 AC Q05906;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE TRANSCRIPTIONAL REGULATOR IE63 HOMOLOG.
 GN UL3.
 OS Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92365125.
 RA Zhao Y., Holden V.R., Harty R.N., O'Callaghan D.J.;
 RT "Identification and transcriptional analyses of the UL3 and UL4 genes
 of equine herpesvirus 1, homologs of the ICP27 and glycoprotein K
 genes of herpes simplex virus";
 RL J. Virol. 66:5363-5372(1992).
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
 CC HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
 CC -----
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 CC -----
 DR EMBL; M95822; AAA46099.1;
 DR PIR; B42746; B42746.
 KW Transcription regulation.
 SQ SEQUENCE 470 AA; 51389 MW; 48DBE440E11363F7 CRC64;
 CC -----
 Query Match 67.3%; Score 35; DB 1; Length 470;
 Best Local Similarity 62.5%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QOSGSWP 8
 Db 127 QSAGSWPK 134
 CC -----
 RESULT 13
 ID CTCL_ACILW STANDARD; PRT; 96 AA.
 AC O33947;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MUCONOLACTONE DELTA-ISOMERASE 1 (EC 5.3.3.4) (MIASE 1).
 GN CATC1.
 OS Acinetobacter lwoffii.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K24;

RX MEDLINE; 97405925.
 RA Kim S.I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
 RA Park Y.K., Lee Y.N., Ha K.-S.;
 RT "Cloning and characterization of two catA genes in Acinetobacter
 RT lwoffii K24";
 RL J. Bacteriol. 179:5226-5231(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K24;
 RX MEDLINE; 98139907.
 RA Kim S.I., Leem S.-H., Choi J.-S., Ha K.-S.;
 RT "Organization and transcriptional characterization of the catI gene
 RT cluster in Acinetobacter lwoffii K24";
 RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
 CC -1- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE =
 CC 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.
 CC -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
 CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
 CC -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
 CC -----
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 CC -----
 DR EMBL; U77658; AAC46227.1; -;
 KW Aromatic hydrocarbons catabolism; Isomerase.
 SQ SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;

Query Match 65.4%; Score 34; DB 1; Length 96;
 Best Local Similarity 71.4%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSWP 7
 Db 35 QKSGKWP 41

RESULT 14
 YFDK_ECOLI
 ID YFDK_ECOLI STANDARD; PRT; 146 AA.
 AC P77656;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 16.4 KDA PROTEIN IN INTC-DSDC INTERGENIC REGION.
 GN YFDK.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12";
 RT Science 277:1453-1474(1997).
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 97349980.
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Ito T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
 RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,

RA Yamagata S., Horiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT DNA Res. 4:91-113(1997).
 CC -1- SIMILARITY: STRONG, TO E.COLI YMFS.
 CC -----
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 CC -----
 DR EMBL; AF000324; AAC75413.1; -;
 DR EMBL; D90866; CAB22145.1; -;
 DR EMBL; D90865; CAB22143.1; -;
 DR ECOGENE; EG14135; YFDK.
 KW Hypothetical protein.
 SQ SEQUENCE 146 AA; 16408 MW; 28F3CA711C5E9C79 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 146;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QOQSWP 7
 Db 23 QAGSWP 28

RESULT 15
 RIML_ECOLI
 ID RIML_ECOLI STANDARD; PRT; 179 AA.
 AC P13857;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RIBOSOMAL-PROTEIN-SERINE ACETYLTRANSFERASE (EC 2.3.1.-) (ACETYLATING
 DE ENZYME FOR N-TERMINAL OF RIBOSOMAL PROTEIN L7/L12).
 GN RIML.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB2052;
 RX MEDLINE; 89364711.
 RA Tanaka S., Matsushita Y., Yoshikawa A., Isono K.;
 RT "Cloning and molecular characterization of the gene rimL which
 RT encodes an enzyme acetylating ribosomal protein L12 of Escherichia
 RT coli K12";
 RL Mol. Gen. Genet. 217:289-293(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12";
 RT Science 277:1453-1474(1997).
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 97251357.
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Mizura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,

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RA  Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA  Yamamoto Y., Horiuchi T.;
RT  "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT  corresponding to the 28.0-40.1 min region on the linkage map.";
RL  DNA Res. 3:363-377(1996).
CC  -!- FUNCTION: THIS ENZYME ACETYLATED THE N-TERMINAL SERINE OF
CC  RIBOSOMAL PROTEIN L7/L12.
CC  -!- CATALYTIC ACTIVITY: ACETYL-COA + RIBOSOMAL-PROTEIN L-SERINE =
CC  COA + RIBOSOMAL-PROTEIN N-ACETYL-L-SERINE.
CC  -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC  -!- SIMILARITY: BELONGS TO THE ACETYLTRANSFERASE FAMILY. RIML
CC  SUBFAMILY.
CC  -----
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CC  -----
DR  EMBL; X15860; CAA33869.1; -.
DR  EMBL; AE000240; AAC74509.1; -.
DR  EMBL; D90781; BAAL5048.1; -.
DR  EMBL; D90782; BAAL5057.1; -.
DR  PIR; S04776; XKECPL.
DR  SWISS-2DPAGE; P13857; COLI.
DR  ECO2DBASE; F037.8; 6TH EDITION.
DR  ECO2DBASE; F038.5; 6TH EDITION.
DR  ECGENE; EGI0853; RIML.
DR  INTERPRO; IPR000182; -.
DR  PFAM; PF00583; Acetyltransf; 1.
KW  Transferase; Acyltransferase.
SQ  SEQUENCE 179 AA; 20680 MW; 9946F97C2A20CB1D CRC64;

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Query Match      65.4%; Score 34; DB 1; Length 179;
Best Local Similarity 75.0%; Pred. NO. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY  1 QOSGSWPQ 8
    III :III
DB  36 QOSLWNPQ 43

```

Search completed: March 28, 2001, 07:35:15
Job time: 152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:27 ; Search time 443.95 Seconds
(without alignments)
2.376 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QQSGSWPQT 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues.

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	76.9	1194	5 Q9VSI2	Q9vsi2 drosophila
2	38	73.1	553	5 O01825	O01825 caenorhabdi
3	37	71.2	327	12 Q67852	Q67852 duck hepati
4	37	71.2	350	10 Q49958	Q49958 triticum tu
5	36	69.2	154	12 Q84631	Q84631 paramecium
6	36	69.2	331	2 Q08246	Q08246 streptomyc
7	36	69.2	613	5 Q9VHU1	Q9vhu1 drosophila
8	36	69.2	764	10 Q9LRH7	Q9lrh7 pisum sativ
9	36	69.2	1456	12 Q85198	Q85198 potato viru
10	36	69.2	1456	12 Q85245	Q85245 potato viru
11	36	69.2	1456	12 Q9JEX8	Q9jex8 potato viru
12	36	69.2	1456	12 Q9IMP2	Q9imp2 potato viru
13	35	67.3	153	13 Q9YH52	Q9yh52 gallus gall
14	35	67.3	164	2 Q34250	Q34250 streptomyc
15	35	67.3	330	12 Q72885	Q72885 duck hepati
16	35	67.3	330	12 Q66405	Q66405 duck hepati
17	35	67.3	366	12 Q66404	Q66404 duck hepati
18	35	67.3	379	4 Q9NR38	Q9nr38 homo sapien
19	35	67.3	399	4 Q9NR37	Q9nr37 homo sapien

20	35	67.3	405	10	Q41516	Q41516 triticum ae
21	35	67.3	405	10	Q9SYI0	Q9syy0 triticum ae
22	35	67.3	447	4	Q9UHD6	Q9und6 homo sapien
23	35	67.3	459	4	Q9Y638	Q9y638 homo sapien
24	35	67.3	471	4	Q9UBL9	Q9ubl9 homo sapien
25	35	67.3	497	4	Q9UHD5	Q9uhd5 homo sapien
26	35	67.3	618	10	Q9LXQ8	Q9lxx8 arabidopsis
27	35	67.3	789	10	Q42451	Q42451 triticum ae
28	35	67.3	815	10	Q41553	Q41553 triticum ae
29	35	67.3	830	10	Q03872	Q03872 triticum ae
30	35	67.3	929	5	Q9VR32	Q9vr32 drosophila
31	35	67.3	2245	2	Q9L6C9	Q9l6c9 pseudomonas
32	34	65.4	94	2	Q9XCE0	Q9xce0 mycobacteri
33	34	65.4	96	2	Q9Z9Y5	Q9z9y5 frateuria s
34	34	65.4	215	5	Q20513	Q20513 caenorhabdi
35	34	65.4	218	2	Q9KZ8	Q9kzs8 streptomyc
36	34	65.4	219	2	Q9R2S9	Q9rzs9 deinococcus
37	34	65.4	256	10	Q9MB72	Q9mb72 volvox cart
38	34	65.4	259	2	Q9RU17	Q9ru17 deinococcus
39	34	65.4	267	10	Q9XJ63	Q9xj63 oryza sativ
40	34	65.4	267	10	Q9SEW9	Q9sew9 oryza sativ
41	34	65.4	295	2	P73598	P73598 synechocyst
42	34	65.4	318	5	Q9VLW5	Q9vlw5 drosophila
43	34	65.4	350	2	Q9RN58	Q9rn58 streptomyc
44	34	65.4	354	5	Q9N5V9	Q9n5v9 caenorhabdi
45	34	65.4	400	1	Q9YEB4	Q9yee4 aeropyrum p

ALIGNMENTS

RESULT 1

Q9VSI2 PRELIMINARY; PRT; 1194 AA.

AC Q9VSI2; 01-MAY-2000 (TREMREL. 13, Created)

DT 01-MAY-2000 (TREMREL. 13, Last sequence update)

DE 01-OCT-2000 (TREMREL. 15, Last annotation update)

DE CG7112 PROTEIN.

GN CG7112.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abrell J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Ciesla M., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira J., Fleischmann W.,

RA Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003555; AAF50437.1; -
DR FLYBASE; FBgn0035879; CG7112.
DR INTERPRO; IPR000195; -
DR PFAM; PF00566; TBC; 1
SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 76.9%; Score 40; DB 5; Length 1194;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 461 QOQSSWFPYT 469

RESULT 2
ID AC 001825 PRELIMINARY; PRT; 553 AA.
AC 001825;
DT 01-JUL-1997 (TREMBLrel. 04, Created);
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update);
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update);
DE SIMILAR TO BETA-CHINAERIN.
GN F57C9.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightings J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Gelsel C., Kramer J., Gibson A.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF003142; AAB54191.1; -
DR HSP; P27986; IPBW.
DR INTERPRO; IPR000198; -

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DR PFAM; PF00620; RhoGAP; 1.
SQ SEQUENCE 553 AA; 60849 MW; A50EDF9C2F560139 CRC64;

Query Match 73.1%; Score 38; DB 5; Length 553;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7
Db 373 QRSQSWP 379

RESULT 3
ID Q67852 PRELIMINARY; PRT; 327 AA.
AC Q67852;
DT 01-NOV-1996 (TREMBLrel. 01, Created);
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update);
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update);
DE SURFACE PROTEIN.
GN PRES.
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi H., Cullen J.M., Newbold J.E.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M95589; AAA45749.1; -
DR INTERPRO; IPR000349; -
DR PFAM; PF00695; VMSA; 2.
SQ SEQUENCE 327 AA; 36356 MW; 6875E959746DADEB CRC64;

Query Match 71.2%; Score 37; DB 12; Length 327;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQ 8
Db 60 QOQGAMPE 67

RESULT 4
ID O49958 PRELIMINARY; PRT; 350 AA.
AC O49958;
DT 01-JUN-1998 (TREMBLrel. 06, Created);
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update);
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update);
DE LOW MOLECULAR WEIGHT GLUTENIN SUBUNIT PRECURSOR (FRAGMENT).
GN LMW-GS.
OS Triticum turgidum subsp. durum (durum wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
OX NCBI_TaxID=4567;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANGDON;
RA D'Ovidio R., Simeone M., Masci S., Porceddu E.;
RL Theor. Appl. Genet. 95:1119-1126(1997).
DR EMBL; Y14104; CAA74550.1; -
DR MENDEL; 24598; Ttridu; 2372; 24598.
DR INTERPRO; IPR001376; -
DR INTERPRO; IPR001954; -
DR INTERPRO; IPR003015; -
DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 >350 POTENTIAL.

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FT NON_TER 350 350
SQ SEQUENCE 350 AA: 39791 MW: 3590FDDFE55545EC CRC64;

Query Match 71.2%; Score 37; DB 10; Length 350;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPQ 8
II IIII

Db 286 QQLGQWPQ 293

RESULT 5

Q84631 PRELIMINARY; PRT; 154 AA.
AC Q84631;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GENOME, PARTIAL SEQUENCE.
GN A317L.

OS Paramexium bursaria chlorella virus 1 (PBCV-1).
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
OX NCBI_TaxID=10506;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95133167; PubMed=7831789;

RA Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;
RT "Analysis of 45 Kb of DNA located at the left end of the chlorella

RT virus PBCV-1 genome.";

RL Virology 206:339-352(1995).

DR EMBL: U42580; AAC96685.1;

SQ SEQUENCE 154 AA; 18564 MW; 7B45EE2E7F518E15 CRC64;

Query Match 69.2%; Score 36; DB 12; Length 154;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWP 7

I IIIII

Db 33 QTSGSWP 39

RESULT 6

O08246 PRELIMINARY; PRT; 331 AA.
AC O08246;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE TDP-D-GLUCOSE-4, 6, -DEHYDRATASE.

GN MTME.

OS Streptomyces argillaceus.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=41951;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 12956;

RX MEDLINE=97294479; PubMed=9150235;

RA Lombo F., Siens K., Brana A.F., Mendez C., Bindsail K., Salas J.A.;

RT "Cloning and insertional inactivation of Streptomyces argillaceus

RT genes involved in the earliest steps of biosynthesis of the sugar

RT moieties of the antitumor polyketide mithramycin.";

RL J. Bacteriol. 179:3354-3357(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 12956;

RA Salas J.A.;

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12956;
RX MEDLINE=96257259; PubMed=8654997;
RA Lombo F., Blanco G., Fernandez E., Mendez C., Salas J.A.;

RT "Characterization of Streptomyces argillaceus genes encoding a
RT polyketide synthase involved in the biosynthesis of the antitumor
RT mithramycin.";
RL Gene 172:87-91(1996).
DR EMBL: Y10907; CAA71847.1; -.
DR EMBL: AJ007932; CAA07755.1; -.
DR HSSP: P27830; IRLX.
DR INTERPRO: IPR001509; -.
DR INTERPRO: IPR002198; -.
DR PFAM: PF01370; Epimerase; 1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN 1.
SQ SEQUENCE 331 AA; 36352 MW; D6F8E881928837AB CRC64;

Query Match 69.2%; Score 36; DB 2; Length 331;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPQT 9

:|:|:|:|

Db 137 AGSWPET 143

RESULT 7

Q9VHU1 PRELIMINARY; PRT; 613 AA.

AC Q9VHU1;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE CG9630 PROTEIN.

GN CG9630.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Phyllozoa; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Paclad J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003678; AAF54208.1; -;
 DR FLYBASE: FBgn0037561; CG9630.
 DR INTERPRO: IPR000629; -;
 DR INTERPRO: IPR001410; -;
 DR INTERPRO: IPR001650; -;
 DR PFAM: PF00270; DEAD; 1.
 DR PFAM: PF00271; helicase.C; 1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 SQ SEQUENCE 613 AA; 69083 MW; C779803336A02879 CRC64;

Query Match 69.2%; Score 36; DB 5; Length 613;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOQSGSWP 7
 : : : : :
 Db 513 EQTGSWP 519

RESULT 8
 Q9LRH7 PRELIMINARY; PRT; 764 AA.
 ID Q9LRH7
 AC Q9LRH7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE MIXED-AMYRIN SYNTHASE.
 GN OSCPSM.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Pisum.
 OC NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morita M., Shibuya M., Kushihiro T., Masuda K., Ebizuka Y.;
 RT "Molecular cloning and functional expression of triterpene synthases
 from pea (*Pisum sativum*): New alpha-amyrin-producing enzyme is a
 multifunctional triterpene synthase.";
 RL Eur. J. Biochem. 267:3453-3460(2000).
 DR EMBL: AB034803; BA897559.1; -;
 SQ SEQUENCE 764 AA; 88276 MW; DED4CAE6CB822197 CRC64;

Query Match 69.2%; Score 36; DB 10; Length 764;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWP 8
 : : : : :
 Db 714 QEEDWQP 721

RESULT 9
 Q85198 PRELIMINARY; PRT; 1456 AA.
 ID Q85198
 AC Q85198
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 16S KDA PROTEIN.
 OS Potato virus X (PVX).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 RN NCBI_TaxID=12183;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB;
 RX MEDLINE=94025577; PubMed=8212565;
 RA Goulden M.G., Kohm B.A., Santa Cruz S., Kavanagh T.A., Baulcombe D.C.;
 RT "A feature of the coat protein of potato virus X affects both induced
 virus resistance in potato and viral fitness.";
 RL Virology 197:293-302(1993).
 DR EMBL: Z23256; CAA80774.1; -;
 DR INTERPRO: IPR000130; -;
 DR INTERPRO: IPR000606; -;
 DR PFAM: PF01443; Viral_helicase1; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.
 SQ SEQUENCE 1456 AA; 165140 MW; 708B4CBE7645CE03 CRC64;

Query Match 69.2%; Score 36; DB 12; Length 1456;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWP 8
 : : : : :
 Db 1361 QKKGWPE 1368

RESULT 10
 Q85245 PRELIMINARY; PRT; 1456 AA.
 ID Q85245
 AC Q85245
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE PUTATIVE REPLICASE COMPONENT.
 OS Potato virus X (PVX).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
 OC NCBI_TaxID=12183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goulden M.G., Kavanagh T., Santa Cruz S., Chapman S., Barker I.,
 RA Baulcombe D.;
 RT "Molecular analysis of a resistance-breaking strain of potato virus
 X.";
 RL Virology 189:609-617(1992).
 DR EMBL: M95516; AAA03489.1; -;
 DR INTERPRO: IPR000130; -;
 DR INTERPRO: IPR000606; -;
 DR INTERPRO: IPR001993; -;
 DR PFAM: PF01443; Viral_helicase1; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN.1.
 SQ SEQUENCE 1456 AA; 165533 MW; 0A50CBCC4ED25446 CRC64;

Query Match 69.2%; Score 36; DB 12; Length 1456;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWP 8
 : : : : :
 Db 1361 QKKGWPE 1368

RESULT 11
 Q9JEX8 PRELIMINARY; PRT; 1456 AA.
 ID Q9JEX8
 AC Q9JEX8
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE REPLICASE.

```

OS Potato virus X (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ROTH1;
RA Malcuit I., Marano M.R., Kavanagh T.A., de Jong W., Forsyth A.,
RA Baulcombe D.C.;
RT "The 25 kDa movement protein of PVX elicits subcellular fragmentation
RT leading to NB-mediated cell death in potato."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ROTH1;
RA Malcuit I., de Jong W., Baulcombe D.C., Shields D.C., Kavanagh T.A.;
RT "Acquisition of multiple virulence/avirulence determinants in potato
RT virus X (PVX) strains has occurred through convergent evolution rather
RT than through recombination."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF111193; AAF67818.1; -
SQ SEQUENCE 1456 AA; 165778 MW; 00479DBA454A77090 CRC64;

Query Match 69.2%; Score 36; DB 12; Length 1456;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQ 8
DB 1361 QKKGWPE 1368
I:||||:

RESULT 12
Q9IMP2 PRELIMINARY; PRT; 1456 AA.
ID Q9IMP2
AC Q9IMP2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE REPLICASE.
OS Potato virus X (PVX).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CP4;
RA Malcuit I., de Jong W., Baulcombe D.C., Shields D.C., Kavanagh T.A.;
RT "Acquisition of multiple virulence/avirulence determinants in potato
RT virus X (PVX) strains has occurred through convergent evolution rather
RT than through recombination."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172259; AAF69747.1; -
SQ SEQUENCE 1456 AA; 165416 MW; 5197CA9105DA9B13 CRC64;

Query Match 69.2%; Score 36; DB 12; Length 1456;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQ 8
DB 1361 QKKGWPE 1368
I:||||:

RESULT 13
Q9YH52 PRELIMINARY; PRT; 153 AA.
ID Q9YH52
AC Q9YH52;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE HYPOTHETICAL 17.4 KDA PROTEIN.
OS Gallus gallus (Chicken).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H.B19;
RX MEDLINE=90077532; PubMed=2592020;
RA Kaufman J., Salomonsen J., Skjoldt K.;
RT "B-G cDNA clones have multiple small repeats and hybridize to both
RT chicken MHC regions."
RL Immunogenetics 30:440-451(1989).
DR EMBL; M27666; AAA69840.1; -
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17404 MW; 6D344F572FA7EE48 CRC64;

Query Match 67.3%; Score 35; DB 13; Length 153;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QSGSWPOT 9
DB 65 QSGHWPLT 72
I:||||:

RESULT 14
Q54250 PRELIMINARY; PRT; 164 AA.
ID Q54250
AC Q54250;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DNDP-GLUCOSE DEHYDRATASE (FRAGMENT).
GN SCHE.
OS Streptomyces ghanaensis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=35758;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 14672;
RX MEDLINE=96313316; PubMed=8768522;
RA Decker H., Gaisser S., Schneider P., Westrich L., Wohlleben W.,
RA Bechtold A.;
RT "A general approach for cloning and characterizing dNDP-glucose
RT dehydratase genes from actinomycetes."
RL FEMS Microbiol. Lett. 141:195-201(1996).
DR EMBL; X97854; CAA66448.1; -
DR HSSP; P27830; 1BXK
DR INTERPRO; IPR001509; -
DR INTERPRO; IPR002198; -
DR PFAM; PFO1370; Epimerase; 1.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
FT NON_TER 1 164
FT NON_TER 164 164
SQ SEQUENCE 164 AA; 17695 MW; F927F461BA6C50A0 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 164;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSWPOT 9
DB 122 GSWPET 127
I:||||:

RESULT 15
Q72885 PRELIMINARY; PRT; 330 AA.
ID Q72885
AC Q72885;
DT 01-AUG-1998 (TReMBLrel. 07, Created)

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DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DE 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE SURFACE PROTEIN.
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AUSTRALIAN DHBV;
RA Triyatni M., Qiao M., Ey P., Burrell C., Jilbert A.R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006350; CAR06988.1; -.
DR INTERPRO; IPR000349; -.
DR PFAM; PF00695; VMSA; 2.
SQ SEQUENCE 330 AA; 36789 MW; EDED4F42373ADA99 CRC64;

Query Match 67.3%; Score 35; DB 12; Length 330;
Best Local Similarity 71.4%; Pred. NO. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQSGSWP 7
|||:||
Db 60 QQGAWP 66

Search completed: March 28, 2001, 07:53:31
Job time: 524 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:53 ; Search time 154.19 Seconds
(without alignments)
1.996 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT:*

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17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	9	W76036	LM609 grafted anti
2	47	90.4	9	W76013	LM609 grafted anti
3	47	90.4	107	W76006	LM609 grafted anti
4	47	90.4	107	W76002	Vitaxin antibody 1
5	47	90.4	107	W76004	LM609 antibody lig
6	45	86.5	9	W76035	LM609 grafted anti
7	41	78.8	9	W76033	LM609 grafted anti
8	41	78.8	9	Y06372	Murine monoclonal
9	41	78.8	107	R25729	Humanised VL regio
10	41	78.8	109	Y06388	Humanised LM609 an
11	41	78.8	109	Y06380	Murine monoclonal
12	41	78.8	109	Y06382	Humanised LM609 an

13	41	78.8	127	15	R54093	Sequence of mouse
14	40	76.9	107	14	R38601	HYH light chain.
15	40	76.9	107	19	W58482	Murine HYH antibody
16	40	76.9	108	12	R15438	Light chain variab
17	40	76.9	109	15	R52033	Light chain variab
18	40	76.9	143	18	W19580	Mouse anti-idiotyp
19	40	76.9	240	12	R15443	Single chain Fv fr
20	39	75.0	9	14	R37604	hIL2R Ab L chain v
21	39	75.0	9	19	W76034	LM609 grafted anti
22	39	75.0	9	20	Y26992	CDR3 domain reshap
23	39	75.0	106	19	W71241	Light chain variab
24	39	75.0	107	14	R37612	hIL2R Ab L chain v
25	39	75.0	107	14	R37610	B-B10 MAb L chain
26	39	75.0	107	15	R50190	Light chain variab
27	39	75.0	107	20	Y26979	Light chain variab
28	39	75.0	107	21	Y70604	Vkappa region of h
29	39	75.0	127	15	R50187	Light chain variab
30	39	75.0	127	15	R50191	Light chain variab
31	39	75.0	127	15	R50192	Light chain variab
32	39	75.0	127	20	Y26980	Light chain variab
33	39	75.0	127	20	Y26981	Light chain variab
34	39	75.0	127	20	Y26982	Light chain variab
35	39	75.0	240	19	W71243	Light chain variab
36	39	75.0	245	21	Y70605	scFv comprising he
37	38	73.1	105	20	W87456	JK gene product.
38	38	73.1	105	20	W87458	Humanised anti-alp
39	38	73.1	107	20	W84098	Humanised anti-alp
40	38	73.1	108	20	W84094	Murine vitronectin
41	38	73.1	112	20	W84100	Vitronectin alpha-
42	38	73.1	179	20	Y74170	Human prostate tum
43	37	71.2	107	14	R32129	Anti-IL2R beta ant
44	37	71.2	240	14	R34510	Fv(TU27). Homo sa
45	36	69.2	9	19	W44180	Monoclonal antibody

ALIGNMENTS

RESULT 1

W76036

ID W76036 standard; Protein; 9 AA.

XX

AC W76036;

XX

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR3 protein fragment #5.

XX

Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-L region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-0501826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

WPI; 1998-437472/37.

DR N-PSDB; V49873.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 62; Page 44; 129pp; English.
XX
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 52; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 1 qqsgswpqt 9

RESULT 2
ID W76013 standard; Protein; 9 AA.
XX W76013;
AC
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-L region CDR3 protein fragment #1.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-L region; CDR;
XX complementarity determining region.
XX
XX Mus sp.
XX
XX W09833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX N-PSDB; V49850.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Disclosure; Page 40; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 9 AA;

Query Match 90.4%; Score 47; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 1 qqsgswpqt 9

RESULT 3
ID W76006 standard; Protein; 107 AA.
XX W76006;
AC
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody light chain variable region protein fragment.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 49
XX FT /label= Arg, Met
XX
XX W09833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX N-PSDB; V49843.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 19; Fig 7; 129pp; English.
XX
XX This sequence represents a LM609 grafted antibody variable light chain
XX region. LM609 and the antibody vitaxin bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
XX and thus block integrin-mediated signal transduction. This is useful in
XX the treatment, prevention and diagnosis of alphavbeta3-mediated disease,

CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.21;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 ||||| |
 Db 89 qqsgswpht 97

RESULT 4

W76002
 ID W76002 standard; Protein; 107 AA.

XX AC W76002;

XX DT 02-NOV-1998 (first entry)

DE DE Vitaxin antibody light chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49821.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX FS Claim 1; Fig 1b; 129pp; English.

XX CC This sequence represents the vitaxin antibody variable light chain
 region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.21;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 ||||| |
 Db 89 qqsgswpht 97

RESULT 5

W76004
 ID W76004 standard; Protein; 107 AA.

XX AC W76004;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody light chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; W76004.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 46; Fig 2b; 129pp; English.

XX CC This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3
 CC and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 107 AA;

Query Match 90.4%; Score 47; DB 19; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.21;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
 ||||| |
 Db 89 qqsgswpht 97

```

RESULT 6
W76035
ID W76035 standard; Protein; 9 AA.
XX
XX W76035;
AC
XX
XX
DT 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-L region CDR3 protein fragment #4.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX W09833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX N-PSDB; V49870.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 44; 129pp; English.
PS
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 9 AA;

Query Match 86.5%; Score 45; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.le+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 1 qqs9swp1t 9

RESULT 7
W76033
ID W76033 standard; Protein; 9 AA.
XX
XX W76033;
AC
XX
XX
DT 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-L region CDR3 protein fragment #2.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX W09833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
PF
XX
XX 30-JAN-1997; 97US-0791391.
PR
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX N-PSDB; V49870.
DR
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
PS
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 9 AA;

Query Match 78.8%; Score 41; DB 19; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.le+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 1 qqs9swp1t 9

RESULT 8
Y06372
ID Y06372 standard; Peptide; 9 AA.
XX
XX Y06372;
AC
XX
XX
DT 06-SEP-1999 (first entry)
XX
XX Murine monoclonal antibody LM609 VL CDR3.
DE
XX
XX Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

```

cancer; therapy; diagnosis.

XX PN WO9211018-A.
XX PD 09-JUL-1992.
XX PF 19-DEC-1991; 91WO-US09711.
XX PR 19-DEC-1990; 90US-0634278.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Co MS, Coellingh KL, Landolfi NF, Queen CL, Schneider WP;
XX WPI; 1992-249842/30.
XX DR New immunoglobulin(s) having murine CDRs in human framework
XX PT regions - have lower antigenicity; useful for treating e.g. HSV,
XX CMV, T-cell disorders, myeloid disorders and auto-immune
XX PT conditions
XX PS Claim 40; Fig 27A; 141pp; English.
XX CC The sequence shows the humanised mature light chain variable
XX CC region of the mouse CMV5 antibody. Murine CDRs were used
XX CC in a human Wol framework to produce a pure humanised immunoglobulin
XX CC (Ig) which is capable of binding to the GH glycoprotein of
XX CC cytomegalovirus. The Ig is non immunogenic, due to the human
XX CC framework, and has a strong affinity for its predetermined
XX CC antigen. They can be produced in large quantities via recombinant
XX CC DNA and monoclonal antibody technology. The humanised Igs may be
XX CC used alone or in combination with chemotherapeutic agents such as
XX CC non-steroidal anti-inflammatory drugs or immunosuppressants.
XX CC See also R25721-32.
XX SQ Sequence 107 AA;

Query Match 78.8%; Score 41; DB 20; Length 9;

Best Local Similarity 77.8%; Pred. No. 2.1e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9
Db 1 qqnswpht 9

RESULT 9

ID R25729 standard; Protein; 107 AA.

XX AC R25729;

XX DT 13-JAN-1993 (first entry)

XX DE Humanised VL region of the mouse CMV5 antibody.

XX KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
XX KW GH; light chain; variable region; framework; human; Wol.
XX OS Mus musculus.

XX FH Key Location/Qualifiers
XX FT Region 24..34
XX FT /note= "CDR"
XX FT Region 50..56
XX FT /note= "CDR"
XX FT Region 89..97
XX FT /note= "CDR"
XX FT Misc-difference 49
XX FT /note= "mutated residue"

Query Match 78.8%; Score 41; DB 13; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9
Db 89 qqnswpht 97

RESULT 10

ID Y06388 standard; Protein; 109 AA.

XX AC Y06388;

XX DT 06-SEP-1999 (first entry)

XX DE Humanised LM609 antibody VL domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.

XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Peptide 1..2
XX FT /note= "vector-encoded residues"
XX FT Region 24..34
XX FT /note= "CDR1"
XX FT Region 50..56
XX FT /note= "CDR2"
XX FT Region 89..97
XX FT /note= "CDR3"

XX
PN W09929888-A1.

XX
PD 17-JUN-1999.

XX
PF 04-DEC-1998; 98WO-US25828.

XX
PR 05-DEC-1997; 97US-0986016.

XX
PA (SCRI) SCRIPPS RES INST.

XX
PI Barbas CF, Rader C;

XX
PR WPI; 1999-394979/33.

XX
PT Production of humanized mouse monoclonal antibodies

XX
PS Disclosure; Page 52; 55pp; English.

XX
CC This sequence represents the light chain variable region of a

XX
CC humanised LM609 antibody. LM609 is directed to human integrin

XX
CC alpha-v beta-3. It selectively promotes apoptosis of vascular

XX
CC cells that have been stimulated to undergo angiogenesis, making it

XX
CC a tool for cancer diagnosis and therapy. The invention provides

XX
CC humanised antibodies, especially humanised LM609. In such humanized

XX
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is

XX
CC grafted onto a human light chain, and a heavy chain CDR from a mouse

XX
CC antibody is grafted onto a human antibody heavy chain to produce

XX
CC libraries from which a humanised murine antibody having the desired

XX
CC specificity is selected. By preserving the original CDR sequences

XX
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the

XX
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 109 AA;

Query Match 78.8%; Score 41; DB 20; Length 109;
Best Local Similarity 77.8%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPQT 9
||| ||| |

Db 89 qqsnswpht 97

RESULT 11

Y06380
ID Y06380 standard; Protein; 109 AA.

XX
AC Y06380;

XX
DT 06-SEP-1999 (first entry)

XX
DE Murine monoclonal antibody LM609 V lambda.

XX
KW Humanised antibody; antibody humanisation; antibody engineering;

XX
KW LM609; monoclonal antibody; complementarity determining region;

XX
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX
KW cancer; therapy; diagnosis.

XX
OS Mus musculus.

XX
FH Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 24..34 /note= "CDR1"

FT Region 50..56 /note= "CDR2"

FT Region 89..97 /note= "CDR3"

XX
PN W09929888-A1.

XX
PD 17-JUN-1999.

XX
PF 04-DEC-1998; 98WO-US25828.

XX
PR 05-DEC-1997; 97US-0986016.

XX
PA (SCRI) SCRIPPS RES INST.

XX
PI Barbas CF, Rader C;

XX
PR WPI; 1999-394979/33.

XX
PT Production of humanized mouse monoclonal antibodies

XX
PS Disclosure; Page 49-50; 55pp; English.

XX
CC This sequence represents the light chain V lambda region of

XX
CC murine monoclonal antibody LM609. LM609 is directed to integrin

XX
CC alpha-v beta-3. It selectively promotes apoptosis of vascular

XX
CC cells that have been stimulated to undergo angiogenesis, making it

XX
CC a tool for cancer diagnosis and therapy. The invention provides

XX
CC humanised antibodies, especially humanised LM609. In such humanized

XX
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is

XX
CC grafted onto a human light chain, and a heavy chain CDR from a mouse

XX
CC antibody is grafted onto a human antibody heavy chain to produce

XX
CC libraries from which a humanised murine antibody having the desired

XX
CC specificity is selected. By preserving the original CDR sequences

XX
CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the

XX
CC humanisation strategy ensures epitope conservation.

XX
SQ Sequence 109 AA;

Query Match 78.8%; Score 41; DB 20; Length 109;
Best Local Similarity 77.8%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPQT 9
||| ||| |

Db 89 qqsnswpht 97

RESULT 12

Y06382
ID Y06382 standard; Protein; 109 AA.

XX
AC Y06382;

XX
DT 06-SEP-1999 (first entry)

XX
DE Humanised LM609 antibody VL domain.

XX
KW Humanised antibody; antibody humanisation; antibody engineering;

XX
KW LM609; monoclonal antibody; complementarity determining region;

XX
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;

XX
KW cancer; therapy; diagnosis.

XX
OS Homo sapiens.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 24..34 /note= "CDR1"

FT Region 50..56 /note= "CDR2"

FT Region 89..97 /note= "CDR3"

XX
PN W09929888-A1.

PD 17-JUN-1999.
 XX
 PF 04-DEC-1998; 98WO-US25828.
 XX
 PR 05-DEC-1997; 97US-0986016.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX
 DR WPI; 1999-394979/33.
 XX
 XX Production of humanized mouse monoclonal antibodies
 PT
 XX
 PS Disclosure; Page 50; 55pp; English.
 XX
 CC This sequence represents the light chain variable region of a
 CC humanised LM609 antibody. LM609 is directed to human integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.
 XX
 SQ Sequence 109 AA;

Query Match 78.8%; Score 41; DB 20; Length 109;
 Best Local Similarity 77.8%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPQT 9
 ||| ||| |
 Db 89 qqsnswpht 97

RESULT 13
 R54093
 ID R54093 standard; Protein; 127 AA.
 XX
 AC R54093;
 XX
 DT 29-DEC-1994 (first entry)
 XX
 DE Sequence of mouse V-kappa showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.
 XX
 DE Feline herpes virus; FHV-1; monoclonal antibody; CDR;
 KW complementarity determining region.
 KW
 XX Mus musculus.
 OS
 XX

Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= leader
 FT Region 21..43
 FT /label= FR1
 FT Region 44..54
 FT /label= CDR1
 FT Region 55..70
 FT /label= FR2
 FT Region 71..76
 FT /label= CDR2
 FT Region 77..108
 FT /label= FR3
 FT Region 109..117
 FT /label= CDR3

FT Region 118..127
 FT /label= FR4
 XX
 PN W09412661-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 25-NOV-1993; 93WO-JP01724.
 XX
 PR 28-NOV-1992; 92JP-0341255.
 XX
 XX (KAGA) CHEMO SERO THERAPEUTIC RES INST.
 PA
 XX Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 PI WPI; 1994-200288/24.
 XX
 DR N-PSDB; Q64167.
 XX
 CC Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.
 XX
 PS Disclosure; Page 18-19; 53pp; Japanese.
 XX
 CC The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.
 XX
 SQ Sequence 127 AA;

Query Match 78.8%; Score 41; DB 15; Length 127;
 Best Local Similarity 77.8%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPQT 9
 ||| ||| |
 Db 109 qqsnswpht 117

RESULT 14
 R38601
 ID R38601 standard; peptide; 107 AA.
 XX
 AC R38601;
 XX
 DT 28-OCT-1993 (first entry)
 XX
 DE HVH light chain.
 XX
 KW Antibody; variable domain; light; L; heavy; H; consensus;
 KW affinity; antigen; immunogenicity; humanisation; framework.
 XX
 OS Homo sapiens.
 XX
 PN W09311794-A.
 XX
 PD 24-JUN-1993..
 XX
 PF 14-DEC-1992; 92WO-US10906.
 XX
 PR 13-DEC-1991; 91US-0808464.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 XX WPI; 1993-213827/26.
 DR

XX Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but
PT retain binding affinity, etc.
XX
XX
PS Disclosure; Page 84; 160pp; English.
XX
XX The amino acid sequences of the light and heavy chains of the
CC variable domains from antibodies HYH [HYHEL-10 Fab-lysozyme complex]
CC (R38601 and R38608, respectively), MCPC [IGA Fab MCP603-phosphocholine
CC complex] (R38602-03 and R38609-10, respectively), NEWM [Ig Fab' NEW]
CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
CC R38612, respectively) may be used to determine an alignment from which
CC appropriate changes may be made.
CC Unlike other methods of humanisation, which advocate the
CC replacement of entire antibody framework regions with those of human
CC antibodies, this method involves only the introduction of human
CC residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody
CC are not diminished.
XX
XX
SQ Sequence 107 AA;

Query Match 76.9%; Score 40; DB 14; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 89 qqsnswpqt 97
||| ||| |

RESULT 15

W58482
ID W58482 standard; protein; 107 AA.

XX
AC W58482;

XX
DT 18-AUG-1998 (first entry)

XX Murine HYH antibody light chain variable domain.

XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
XX depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
XX autoimmune disease; rheumatoid arthritis; type I diabetes.

XX Mus sp.

XX US5770196-A.

XX 23-JUN-1998.

XX PF 07-JUN-1995; 95US-0472788.

XX PR 23-JUN-1993; 93US-0082842.

XX PR 13-DEC-1991; 91US-0808464.

XX PR 14-DEC-1992; 92WO-US10906.

XX PR 07-JUN-1995; 95US-0472788.

XX (XOMA) XOMA CORP.

XX Studnicka GM;

XX WPI; 1998-376744/32.

XX Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
XX with humanised variable regions

XX Disclosure; Column 43-44; 77pp; English.

XX A method has been developed of depleting CD5+ cells in an animal. The
XX method comprises administering a cytotoxic protein containing a modified

CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at
CC least one of (a) a modified light chain variable region (see W58478 or
CC W58480), and (b) a modified heavy chain variable region (see W58479 or
CC W58481), where W58478 and W58479 are humanised forms of the H65 light
CC and heavy chain variable domains with low risk amino acid substitutions
CC [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC W58481 are humanised forms of the H65 light and heavy chain variable
CC domains with moderate risk amino acid substitutions and are present in
CC humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
CC treating autoimmune diseases, especially systemic lupus erythematosus,
CC rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC represents the murine HYH antibody light chain variable domain.
XX

SQ Sequence 107 AA;

Query Match 76.9%; Score 40; DB 19; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 89 qqsnswpqt 97
||| ||| |

Search completed: March 28, 2001, 06:59:53
Job time: 1389 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:58 ; Search time 113.49 Seconds
(without alignments)
1.424 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*

2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*

3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*

4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	78.8	100	1	US-08-436-463-19
2	41	78.8	107	1	US-07-634-278-62
3	41	78.8	107	1	US-07-634-278-63
4	41	78.8	107	1	US-07-634-278-87
5	41	78.8	107	1	US-08-477-728-62
6	41	78.8	107	1	US-08-477-728-63
7	41	78.8	107	1	US-08-477-728-87
8	41	78.8	107	1	US-08-474-040-62
9	41	78.8	107	1	US-08-474-040-63
10	41	78.8	107	1	US-08-474-040-87
11	41	78.8	107	1	US-08-487-200-62
12	41	78.8	107	1	US-08-487-200-63
13	41	78.8	107	1	US-08-487-200-87
14	41	78.8	127	1	US-07-634-278-83
15	41	78.8	127	1	US-08-474-040-83
16	41	78.8	127	1	US-08-474-040-83
17	41	78.8	127	1	US-08-487-200-83
18	41	78.8	127	1	US-08-436-463-4
19	40	76.9	107	1	US-08-436-463-20
20	40	76.9	107	1	US-08-107-669D-1
21	40	76.9	107	1	US-08-472-788A-1
22	40	76.9	107	2	US-08-477-531B-1
23	40	76.9	107	2	US-08-082-842A-1
24	40	76.9	109	1	US-07-942-245-4
25	40	76.9	143	2	US-08-653-402B-8
26	39	75.0	9	2	US-08-232-081B-6
27	39	75.0	9	2	US-08-476-176B-55
28	39	75.0	9	3	US-08-127-721A-55

29 39 75.0 9 3 US-08-485-246A-55 Sequence 55, Appl
30 39 75.0 103 1 US-08-436-463-21 Sequence 21, Appl
31 39 75.0 106 2 US-08-800-198-4 Sequence 4, Appl
32 39 75.0 106 3 US-09-296-595-4 Sequence 4, Appl
33 39 75.0 107 2 US-08-232-081B-9 Sequence 9, Appl
34 39 75.0 107 2 US-08-232-081B-40 Sequence 40, Appl
35 39 75.0 107 2 US-08-476-176B-4 Sequence 4, Appl
36 39 75.0 107 3 US-08-127-721A-4 Sequence 4, Appl
37 39 75.0 107 3 US-08-485-246A-4 Sequence 4, Appl
38 39 75.0 127 1 US-08-436-463-18 Sequence 18, Appl
39 39 75.0 127 2 US-08-476-176B-6 Sequence 6, Appl
40 39 75.0 127 2 US-08-476-176B-8 Sequence 8, Appl
41 39 75.0 127 2 US-08-476-176B-10 Sequence 10, Appl
42 39 75.0 127 3 US-08-127-721A-6 Sequence 6, Appl
43 39 75.0 127 3 US-08-127-721A-8 Sequence 8, Appl
44 39 75.0 127 3 US-08-127-721A-10 Sequence 10, Appl
45 39 75.0 127 3 US-08-485-246A-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROUDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-19

Query Match 78.8%; Score 41; DB 1; Length 100;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 89 QOQNSWPHT 97

RESULT 2

US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 89 QOQNSWPHT 97

RESULT 3

US-07-634-278-63
; Sequence 63, Application US/07634278

; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 89 QOQNSWPHT 97

RESULT 4

US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPOT 9
Db 89 QQSNWPHT 97

RESULT 5
US-08-477-728-62
Sequence 62, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-62

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPOT 9
Db 89 QQSNWPHT 97

RESULT 6
US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
-LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGWPQT 9
Db 89 QOQSNWPHT 97

RESULT 7
US-08-477-728-87
Sequence 87, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
-LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGWPQT 9
Db 89 QOQSNWPHT 97

RESULT 8
US-08-474-040-62
Sequence 62, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-62

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPQT 9
DB 89 QOSNSWPHT 97

RESULT 9
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version: #1.25
; CURRENT APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPQT 9
DB 89 QOSNSWPHT 97

RESULT 10
US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPQT 9

```

Db      89  QQSNSWPHT 97

RESULT 11
US-08-487-200-62
; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-62

Query Match      78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  QQSGSWPQT 9
Db      89  QQSNSWPHT 97

RESULT 12
US-08-487-200-63
; Sequence 63, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-63

Query Match      78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  QQSGSWPQT 9
Db      89  QQSNSWPHT 97

RESULT 13
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.

```

APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-87

Query Match 78.8%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPQT 9
11111111
Db 89 QOQNSWPHT 97

RESULT 14
US-07-634-278-83
Sequence 83, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas L.
APPLICANT: COELING, Kathleen E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-83

Query Match 78.8%; Score 41; DB 1; Length 127;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPQT 9
11111111
Db 109 QOQNSWPHT 117

RESULT 15
US-08-477-728-83
Sequence 83, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728

; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-728-83

Query Match 78.8%; Score 41; DB 1; Length 127;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPQT 9
Db 109 QQNSWPHT 117

Search completed: March 28, 2001, 07:01:59
Job time: 1338 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:33 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSPAS 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	69.1	196	2 H64968	acetyl CoA acetyl
2	38	69.1	219	1 QCEC35	hypothetical 23.4K
3	37	67.3	731	1 JC2464	probable copper-tr
4	36	65.5	322	1 A29928	membrane-associate
5	36	65.5	360	2 S48566	hypothetical prote
6	36	65.5	470	2 H71667	glutamate--tRNA li
7	36	65.5	473	2 D70405	glutamate--tRNA li
8	35	63.6	233	2 H82163	arginyl-tRNA-prote
9	35	63.6	272	2 S27819	vitelline B1 precu
10	35	63.6	272	2 S27820	vitelline B2 precu
11	35	63.6	446	2 T19625	hypothetical prote
12	35	63.6	448	1 A60003	nucleocapsid prote
13	35	63.6	538	2 T28874	hypothetical prote
14	35	63.6	628	1 A56707	protein-tyrosine k
15	35	63.6	722	2 S64492	hypothetical prote
16	35	63.6	1291	2 T13389	MHC class II histo
17	34	61.8	89	2 S38688	MHC class II histo
18	34	61.8	89	2 S38683	MHC class II histo
19	34	61.8	89	2 S38684	MHC class II histo
20	34	61.8	127	2 D54759	terminal oxidase (
21	34	61.8	170	2 D75554	hypothetical prote
22	34	61.8	225	2 T47095	MHC class II OVAR-
23	34	61.8	236	2 S16389	sporamin - sweet p
24	34	61.8	284	2 S62931	probable membrane
25	34	61.8	284	2 S62955	probable membrane
26	34	61.8	379	1 F64633	site-specific DNA-
27	34	61.8	381	2 A71882	type II DNA modifi
28	34	61.8	1446	1 A45344	immediate-early pr
29	34	61.8	1460	1 EDBE1F	immediate-early pr

RESULT 1
H64968
acetyl CoA acetyltransferase - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Jun-1999
C:Accession: H64968; I69646; I69656
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64968
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <BLAT>
A:Cross-references: GB:AE000294; GB:U00096; NID:g1788338; PIDN:AAC75094.1; PID:g17883
A:Experimental source: strain K-12, substrain MGL1655
R:Yao, Z.; Valvano, M.A.
J. Bacteriol. 176, 4133-4143, 1994
A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r
erotypes Y and 4a.
A:Reference number: I55053; MUID:94292434
A:Accession: I69646
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>
A:Cross-references: EMBL:U03041; NID:g501028; PIDN:AAC31635.1; PID:g510256
R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W
J. Bacteriol. 176, 4144-4156, 1994
A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its
A:Reference number: I55054; MUID:94292435
A:Accession: I69656
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RE2>
A:Cross-references: EMBL:U09876; NID:g508236; PID:g508245
C:Genetics:
A:Gene: yefH
A:Map position: 45 min
C:Superfamily: galactoside acetyltransferase
Query Match 69.1%; Score 38; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8

Db 105 HNHGSF 110

RESULT 2

Q9BCA5

hypothetical 23.4K protein (ansa 3' region) - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 C:Accession: H64936; J00048
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: H64936
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-219 <BLAT>
 A:Cross-references: GB:AE000271; GB:U00096; NID:U00096; PIDN:AACT4838.1; PID:g1788066;
 A:Experimental source: strain K-12, substrain MG1655
 R:Jerlstrom, P.G.; Bezjak, D.A.; Jennings, M.P.; Beacham, I.R.
 Gene 78, 37-46, 1989
 A:Title: Structure and expression in Escherichia coli K-12 of the L-asparaginase I-encoding gene
 A:Reference number: JU0047; MUID:89357501
 A:Accession: JU0048
 A:Molecule type: DNA
 A:Residues: 7-219 <JER>
 A:Cross-references: GB:M26934; NID:g145278; PIDN:AAA23447.1; PID:g145280
 C:Genetics:
 A:Gene: ydJB
 A:Map position: 39 min
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)

Query Match 69.1%; Score 38; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY -4 NHGSEFAS 10

| | | | |

Db 63 NHGSEFAS 69

RESULT 3

JC2464
 probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.
 C>Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
 C:Accession: JC2464
 R:Trenor III, C.; Lin, W.; Andrews, N.C.
 Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
 A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
 A:Reference number: JC2464; MUID:95110304
 A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <TRE>
 A:Cross-references: GB:U16658; NID:g643612; PIDN:AAA62113.1; PID:g643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain
 C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembrane
 F;7-92/Region: His-rich
 F;135-477/Domain: ATPase transduction domain homology <ATT>
 F;544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
 F;287/Active site: Glu #status predicted
 F;431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 67.3%; Score 37; DB 1; Length 731;
 Best Local Similarity 75.0%; Pred. No. 36;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEF 8

| | | | |

Db 88 ARNHGSEF 95

RESULT 4

A29928
 membrane-associated 40K protein precursor - Vibrio anguillarum plasmid pJM1
 C:Species: Vibrio anguillarum
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
 C:Accession: A29928; C41671
 R:Actis, L.A.; Tolmasky, M.E.; Farrell, D.H.; Crosa, J.H.
 J. Biol. Chem. 263, 2853-2860, 1988
 A:Title: Genetic and molecular characterization of essential components of the Vibrio
 A:Reference number: A92707; MUID:88139336
 A:Accession: A29928
 A:Molecule type: DNA
 A:Residues: 1-322 <ACT>
 A:Cross-references: GB:J03529; NID:g150755; PIDN:AAA91580.1; PID:g150756
 R:Koester, W.L.; Actis, L.A.; Waldbeser, L.S.; Tolmasky, M.E.; Crosa, J.H.
 J. Biol. Chem. 266, 23829-23833, 1991
 A:Title: Molecular characterization of the iron transport system mediated by the pJM1
 A:Reference number: A41671; MUID:92084677
 A:Accession: C41671
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <KOE>
 A:Cross-references: GB:M74068
 C:Superfamily: iron(III) diclitate transport protein
 C:Keywords: membrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-322/Product: membrane-associated 40K protein #status predicted <MAT>

Query Match 65.5%; Score 36; DB 1; Length 322;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSEFAS 10

| | | | |

Db 203 HNHGSEFAS 210

RESULT 5

S48566
 hypothetical protein YLR215c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein L8167.23
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Nov-1999
 C:Accession: S48566
 R:Pauley, A.
 submitted to the EMBL Data Library, September 1994
 A:Description: The sequence of S. cerevisiae cosmid 8167.
 A:Reference number: S48545
 A:Accession: S48566
 A:Molecule type: DNA
 A:Residues: 1-360 <PAU>
 A:Cross-references: EMBL:U14913; NID:g544497; PIDN:AAB67444.1; PID:g544519; GSPDB:GNO
 C:Genetics:
 A:Gene: MIPS:YLR215c
 A:Map position: 12R
 C:Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215c

Query Match 65.5%; Score 36; DB 2; Length 360;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHHGSEFAS 10

| | | | |

Db 304 RHHGSEFAS 312

RESULT 6

H71667
 glutamate--tRNA ligase (EC 6.1.1.17) (gltX2) RP623 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 20-Jun-2000

C:Accession: H71667
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U. Nature 396, 133-140, 1998
A:Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: H71667
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-470 <AND>
A:Cross-references: GB:AJ235272; GB:AJ235269; NID:G3861033; PIDN:CAAL5066.1; PID:G386116
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: gltX2; RP623
C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F:4-281/Domain: glutamine--tRNA ligase homology <EGL>

Query Match 65.58; Score 36; DB 2; Length 470;
Best Local Similarity 75.08; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
|||||
DB 31 ARHNGKF 38

RESULT 7
D70405
glutamate--tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C:Accession: D70405
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A:Reference number: A70300; MUID:9819666
A:Accession: D70405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-473 <AOQ>
A:Cross-references: GB:AE000729; NID:G2983659; PIDN:AAC07230.1; PID:G2983664; GB:AE00069
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gltX
C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F:4-276/Domain: glutamine--tRNA ligase homology <EGL>

Query Match 65.58; Score 36; DB 2; Length 473;
Best Local Similarity 75.08; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
|||||
DB 31 ARHNGKF 38

RESULT 8
H82163
arginyl-tRNA-protein transferase-related protein Vcl1736 [imported] - *Vibrio cholerae* (92
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: H82163
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833
A:Accession: H82163

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <HEI>
A:Cross-references: GB:AE004251; GB:AE003852; NID:G9656248; PIDN:AAF94886.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: Vcl1736
A:Map position: 1

Query Match 63.6%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGS 7
|||||
DB 117 ARRHGGS 123

RESULT 9
S27819
vitelline B1 precursor - liver fluke
N:Alternate names: eggshell protein B1
C:Species: *Fasciola hepatica* (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: A48436; A48437; B48437; A59161; S27819
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
Mol. Biochem. Parasitol. 54, 129-141, 1992
A:Title: Eggshell precursor proteins of *Fasciola hepatica*, I. Structure and expressio
A:Reference number: A48436; MUID:93063029
A:Accession: A48436
A:Molecule type: mRNA; protein
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M93024; NID:G159065; PIDN:AAA29143.1; PID:G159066
A:Note: sequence extracted from NCBI backbone (NCBIN:117208, NCBIPI:117210)
R:Waite, J.H.; Rice-Ficht, A.C.
Mol. Biochem. Parasitol. 54, 143-151, 1992
A:Title: Eggshell precursor proteins of *Fasciola hepatica*, II. Microheterogeneity in
A:Reference number: A48437; MUID:93063030
A:Accession: A48437
A:Status: preliminary
A:Molecule type: protein
A:Residues: 20-47 <WAI1>
A:Cross-references: PID:G259030; PIDN:AAB23982.1
A:Note: sequence extracted from NCBI backbone (NCBIPI:117211)
A:Accession: B48437
A:Status: preliminary
A:Molecule type: protein
A:Residues: 172-193 <WA2>
A:Cross-references: PID:G259031; PIDN:AAB23983.1
A:Note: sequence extracted from NCBI backbone (NCBIPI:117213)
R:Waite, J.H.
Anal. Biochem. 192, 429-433, 1991
A:Title: Detection of peptidyl-3,4-dihydroxyphenylalanine by amino acid analysis and
A:Reference number: A59161; MUID:91241559
A:Accession: A59161
A:Molecule type: protein
A:Residues: 62-70 <WA3>
A:Experimental source: egg shell
C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B1 #status predicted <WAT>
F:63/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 63.6%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
|||||
DB 19 ARRHGKF 26

```
RESULT 10
S27820
vitelline B2 precursor - liver fluke
N:Alternate names: eggshell protein B2
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Feb-2000
C:Accession: S27820
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
submitted to the EMBL Data Library, May 1992
A:Description: Eggshell precursor proteins of Fasciola hepatica: I. structure and expres
A:Reference number: S27819
A:Accession: S27820
A:Molecule type: mRNA
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M93025; NID:g159067; PIDN:AAA29144.1; PID:g159068
C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B2 #status predicted <MAT>

Query Match          63.6%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
   ||| || |
Db 19 ARHPHGKF 26

RESULT 11
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-446 <MIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match          63.6%; Score 35; DB 2; Length 446;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSFAS 10
   ||| || |
Db 51 RHNYGSHAA 59

RESULT 12
A60003
nucleocapsid protein - human coronavirus (strain OC43)
C:Species: human coronavirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999
C:Accession: A60003
R:Kamahora, T.; Soe, L.H.; Lai, M.M.C.
Virus Res. 12, 1-9, 1989
A:Title: Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus OC43
A:Reference number: A60003; MUID:89243809
A:Accession: A60003
A:Molecule type: genomic RNA
```

```
A:Residues: 1-448 <KAM>
C:Genetics:
A:Gene: N
C:Superfamily: coronavirus nucleocapsid protein
C:Keywords: glycoprotein; nucleocapsid
F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          63.6%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
   ||| || |
Db 103 RHNRGSF 109

RESULT 13
T28874
hypothetical protein R04E5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28874
R:Miller, N.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z20535
A:Accession: T28874
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-538 <MIL>
A:Cross-references: EMBL:U41538; PIDN:AAC48179.1; GSPDB:GN00028; CESP:R04E5.2
A:Experimental source: strain Bristol N2; clone R04E5
C:Genetics:
A:Gene: CESP:R04E5.2
A:Map position: X
A:Introns: 28/2; 52/3; 91/2; 133/3; 169/1; 199/3; 240/2; 269/3; 302/3; 329/3; 368/3;

Query Match          63.6%; Score 35; DB 2; Length 538;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSFA 9
   ||| || |
Db 434 KHHGKFA 441

RESULT 14
A56707
protein-tyrosine kinase (EC 2.7.1.112) syk, splice form B - rat
N:contains: protein-tyrosine kinase syk, splice form A
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Oct-1995 #sequence_revision 23-May-1997 #text_change 10-Sep-1999
C:Accession: A56707; B56707; A48875
R:Rowley, R.B.; Bolen, J.B.; Fargnoli, J.
J. Biol. Chem. 270, 12659-12664, 1995
A:Title: Molecular cloning of rodent p72(Syk). Evidence of alternative mRNA splicing.
A:Reference number: A56707; MUID:95279402
A:Accession: A56707
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-628 <ROW>
A:Cross-references: GB:U21684
A:Accession: B56707
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-275,299-628 <RO2>
A:Cross-references: GB:U21683
R:Benhamou, M.; Ryba, N.J.P.; Nishikata, H.; Kihara, H.; Siraganian, R.P.
J. Biol. Chem. 268, 23318-23324, 1993
A:Title: Protein tyrosine kinase p72syk in high affinity IgE receptor signaling: iden
```

A:Reference number: A48875; MUID:94043123
 A:Accession: A48875
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 15-22,'E','23-263,'M',265-269,'S',271-444,'EL',447-628 <RES>
 A:Cross-references: GB:L20838; NID:g416152; PIDN:AAA42308.1; PID:g416153
 C:Superfamily: protein-tyrosine kinase ZAP-70; protein kinase homology; SH2 homology
 C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
 F:1-628/Product: protein-tyrosine kinase syk, splice form B #status predicted <PRB>
 F:1-275,299-628/Product: protein-tyrosine kinase syk, splice form A #status predicted <R
 F:14-105/Domain: SH2 homology <SH2A>
 F:166-257/Domain: SH2 homology <SH2B>
 F:362-626/Domain: protein kinase homology <KIN>
 F:370-378/Region: protein kinase ATP-binding motif

Query Match 63.6%; Score 35; DB 1; Length 628;
 Best Local Similarity 77.8%; Pred. No. 72;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 ||| |
 Db 194 ARDNGSFA 202

RESULT 15
 S64492
 hypothetical protein YGR178c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein G7139
 C:Species: Saccharomyces cerevisiae
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
 C:Accession: S64492
 R:Hebling, U.; Hofmann, B.; Delli, H.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64003
 A:Accession: S64492
 A:Molecule type: DNA
 A:Residues: 1-722 <HEB>
 A:Cross-references: EMBL:Z72963; NID:g1323314; PIDN:CAA97204.1; PID:e243559; PID:g132331
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:PPB1
 A:Cross-references: SGD:S0003410; MIPS:YGR178c
 A:Map position: 7R

Query Match 63.6%; Score 35; DB 2; Length 722;
 Best Local Similarity 85.7%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHHGGSF 8
 | | | | |
 Db 474 RHHGGSF 480

Search completed: March 28, 2001, 07:04:35
 Job time: 1073 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:15 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSFAS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	69.1	196	1 WBBJ_ECOLI	P37750 escherichia
2	38	69.1	213	1 PNCA_ECOLI	P21369 escherichia
3	36	65.5	218	1 YAVH_RHISN	Q53216 rhizobium s
4	36	65.5	322	1 FATB_VIBAN	P11460 vibrio angu
5	36	65.5	470	1 SYE2_RICPR	Q9zct8 rickettsia
6	36	65.5	473	1 SYE_AQUAE	P67271 aquifex aeo
7	35	63.6	197	1 EGS_FASHE	P07915 fasciola he
8	35	63.6	448	1 NCAP_CVHOC	P33469 human coron
9	35	63.6	567	1 CC45_XENLA	Q9yh26 xenopus lae
10	35	63.6	629	1 KSVK_RAT	Q64725 rattus norv
11	35	63.6	722	1 PBP1_YEAST	P53297 saccharomyc
12	34	61.8	284	1 YNB9_YEAST	P53975 saccharomyc
13	34	61.8	284	1 YND3_YEAST	P53964 saccharomyc
14	34	61.8	1446	1 IE18_PPRKA	P33479 pseudorabie
15	34	61.8	1461	1 IE18_PPRVF	P11675 pseudorabie
16	33	60.0	339	1 YD0N_BACSU	P96651 bacillus su
17	33	60.0	369	1 RF2_THEMA	Q9xlr5 thermotoga
18	33	60.0	480	1 SYE_HAEIN	P43818 haemophilus
19	33	60.0	927	1 CC15_SCHPO	Q09822 schizosacch
20	33	60.0	966	1 M172_HUMAN	Q14596 homo sapien
21	33	60.0	1403	1 YDF3_SCHPO	Q10475 schizosacch
22	33	60.0	2109	1 RPL_VSVSJ	P03523 vesicular s
23	32	58.2	129	1 YP56_MYCTU	Q50742 mycobacteri
24	32	58.2	190	1 SLVD_HAEIN	P48430 haemophilus
25	32	58.2	231	1 ARAD_ECOLI	P08203 escherichia
26	32	58.2	231	1 ARAD_SALTY	P06190 salmonella
27	32	58.2	231	1 SGBE_ECOLI	P37680 escherichia
28	32	58.2	231	1 SGBE_HAEIN	P44989 haemophilus
29	32	58.2	376	1 HPPD_RAT	P32755 rattus norv
30	32	58.2	392	1 HPPD_HUMAN	P32754 homo sapien
31	32	58.2	392	1 HPPD_MOUSE	P49429 mus musculu
32	32	58.2	434	1 TA47_TREPA	P29723 treponema p
33	32	58.2	473	1 SYTM_SCHPO	O13969 schizosacch

RESULT 1

ID	WBBJ_ECOLI	STANDARD;	PRT;	196 AA.
AC	P37750; P76375;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	POTATIVE LIPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ			
DE	(EC 2.3.1.-).			
GN	WBBJ.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
[1]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / W3110;			
RC	MEDLINE: 94292434.			
RX	Yao Z., Valvano M.A.;			
RA	"Genetic analysis of the O-specific lipopolysaccharide biosynthesis			
RT	region (rfb) of Escherichia coli K-12 W3110: identification of genes			
RT	that confer group 6 specificity to Shigella flexneri serotypes Y and			
RT	4a.";			
RL	J. Bacteriol. 176:4133-4143(1994).			
[2]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / WGI;			
RC	MEDLINE: 94292435.			
RX	Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,			
RA	Redmond J.W., Lindquist L., Reeves P.R.;			
RT	"Structure of the O antigen of Escherichia coli K-12 and the sequence			
RT	of its rfb gene cluster.";			
RL	J. Bacteriol. 176:4144-4156(1994).			
[3]				
RN	REVISIONS TO 168-176 AND 187-189.			
RP	STRAIN=K12 / WGI;			
RC	Stevenson G.;			
RA	Submitted (Dec-1997) to the EMBL/GenBank/DBJ databases.			
[4]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / MGI655;			
RC	MEDLINE: 97426617.			
RX	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RT	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RT	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474(1997).			
[5]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12;			
RC	MEDLINE: 97251358.			
RX	Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,			
RA	Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,			
RA	Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,			
RA	Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,			
RA	Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,			

34	32	58.2	593	1	ARSD_HUMAN	P51689 homo sapien
35	32	58.2	635	1	KSYK_HUMAN	P43405 homo sapien
36	32	58.2	676	1	HS7C_TRYBB	P20030 trypanosoma
37	32	58.2	1178	1	RPOB_MYCTU	P47766 mycobacteri
38	32	58.2	1179	1	RPOB_MYCLE	P30760 mycobacteri
39	31	56.4	65	1	CCSA_PEA	P31172 pisum sativ
40	31	56.4	69	1	GLUC_CANFA	P29794 canis famil
41	31	56.4	141	1	HBAI_IGUIG	P18974 iguana igua
42	31	56.4	151	1	GLUC_CHICK	P01277 gallus gall
43	31	56.4	158	1	GLUC_PIG	P01274 sus scrofa
44	31	56.4	161	1	PTB1_XENLA	P48532 xenopus lae
45	31	56.4	180	1	GLUC_BOVIN	P01272 bos taurus

ALIGNMENTS

RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 RL corresponding to the 40.1-50.0 min region on the linkage map.";
 CC DNA Res. 3:379-392(1996).
 CC -1- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
 CC ON THE O ANTIGEN.
 CC -1- PATHWAY: LIPOPOLYSACCHARIDE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LFXA/NOFL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC -----
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 CC -----
 DR EMBL; U03041; AAC31635.1; -;
 DR EMBL; U09876; AAB88406.1; -;
 DR EMBL; AE000294; AAC75094.1; -;
 DR EMBL; D90841; CAB21803.1; -;
 DR EMBL; D90842; CAB21811.1; -;
 DR EMBL; D90843; CAB21811.1; -;
 DR EMBL; EG11984; WBBJ.
 DR INTERPRO; IPR001451; -;
 DR PFAM; PF00132; hexapep; 1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
 KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
 FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
 FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
 SQ SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1B1 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGGSF 8
 |||||
 DB 105 HHGGSF 110

RESULT 2
 PNCA_ECOLI STANDARD; PRT; 213 AA.
 ID PNCA_ECOLI STANDARD; PRT; 213 AA.
 AC P21369; P76229; P76910;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRAZINAMIDASE/NICOTINAMIDASE [INCLUDES: PYRAZINAMIDASE (EC 3.5.1.-)
 DE (PZAS); NICOTINAMIDASE (EC 3.5.1.19) (NICOTINE DEAMIDASE)].
 GN PNCA OR NAM.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12;
 RX MEDLINE; 89357501.
 RA Jerlstroem P.G., Bezjak D.A., Jennings M.P., Beacham I.R.;
 RT "Structure and expression in *Escherichia coli* K-12 of the
 RT L-asparaginase I-encoding ansA gene and its flanking regions.";
 RL Gene 78:37-46(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96338362.
 RA Frothingham R., Meeker-O'Connell W.A., Talbot E.A., George J.W.,
 RA Kreuzer K.N.;
 RT "Identification, cloning, and expression of the *Escherichia coli*
 RT pyrazinamidase and nicotinamidase gene, *pncA*.";
 RL Antimicrob. Agents Chemother. 40:1426-1431(1996).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
 RA Ikenoto K., Inada T., Isono K., Itoh S., Itoh T., Kanai K.,
 RA Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,
 RA Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,
 RA Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Salto N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,
 RA Yamamoto Y., Yano M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NICOTINAMIDE + H(2)O = NICOTINATE + NH(3).
 CC -1- PATHWAY: PYRIDINE NUCLEOTIDE CYCLE.
 CC -1- SIMILARITY: TO YEAST YGL037C.
 CC -----
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 CC -----
 DR EMBL; M26934; AAA23447.1; -;
 DR EMBL; AE000271; AAC74838.1; ALT_INIT.
 DR EMBL; D90820; BAA15559.1; -;
 DR EMBL; D90821; BAA15566.1; -;
 DR PIR; JU0048; QOECAS.
 DR ECGENE; EG11135; PNCA.
 DR INTERPRO; IPR000868; -;
 DR PFAM; PF00857; Isochorismatase; 1.
 KW Hydrolase.
 SQ SEQUENCE 213 AA; 23362 MW; B9F8D946FA18433F CRC64;

Query Match 69.1%; Score 38; DB 1; Length 213;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGGSFAS 10
 |||||
 DB 57 NHGGSFAS 63

RESULT 3
 Y4VH_RHISN STANDARD; PRT; 218 AA.
 ID Y4VH_RHISN STANDARD; PRT; 218 AA.
 AC Q53216;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 24.6 KDA PROTEIN Y4VH.
 GN Y4VH.
 OS *Rhizobium* sp. (strain NGR234).
 OC Plasmid sym pNGR234a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97305956.
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between *Rhizobium* and legumes.";
 RL Nature 387:394-401(1997).
 RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE; 96389014.
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of *Rhizobium* sp.
NR234 using dye terminators and a thermostable 'sequenase': a
beginning.";
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
DR EMBL; Z68203; CAA92423.1; -;
DR EMBL; AE000101; AAB91896.1; -;
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSPA 9
IIIIII:
Db 68 ARDNHGSYS 76

RESULT 4
FATB_VIBAN
ID FATB_VIBAN STANDARD; PRT; 322 AA.
AC P11460;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE FERRIC ANGUIBACTIN-BINDING PROTEIN PRECURSOR.
GN FATB.
OS Vibrio anguillarum.
OG Plasmid pJMI.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-775;
RX MEDLINE; 88139336.
RA Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
RT "Genetic and molecular characterization of essential components of
the Vibrio anguillarum plasmid-mediated iron-transport system.";
RL J. Biol. Chem. 263:2853-2860(1988).
RN [2]
RP SEQUENCE OF 1-154 FROM N.A.
RC STRAIN-775;
RX MEDLINE; 92084677.
RA Koester W.L., Actis L.A., Waldbeser L.S., Tolmasky M.E., Crosa J.H.;
RT "Molecular characterization of the iron transport system mediated by
the pJMI plasmid in *Vibrio anguillarum* 775.";
RL J. Biol. Chem. 266:23829-23833(1991).
CC -1- FUNCTION: BINDS FERRIC ANGUIBACTIN; PART OF THE BINDING-PROTEIN-
DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIC ANGUIBACTIN.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE INNER MEMBRANE BY A LIPID
CC ANCHOR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 8.
CC -----
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DR EMBL; J03529; AAA91580.1; -;
DR EMBL; M74068; AAA25643.1; ALT_INIT.
DR PIR; A29928; A29928.
DR INTERPRO; IPR002491; -;
DR PFAM; PF01497; Peripla_BP_2; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; Iron transport; Signal; Inner membrane; Lipoprotein;
KW Plasmid.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 322 FERRIC ANGUIBACTIN-BINDING PROTEIN.
FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 322 AA; 35635 MW; FB8674EED5CF73F7 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 322;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSPAS 10
IIIIII:
Db 203 HNHGSPSS 210

RESULT 5
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Scheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of *Rickettsia prowazekii* and the origin of
mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -;
DR HSP; P27000; IGLN.
DR INTERPRO; IPR000924; -;
DR INTERPRO; IPR001412; -;
DR PFAM; PF00749; trna-synt_lc; 1.
DR PRINTS; PS00967; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
CC -----

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SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 65.5%; Score 36; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
   |||||
DB 31 ARHNGGKF 38

RESULT 6
ID SVE-AQUAE STANDARD; PRT; 473 AA.
AC 06271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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-----
DR EMBL; M15871; AAA29138.1; -.
KW Eggshell; Signal.
FT SIGNAL 1 17
FT CHAIN 18 197 PUTATIVE EGGSHELL PROTEIN.
FT SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 63.6%; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
   |||||
DB 17 ARHNGGKF 24

RESULT 8
NCAP_CVHOC STANDARD; PRT; 448 AA.
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43."
RL Virus Res. 12:1-9(1989).
PIR: A60003; A60003.
DR INTERPRO: IPR001218; -.
DR PFAM: PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARNHGGSF 8
   |||||
DB 103 RHNGGSF 109

RESULT 7
EGGS_FASHE STANDARD; PRT; 197 AA.
ID EGGS_FASHE STANDARD; PRT; 197 AA.

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RESULT 9
CC45_XENLA STANDARD; PRT; 567 AA.
ID CC45_XENLA STANDARD; PRT; 567 AA.
AC Q9YH26;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CDC45-RELATED PROTEIN.
GN CDC45.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98429493.
RA Minura S., Takisawa H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
chromatin under the control of S-phase Cdk.";
RL EMBO J. 17:5699-5707(1998).
CC -!- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
CC -----
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CC -----
CC EMBL; AF062494; AAC67520.1; -
CC DNA replication; Cell cycle; Nuclear protein.
CC SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 567;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARNHNGS 7
Db 251 SRHNGN 257
:|||||:

RESULT 10
KSYK_RAT STANDARD; PRT; 629 AA.
ID KSYK_RAT STANDARD; PRT; 629 AA.
AC O64725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
GN SYK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95279402.
RA Rowley R.B., Bolen J.B., Fargnoli J.;
RT "Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
splicing.";
RL J. Biol. Chem. 270:12659-12664(1995).
CC -!- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
CC LYMPCYTOCYTE ACTIVATION.
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYKA AND SYKB (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE SYK/ZAP-70 SUBFAMILY.
CC -----
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CC -----
CC EMBL; U21684; AAA75167.1; -
CC EMBL; U21683; AAA75166.1; -
CC HSSP; P43405; ICSY.
CC INTERPRO; IPR000719; -
CC INTERPRO; IPR000980; -
CC INTERPRO; IPR001245; -
CC PFAM; PF00017; SH2; 2.
CC PFAM; PF00069; kinase; 1.
CC PRINTS; PR00401; SH2DOMAIN.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50001; SH2; 2.
CC Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC SH2 domain; Alternative splicing.
CC DOMAIN 14 106
CC DOMAIN 167 258
CC DOMAIN 365 625
CC NP_BIND 371 379
CC BINDING 396 396
CC ACT_SITE 488 488
CC MOD_RES 519 519
CC VARSPIC 277 299
CC SEQUENCE 629 AA; 71528 MW; 81169A643EC6A6FE CRC64;

Query Match 63.6%; Score 35; DB 1; Length 629;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

Oy 1 ARNHNGSFA 9
Db 195 ARDNNGSFA 203
|||:|||||

RESULT 11
PBPL_YEAST STANDARD; PRT; 722 AA.
ID PBPL_YEAST STANDARD; PRT; 722 AA.
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAB1-BINDING PROTEIN 1.
GN PBPL OR MRS16 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mecklenbrauer I.;
RT "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns.";
RL Thesis (1996), Vienna Biocentre, Austria.
RN [3]

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RP CHARACTERIZATION.
RX MEDLINE; 99038243.
RA Mangus D.A., Amrani N., Jacobson A.;
RT "Pb1p, a factor interacting with Saccharomyces cerevisiae poly(A)-
RL binding protein, regulates polyadenylation.";
RL Mol. Cell. Biol. 18:7383-7396(1998).
CC -!- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
CC ABSENCE OF PB1P, THE 3' TERMINI OF PRE-MRNAs ARE PROPERLY CLEAVED
CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
CC OF PB1 TO NEGATIVELY REGULATE POLYADENYLATION.
CC -!- SUBUNIT: INTERACTS WITH PB1.
CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -----
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CC -----
DR EMBL; Z72963; CAA97204.1; -;
DR EMBL; U46931; AAB94294.1; -;
DR SGD; S0003410; PB1.
KW Nuclear protein.
SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match 63.6%; Score 35; DB 1; Length 722;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 RHNHGSF 8
I I I I I I
Db 474 RHNHGSF 480

RESULT 12
YNB9_YEAST STANDARD; PRT; 284 AA.
AC P53975;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 31.3 KDA PROTEIN IN HDAL-PUB1 INTERGENIC REGION
DE PRECURSOR.
GN YNL019C OR N2827.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Andre B., Iraqi Housaini I., Urrestazu L.A., Vissers S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YNL033W.
CC -----
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CC -----
DR EMBL; Z71295; CAA95881.1; -;
DR SGD; S0004964; YNL019C.
KW Hypothetical protein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 284 HYPOTHETICAL PROTEIN YNL019C.
FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 284 AA; 31326 MW; 0AD55E3495B2B284 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ARNHGSFA 9
I I I I I I
Db 194 SHNHGSIS 202

RESULT 13
YND3_YEAST STANDARD; PRT; 284 AA.
AC P53964;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 31.4 KDA PROTEIN IN NCE3-HHT2 INTERGENIC REGION
DE PRECURSOR.
GN YNL033W OR N2743.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Dueterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YNL019C.
CC -----
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CC -----
DR EMBL; Z71309; CAA95896.1; -;
DR SGD; S0004978; YNL033W.
KW Hypothetical protein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 284 HYPOTHETICAL PROTEIN YNL033W.
FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 284 AA; 31386 MW; 1BC45E3495B2A395 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ARNHGSFA 9
I I I I I I
Db 194 SHNHGSIS 202

RESULT 14
IE18_PVKA STANDARD; PRT; 1446 AA.
AC P33479;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE IMMEDIATE-EARLY PROTEIN IE180.
GN IE.
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91021039.
RA Vleck C., Kozmik Z., Paces V., Schirm S., Schwyzler M.;
RT "Pseudorabies virus immediate-early gene overlaps with an oppositely
oriented open reading frame: characterization of their promoter and

```
RT enhancer regions."
RL Virology 179:365-377(1990).
CC -!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
CC -!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
CC -!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
CC PHOSPHORYLATION.
CC -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
CC
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CC
CC EMBL; M34651; AAA47470.1; -.
DR PIR; A45344; A45344.
DR
KW Early protein; Transcription regulation; Trans-acting factor;
KW DNA-binding; Phosphorylation; Nuclear protein.
FT DOMAIN 347 354 POLY-SER.
FT DOMAIN 379 397 POLY-SER.
SQ SEQUENCE 1446 AA; 148640 MW; 81F43A3DE3DDA068 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1446;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
| | | | |
Db 583 APHGGSF 590

RESULT 15
IE18_PRVIF IE18_PRVIF STANDARD; PRT; 1461 AA.
AC P11675;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE IMMEDIATE-EARLY PROTEIN IE180.
GN IE.
OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89315207.
RA Cheung A.K.;
RT "DNA nucleotide sequence analysis of the immediate-early gene of
RL pseudorabies virus."
RL Nucleic Acids Res. 17:4637-4646(1989).
RN [2]
RP REVISIONS.
RA Cheung A.K.;
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
CC -!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
CC -!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
CC PHOSPHORYLATION.
CC -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
CC
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CC
CC EMBL; X15120; CAA33214.1; -.
DR PIR; S04713; EDBE1F.
KW Early protein; Transcription regulation; Trans-acting factor;
KW DNA-binding; Phosphorylation; Nuclear protein.
FT DOMAIN 390 405 POLY-SER.
FT DOMAIN 958 966 POLY-SER.
SQ SEQUENCE 1461 AA; 149833 MW; 7F31E7ABE403B208 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1461;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
| | | | |
Db 594 APHGGSF 601

Search completed: March 28, 2001, 07:35:16
Job time: 153 sec
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:31 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	69.1	839	10 Q9LIE5	Q9LIE5 arabidopsis
2	37	67.3	227	5 Q9VNI9	Q9VNI9 drosophila
3	37	67.3	326	2 Q9RJG3	Q9RJG3 streptomyc
4	37	67.3	731	2 Q93359	Q93359 escherichia
5	36	65.5	89	7 Q19495	Q19495 gallus gall
6	36	65.5	360	3 Q05791	Q05791 saccharomyc
7	35	63.6	161	5 Q9VZ39	Q9VZ39 drosophila
8	35	63.6	233	2 Q9KRA6	Q9KRA6 vibrio chol
9	35	63.6	272	5 Q24950	Q24950 fasciola he
10	35	63.6	272	5 Q24951	Q24951 fasciola he
11	35	63.6	446	5 Q62086	Q62086 caenorhabdi
12	35	63.6	615	11 Q63614	Q63614 rattus norv
13	35	63.6	1291	5 Q77261	Q77261 drosophila
14	35	63.6	1300	5 Q9W5E0	Q9W5E0 drosophila
15	34	61.8	39	7 P79474	P79474 cervus elap
16	34	61.8	39	7 P79477	P79477 cervus elap
17	34	61.8	39	7 P79478	P79478 cervus elap
18	34	61.8	39	7 P79479	P79479 cervus elap
19	34	61.8	76	7 Q9TPC2	Q9TPC2 macaca mula

20	34	61.8	82	7	Q30606	Q30606 macaca mula
21	34	61.8	82	7	Q30608	Q30608 macaca mula
22	34	61.8	82	7	Q30637	Q30637 macaca mula
23	34	61.8	82	7	Q30638	Q30638 macaca mula
24	34	61.8	82	7	Q30658	Q30658 macaca mula
25	34	61.8	82	7	Q30659	Q30659 macaca mula
26	34	61.8	82	7	Q30666	Q30666 macaca mula
27	34	61.8	82	7	Q30667	Q30667 macaca mula
28	34	61.8	82	7	Q30668	Q30668 macaca mula
29	34	61.8	82	7	Q19287	Q19287 macaca mula
30	34	61.8	82	7	Q19288	Q19288 macaca mula
31	34	61.8	82	7	Q9TFC9	Q9TFC9 callicebus
32	34	61.8	82	7	Q9MXN1	Q9MXN1 macaca mula
33	34	61.8	83	6	Q9TSS5	Q9TSS5 bos indicus
34	34	61.8	83	7	Q98002	Q98002 ovis aries
35	34	61.8	85	7	Q30796	Q30796 ovis aries
36	34	61.8	85	7	Q30800	Q30800 ovis aries
37	34	61.8	85	7	Q30803	Q30803 ovis aries
38	34	61.8	85	7	Q30812	Q30812 ovis aries
39	34	61.8	85	7	P79966	P79966 capra aegag
40	34	61.8	85	7	P79967	P79967 capra aegag
41	34	61.8	85	7	P79968	P79968 capra aegag
42	34	61.8	86	7	Q30326	Q30326 bos taurus
43	34	61.8	89	7	Q19210	Q19210 capra hircu
44	34	61.8	89	7	Q19212	Q19212 capra hircu
45	34	61.8	89	7	Q30521	Q30521 galago sene

ALIGNMENTS

RESULT 1

Q9LIE5 PRELIMINARY; PRT; 839 AA.

AC Q9LIE5;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSDUCTION-LIKE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; OC Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;

RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones."

RL DNA Res. 7:217-221(2000).

DR EMBL; AP001306; BAB03065.1; .

SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 69.1%; Score 38; DB 10; Length 839;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPF 8

Db 274 SRHNGSPF 281

RESULT 2

Q9VNI9

ID Q9VNI9 PRELIMINARY; PRT; 227 AA.
 AC Q9VNI9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE CG2023 PROTEIN.
 GN CG2023.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey L.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottiler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003601; AAF51945.1; -
 DR FLYBASE; FBgn0037383; CG2023.
 SQ SEQUENCE 227 AA; 25695 MW; 768718C22AE7C60E CRC64;

Query Match 67.3%; Score 37; DB 5; Length 227;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFAS 10
 II II II I
 Db 126 ARHNGGSFAS 135

RESULT 3
 ID Q9RJG3 PRELIMINARY; PRT; 326 AA.
 AC Q9RJG3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE PUTATIVE ARAC FAMILY TRANSCRIPTIONAL REGULATOR.
 GN SCF76.11.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Murphy L., Harris D.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL121600; CAB56731.1; -
 DR INTERPRO; IPR000005; -
 DR PFAM; PF00165; HTH_Arac; 1.
 SQ SEQUENCE 326 AA; 34425 MW; 2FEF5346ACAC80D6 CRC64;

Query Match 67.3%; Score 37; DB 2; Length 326;

Best Local Similarity 85.7%; Pred. No. 23; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
 II II II II
 Db 85 RHGHSF 91

RESULT 4
 ID Q59369 PRELIMINARY; PRT; 731 AA.
 AC Q59369
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE HISTIDINE RICH P TYPE APPASE.
 GN HRA-1.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95110304; PubMed=7811248;
 RA Trenor C.C., Lin W., Andrews N.C.;
 RT "Novel bacterial P-type APPases with histidine-rich heavy-metal-
 RT associated sequences."
 RL Biochem. Biophys. Res. Commun. 205:1644-1650(1994).
 DR EMBL; U16658; AAA62113.1; -
 DR INTERPRO; IPR001757; -
 DR PFAM; PF00122; EI-E2_APPase; 1.
 DR PROSITE; PS00154; ATPASE_EI_E2; UNKNOWN1.
 KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 731 AA; 78453 MW; 06237F155E151F0D CRC64;

Query Match 67.3%; Score 37; DB 2; Length 731;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ARHHGSF 8
Db 88 AHHHGSF 95

RESULT 5
O19495 PRELIMINARY: PRT: 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -
DR INTERPRO; IPR000353; -
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 65.5%; Score 36; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. NO. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
Db 75 RHNYGDFES 83

RESULT 6
O05791 PRELIMINARY: PRT: 360 AA.
AC O05791;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CHROMOSOME XII COSMID 8167.
GN L8167.23.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoerge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kottler P.,
RA Louis E.J., Messinguy F., Mewes H.W., Miosga T., Mostl D.,
RA Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambui R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:0-0(0).
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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Pauley A.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Waterston R.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14913; AAB67444.1; -
SQ SEQUENCE 360 AA; 41852 MW; 61CCC9DCEAFA1197 CRC64;

Query Match 65.5%; Score 36; DB 3; Length 360;
Best Local Similarity 77.8%; Pred. NO. 38;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
Db 304 RHNTGFEAS 312

RESULT 7
Q9VZ39 PRELIMINARY: PRT: 161 AA.
AC Q9VZ39;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG1545 PROTEIN.
GN CG1545.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hanks N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kaul S., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003484; AAF47989.1; -.
DR FLYBASE; FBgn0030259; CG1545.
SQ SEQUENCE 161 AA; 18109 MW; 2B17085850A450E3 CRC64;

Query Match 63.6%; Score 35; DB 5; Length 161;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGSPFAS 10
Db 77 YNHGSWAS 84

RESULT 8
Q9KRA6 PRELIMINARY; PRT; 233 AA.
ID Q9KRA6
AC Q9KRA6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ARGINYL-TRNA-PROTEIN TRANSFERASE-RELATED PROTEIN.
GN VC1736.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Rhee T.D., Tettelin H., Richardson D.,
RA Emolaeova M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004251; AAF94886.1; -.
DR TIGR; VC1736; -.
KW Transferase.
SQ SEQUENCE 233 AA; 27350 MW; AEB6E95905EC2C3C CRC64;

Query Match 63.6%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGS 7
Db 117 ARHRGS 123

RESULT 9
Q24950 PRELIMINARY; PRT; 272 AA.
ID Q24950
AC Q24950
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003484; AAF47989.1; -.
DR FLYBASE; FBgn0030259; CG1545.
SQ SEQUENCE 161 AA; 18109 MW; 2B17085850A450E3 CRC64;

Query Match 63.6%; Score 35; DB 5; Length 161;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGSPFAS 10
Db 77 YNHGSWAS 84

RESULT 8
Q9KRA6 PRELIMINARY; PRT; 233 AA.
ID Q9KRA6
AC Q9KRA6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ARGINYL-TRNA-PROTEIN TRANSFERASE-RELATED PROTEIN.
GN VC1736.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Rhee T.D., Tettelin H., Richardson D.,
RA Emolaeova M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004251; AAF94886.1; -.
DR TIGR; VC1736; -.
KW Transferase.
SQ SEQUENCE 233 AA; 27350 MW; AEB6E95905EC2C3C CRC64;

Query Match 63.6%; Score 35; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGS 7
Db 117 ARHRGS 123

RESULT 9
Q24950 PRELIMINARY; PRT; 272 AA.
ID Q24950
AC Q24950
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

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DE VITELLINE PROTEIN B1 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93063029; PubMed=1435854;
RA Rice-Ficht A.C., Dusek K.A., Kochevar G.J., Waite J.H.;
RT "Eggshe'll precursor proteins of Fasciola hepatica, I. Structure and
RT expression of vitelline protein B.";
RL MOL. Biochem. Parasitol. 54:129-141(1992).
DR EMBL; M93024; AAA29143.1; -.
KW SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 272 VITELLINE PROTEIN B1.
SQ SEQUENCE 272 AA; 31211 MW; BFCFDBEF6736BDCA CRC64;

Query Match 63.6%; Score 35; DB 5; Length 272;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
Db 19 ARHPHGKF 26

RESULT 10
Q24951 PRELIMINARY; PRT; 272 AA.
ID Q24951
AC Q24951
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE VITELLINE PROTEIN B2 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93063029; PubMed=1435854;
RA Rice-Ficht A.C., Dusek K.A., Kochevar G.J., Waite J.H.;
RT "Eggshe'll precursor proteins of Fasciola hepatica, I. Structure and
RT expression of vitelline protein B.";
RL MOL. Biochem. Parasitol. 54:129-141(1992).
DR EMBL; M93025; AAA29144.1; -.
KW SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 272 VITELLINE PROTEIN B2.
SQ SEQUENCE 272 AA; 31418 MW; 27D51230F278F6CC CRC64;

Query Match 63.6%; Score 35; DB 5; Length 272;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
Db 19 ARHPHGKF 26

RESULT 11
Q62086 PRELIMINARY; PRT; 446 AA.
ID Q62086
AC Q62086
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.
OS Caenorhabditis elegans.

```


RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003418; AAF4537.1; -
 DR FLYBASE: FBgn0025639; EG:115C2.10.
 DR INTERPRO: IPR001214; -
 SQ SEQUENCE 1300 AA; 137524 MW; 7186D0198CC16926 CRC64;

Query Match 63.6%; Score 35; DB 5; Length 1300;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFAS 10
 DB 554 HNHGQHAS 561

RESULT 15
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 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoides;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.:
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U63077; AAB3777.1; -
 KW MHC.
 FT NON_TER 1 1
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 SQ SEQUENCE . 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 61.8%; Score 34; DB 7; Length 39;
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QY 2 RHNHGSFAS 10
 DB 25 RHNHGVFES 33

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 Job time: 526 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:53 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSEFAS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	19 W76037	LM609 grafted anti
2	51	92.7	10	19 W76020	LM609 grafted anti
3	49	89.1	10	19 W76038	LM609 grafted anti
4	49	89.1	10	19 W76024	LM609 grafted anti
5	46	83.6	10	19 W76025	LM609 grafted anti
6	46	83.6	10	19 W76030	LM609 grafted anti
7	45	81.8	10	19 W76026	LM609 grafted anti
8	45	81.8	10	19 W76027	LM609 grafted anti
9	45	81.8	10	19 W76028	LM609 grafted anti
10	45	81.8	10	19 W76029	LM609 grafted anti
11	45	81.8	10	19 W76010	LM609 grafted anti
12	45	81.8	117	19 W76001	Vitaxin antibody h

13	45	81.8	117	19 W76003	LM609 antibody hea
14	45	81.8	117	20 Y06381	Murine monoclonal
15	45	81.8	117	20 Y06387	Humanised LM609 an
16	45	81.8	118	20 Y06384	Humanised LM609 an
17	45	81.8	118	20 Y06385	Humanised LM609 an
18	45	81.8	118	20 Y06386	Humanised LM609 an
19	45	81.8	118	20 Y06383	Humanised LM609 an
20	45	81.8	130	20 Y06379	Murine monoclonal
21	43	78.2	10	19 W76040	LM609 grafted anti
22	42	76.4	10	19 W76021	LM609 grafted anti
23	41	74.5	10	19 W76039	LM609 grafted anti
24	41	74.5	10	19 W76022	LM609 grafted anti
25	41	74.5	10	19 W76023	LM609 grafted anti
26	37	67.3	110	20 W84099	Vitronectin alpha-
27	37	67.3	117	20 W84093	Murine vitronectin
28	37	67.3	117	20 W84097	Humanised anti-alp
29	36	65.5	8	20 Y06371	Murine monoclonal
30	35	63.6	286	20 Y43477	Amino acid sequenc
31	34	61.8	99	20 Y29137	DNA-binding/dimeri
32	34	61.8	204	19 W59609	H. pylori GPHO 403
33	34	61.8	358	19 W98649	Streptococcus pneu
34	34	61.8	827	21 Y81662	Vesiculovirus larg
35	33	60.0	2109	17 W04540	S. pneumoniae deri
36	32	58.2	119	19 Y86109	Sequence of the hu
37	32	58.2	120	15 R48621	Region for produci
38	32	58.2	121	16 R65173	Chlamydia pneumoni
39	32	58.2	165	20 Y34655	Human 35 kDa opson
40	32	58.2	218	17 R94178	Klebsiella oxytoca
41	32	58.2	238	21 Y70730	Human 35 kDa opson
42	32	58.2	288	17 R94179	Membrane-bound pro
43	32	58.2	299	21 Y66687	Human 35 kDa opson
44	32	58.2	313	17 R94183	Neisseria gonorrhoe
45	32	58.2	360	20 Y38857	

ALIGNMENTS

RESULT 1

W76037
ID W76037 standard; Protein; 10 AA.

XX W76037;

XX W76037;

DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #13.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

XX Mus sp.

XX W09833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49874.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 43; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC vitaxin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 55; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGGSFAS 10
 Db | | | | | | | | | |
 1 arnhggsfas 10
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 ID W76020 standard; Protein; 10 AA.
 XX
 AC W76020;
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB: V49857.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
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 SQ Sequence 10 AA;
 Query Match 92.7%; Score 51; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGGSFA 9
 Db | | | | | | | | | |
 1 arnhggsfa 9
 RESULT 3
 ID W76038 standard; Protein; 10 AA.
 XX
 AC W76038;
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN W09833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI: 1998-437472/37.
 DR N-PSDB: V49875.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 43; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 89.1%; Score 49; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0026;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNHGSFAS 10
 |||||I
 Db 1 arnhgsfys 10

RESULT 4

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 ID W76024 standard; Protein; 10 AA.

XX AC W76024;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49861.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 89.1%; Score 49; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0026;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNHGSFAS 10
 |||||I
 Db 1 arnhgsfys 10

RESULT 5

W76025
 ID W76025 standard; Protein; 10 AA.

XX AC W76025;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49862.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 19; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0094;
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OY 1 ARHNHGSFAS 10
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Db      1 arhnygsfat 10

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ID      W76030 standard; Protein; 10 AA.
AC      W76030;
XX
XX      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #12.
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
XX      Mus sp.
OS
XX
XX      WO9833919-A2.
PN
XX
XX      06-AUG-1998.
PD
XX
XX      30-JAN-1998; 98WO-US01826.
PF
XX
XX      30-JAN-1997; 97US-0791391.
PR
XX
XX      (IXSY-) IXSYS INC.
PA
XX
XX      Glaser SM, Huse WD;
PI
XX
XX      WPI; 1998-437472/37.
DR
XX
XX      N-PSDB; V49867.
DR
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
XX      Claim 62; Page 41; 129pp; English.
PS
XX
XX      W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC      LM609 heavy and light chain variable region. LM609 and the antibody
CC      vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC      inhibit binding of alphavbeta3 to a ligand and thus block
CC      integrin-mediated signal transduction. This is useful in the treatment,
CC      prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC      arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC      contain non-murine framework regions so are suitable for use in humans.
CC      Enhanced types of LM609 have affinity more than 90 times greater than
CC      that of parent the parent antibody.
XX
XX      Sequence 10 AA;
SQ

Query Match      83.6%; Score 46; DB 19; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.0094;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ARHNHGSFAS 10
      ||||:||||
Db      1 arhnygsfaa 10

RESULT  7
W76026
ID      W76026 standard; Protein; 10 AA.
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

```

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AC      W76026;
XX
XX      02-NOV-1998 (first entry)
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
XX
XX      Mus sp.
OS
XX
XX      WO9833919-A2.
PN
XX
XX      06-AUG-1998.
PD
XX
XX      30-JAN-1998; 98WO-US01826.
PF
XX
XX      30-JAN-1997; 97US-0791391.
PR
XX
XX      (IXSY-) IXSYS INC.
PA
XX
XX      Glaser SM, Huse WD;
PI
XX
XX      WPI; 1998-437472/37.
DR
XX
XX      N-PSDB; V49863.
DR
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
XX      Claim 62; Page 41; 129pp; English.
PS
XX
XX      W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC      LM609 heavy and light chain variable region. LM609 and the antibody
CC      vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC      inhibit binding of alphavbeta3 to a ligand and thus block
CC      integrin-mediated signal transduction. This is useful in the treatment,
CC      prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC      angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC      diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC      arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC      contain non-murine framework regions so are suitable for use in humans.
CC      Enhanced types of LM609 have affinity more than 90 times greater than
CC      that of parent the parent antibody.
XX
XX      Sequence 10 AA;
SQ

Query Match      81.8%; Score 45; DB 19; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.014;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ARHNHGSFA 9
      ||||:||||
Db      1 arhnygsfa 9

RESULT  8
W76027
ID      W76027 standard; Protein; 10 AA.
XX
XX      W76027;
AC
XX
XX      02-NOV-1998 (first entry)
DT
XX
XX      LM609 grafted antibody V-H region CDR3 protein fragment #9.
DE
XX
XX      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW

```

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 XX OS
 XX WO9833919-A2.
 PN 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 PR (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 DR N-PSDB; V49864.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ
 Query Match 81.8%; Score 45; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNHGSPA 9
 Db ||||:||||
 1 arhnygsfa 9
 RESULT 9
 W76028
 ID W76028 standard; Protein; 10 AA.
 AC W76028;
 XX 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #10.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 XX OS

XX WO9833919-A2.
 PN 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 PR (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 DR N-PSDB; V49865.
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ
 Query Match 81.8%; Score 45; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNHGSPA 9
 Db ||||:||||
 1 arhnygsfa 9
 RESULT 10
 W76029
 ID W76029 standard; Protein; 10 AA.
 XX W76029;
 AC 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #11.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 XX OS
 XX WO9833919-A2.
 PN 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX

PR 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 DR N-PSDB; V49866.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 62; Page 41; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 81.8%; Score 45; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.014; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSFA 9
 |||||
 Db 1 arhnygsfa 9

RESULT 11
 W76010
 ID W76010 standard; Protein; 10 AA.
 XX
 AC W76010;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 1; Fig 1a; 129pp; English.

DR N-PSDB; V49847.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Disclosure; Page 40; 129pp; English.
 XX
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 81.8%; Score 45; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.014; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSFA 9
 |||||
 Db 1 arhnygsfa 9

RESULT 12
 W76001
 ID W76001 standard; Protein; 117 AA.
 XX
 AC W76001;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE Vitaxin antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 XX WPI; 1998-437472/37.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 1; Fig 1a; 129pp; English.

XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 19; Length 117;
 Best Local Similarity 88.9%; Pred. No. 0.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
 ||||:||||
 Db 97 arhnygsfa 105

RESULT 13
 W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 XX
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX

OS Mus sp.

PN W09833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 1998-437472/37.

DR N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 19; Length 117;
 Best Local Similarity 88.9%; Pred. No. 0.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
 ||||:||||
 Db 97 arhnygsfa 105

RESULT 14
 Y06381
 ID Y06381 standard; Protein; 117 AA.

XX Y06381;

XX AC
 DT 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 VH region.

XX Humanised antibody; antibody humanisation; antibody engineering;
 KW LM609; monoclonal antibody; complementarity determining region;
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
 KW cancer; therapy; diagnosis.

XX OS Mus musculus.

XX PN W09929888-A1.

XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.

XX PR 05-DEC-1997; 97US-0986016.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI: 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 52-53; 55pp; English.

XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody LM609. LM609 is directed to integrin
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular
 CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 20; Length 117;
 Best Local Similarity 88.9%; Pred. No. 0.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9

Db 97 arhnygsfa 105

Db 97 arhnygsfa 105

Search completed: March 28, 2001, 06:59:55
Job time: 1391 sec

RESULT 15
Y06387
ID Y06387 standard; Protein; 117 AA.

XX AC Y06387;
XX DT 06-SEP-1999 (first entry)
XX DE Humanised LM609 antibody VH domain.

XX KW Humanised antibody; antibody humanisation; antibody engineering;
XX KW LM609; monoclonal antibody; complementarity determining region;
XX KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
XX KW cancer; therapy; diagnosis.

XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..2
FT Region 31..35 /note= "vector-encoded residues"
FT Region 50..66 /note= "CDR1"
FT Region 107..117 /note= "CDR2"
FT Region /note= "CDR3"

XX PN W09929888-A1.
XX PD 17-JUN-1999.

XX PF 04-DEC-1998; 98WO-US25828.
XX PR 05-DEC-1997; 97US-0986016.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 1999-394979/33.

XX PT Production of humanized mouse monoclonal antibodies

XX PS Disclosure; Page 52; 55pp; English.

XX CC This sequence represents the heavy chain variable region of a
XX CC humanised LM609 antibody. LM609 is directed to human integrin
XX CC alpha-v beta-3. It selectively promotes apoptosis of vascular
XX CC cells that have been stimulated to undergo angiogenesis, making it
XX CC a tool for cancer diagnosis and therapy. The invention provides
XX CC humanised antibodies, especially humanised LM609. In such humanized
XX CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
XX CC grafted onto a human light chain, and a heavy chain CDR from a mouse
XX CC antibody is grafted onto a human antibody heavy chain to produce
XX CC libraries from which a humanised murine antibody having the desired
XX CC specificity is selected. By preserving the original CDR sequences
XX CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
XX CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 20; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.2;
Matches: 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNGSFA 9
||||:||||

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:01:59 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSFAS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*

1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep:*

2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep:*

3: /cgnl_7/ptodata/1/iaa/6_COMB.pep:*

4: /cgnl_7/ptodata/1/iaa/PCPTUS_COMB.pep:*

5: /cgnl_7/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	69.1	213	2	US-08-655-821-16
2	34	61.8	94	3	US-09-147-550-14
3	34	61.8	94	3	US-09-147-550-45
4	34	61.8	94	3	US-09-147-550-48
5	34	61.8	94	3	US-09-147-550-77
6	34	61.8	94	3	US-09-147-550-84
7	34	61.8	94	3	US-09-147-550-90
8	34	61.8	94	3	US-09-147-550-101
9	34	61.8	204	1	US-08-591-989-4
10	33	60.0	907	3	US-08-938-830-26
11	33	60.0	907	3	US-09-020-222-26
12	33	60.0	2109	4	PCT-US96-06053-6
13	32	58.2	103	2	US-08-596-319-31
14	32	58.2	120	1	US-08-111-080-28
15	32	58.2	120	1	US-08-211-980-28
16	32	58.2	120	4	PCT-US93-07967-28
17	32	58.2	121	1	US-08-275-053-13
18	32	58.2	231	3	US-08-926-842B-20
19	32	58.2	240	3	US-08-926-842B-21
20	32	58.2	384	1	US-08-707-793A-5
21	32	58.2	384	1	US-08-707-792A-5
22	32	58.2	392	3	US-08-979-917A-2
23	32	58.2	393	3	US-08-979-917A-3
24	32	58.2	443	1	US-07-940-245-2
25	32	58.2	443	1	US-08-226-486-2
26	32	58.2	466	1	US-08-785-066-2
27	32	58.2	466	3	US-09-007-355-2
28	32	58.2	466	3	US-08-913-489-2

29 58.2 536 2 US-08-551-211-3 Sequence 3, Appli
30 58.2 630 2 US-08-394-177-5 Sequence 5, Appli
31 58.2 630 2 US-08-596-319-2 Sequence 2, Appli
32 58.2 630 3 US-08-394-912A-5 Sequence 5, Appli
33 58.2 1148 2 US-08-313-185-58 Sequence 58, Appli
34 58.2 1148 3 US-09-082-614A-58 Sequence 58, Appli
35 56.4 14 3 US-08-956-307B-3 Sequence 3, Appli
36 56.4 69 1 US-08-193-863-1 Sequence 1, Appli
37 56.4 69 1 US-08-377-833-1 Sequence 1, Appli
38 56.4 69 1 US-08-324-502-1 Sequence 1, Appli
39 56.4 69 1 US-08-083-501-1 Sequence 1, Appli
40 56.4 69 1 US-08-415-939-1 Sequence 1, Appli
41 56.4 69 1 US-08-548-152-1 Sequence 1, Appli
42 56.4 70 1 US-08-193-863-2 Sequence 2, Appli
43 56.4 70 1 US-08-377-833-2 Sequence 2, Appli
44 56.4 70 1 US-08-324-502-2 Sequence 2, Appli
45 56.4 70 1 US-08-083-501-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-655-821-16
; Sequence 16, Application US/08655821
; Patent No. 5846718
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ying
; APPLICANT: Scorio, Angelo
; TITLE OF INVENTION: IDENTIFICATION OF PYRAZINAMIDE-RESISTANT
; TITLE OF INVENTION: MYCOBACTERIA AND METHODS FOR TREATING
; TITLE OF INVENTION: MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,821
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07662/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-821-16

Query Match 69.1%; Score 38; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSFAS 10
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DB 57 NHGSFAS 63

RESULT 2
 US-09-147-550-14
 ; Sequence 14, Application US/09147550
 ; Patent No. 6090540
 ; GENERAL INFORMATION:
 ; APPLICANT: Alda, Yokoi
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 ; CURRENT APPLICATION NUMBER: US/09/147,550
 ; CURRENT FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: PCT/JP97/02485
 ; EARLIER FILING DATE: 1997-07-17
 ; EARLIER APPLICATION NUMBER: JP 8-190933
 ; EARLIER FILING DATE: 1996-07-19
 ; EARLIER APPLICATION NUMBER: JP 9-77979
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 ; US-09-147-550-14

Query Match 61.8%; Score 34; DB 3; Length 94;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNGSFAS 10
 DB 80 RHNGVFES 88

RESULT 3
 US-09-147-550-45
 ; Sequence 45, Application US/09147550
 ; Patent No. 6090540
 ; GENERAL INFORMATION:
 ; APPLICANT: Alda, Yokoi
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 ; CURRENT APPLICATION NUMBER: US/09/147,550
 ; CURRENT FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: PCT/JP97/02485
 ; EARLIER FILING DATE: 1997-07-17
 ; EARLIER APPLICATION NUMBER: JP 8-190933
 ; EARLIER FILING DATE: 1996-07-19
 ; EARLIER APPLICATION NUMBER: JP 9-77979
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 ; US-09-147-550-45

Query Match 61.8%; Score 34; DB 3; Length 94;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNGSFAS 10
 DB 80 RHNGVFES 88

RESULT 4

US-09-147-550-48
 ; Sequence 48, Application US/09147550
 ; Patent No. 6090540
 ; GENERAL INFORMATION:
 ; APPLICANT: Alda, Yokoi
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 ; CURRENT APPLICATION NUMBER: US/09/147,550
 ; CURRENT FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: PCT/JP97/02485
 ; EARLIER FILING DATE: 1997-07-17
 ; EARLIER APPLICATION NUMBER: JP 8-190933
 ; EARLIER FILING DATE: 1996-07-19
 ; EARLIER APPLICATION NUMBER: JP 9-77979
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 48
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 ; US-09-147-550-48

Query Match 61.8%; Score 34; DB 3; Length 94;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNGSFAS 10
 DB 80 RHNGVFES 88

RESULT 5
 US-09-147-550-77
 ; Sequence 77, Application US/09147550
 ; Patent No. 6090540
 ; GENERAL INFORMATION:
 ; APPLICANT: Alda, Yokoi
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
 ; CURRENT APPLICATION NUMBER: US/09/147,550
 ; CURRENT FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: PCT/JP97/02485
 ; EARLIER FILING DATE: 1997-07-17
 ; EARLIER APPLICATION NUMBER: JP 8-190933
 ; EARLIER FILING DATE: 1996-07-19
 ; EARLIER APPLICATION NUMBER: JP 9-77979
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 77
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 ; US-09-147-550-77

Query Match 61.8%; Score 34; DB 3; Length 94;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNGSFAS 10
 DB 80 RHNGVFES 88

RESULT 6
 US-09-147-550-84
 ; Sequence 84, Application US/09147550
 ; Patent No. 6090540

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; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 7
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 8
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

```

```

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 61.8%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 9
US-08-591-989-4
; Sequence 4, Application US/08591989
; Patent No. 5795721
; GENERAL INFORMATION:
; APPLICANT: Ross S. Rabin, Sumedha Jayasena
; APPLICANT: and Larry Gold
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS OF ICP4
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591.989
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX 49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-591-989-4

Query Match 61.8%; Score 34; DB 1; Length 204;
Best Local Similarity 75.0%; Pred. No. 36;

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Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8

Db 137 APHGHGSF 144

RESULT 10

US-08-938-830-26
; Sequence 26, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Doshenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
; LENGTH: 907 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-938-830-26

Query Match 60.0%; Score 33; DB 3; Length 907;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARNHGGSFAS 10

Db 464 SRHGHGSQTS 473

RESULT 11

US-09-020-222-26
; Sequence 26, Application US/09020222
; Patent No. 6111073
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 26:

STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,222
; FILING DATE: 06-Feb-1998
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 02/07/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
; LENGTH: 907 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-020-222-26

Query Match 60.0%; Score 33; DB 3; Length 907;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARNHGGSFAS 10

Db 464 SRHGHGSQTS 473

RESULT 12

PCT-US96-06053-6
; Sequence 6, Application PC/TUS9606053
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06053
; FILING DATE: 01-MAY-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-009-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 2109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-06053-6

Query Match 60.0%; Score 33; DB 4; Length 2109;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSEFAS 10
Db 1232 SRMSGGFAS 1241

RESULT 13

US-08-596-319-31
; Sequence 31, Application US/08596319
; Patent No. 5981262
; GENERAL INFORMATION:
; APPLICANT: Brugg, Joan
; APPLICANT: Morgenstern, Jay
; APPLICANT: Shue, Lily
; APPLICANT: Zydowsky, Lynne
; APPLICANT: Zoller, Mark
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: HUMAN syk
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,319
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/04540
; FILING DATE: 25-APR-1994
; CLASSIFICATION: 435
; APPLICATION DATA:
; FILING DATE: 23-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERSTEIN, David L.
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCKET NUMBER: ARIAD305A-PCT/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0400
; TELEFAX: (617) 494-0208
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-596-319-31

Query Match 58.2%; Score 32; DB 2; Length 103;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEFA 9
Db 29 ARDNGSYA 37

RESULT 14

US-08-111-080-28
; Sequence 28, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-111-080-28

Query Match 58.2%; Score 32; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSEFAS 10
Db 98 ARENHGTTS 107

RESULT 15

US-08-211-980-28
; Sequence 28, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-980-28

Query Match 58.2%; Score 32; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSFAS 10
|||
Db 98 ARENHGTTTS 107

Search completed: March 28, 2001, 07:02:00
Job time: 1339 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:35 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-96

Perfect score: 58

Sequence: 1 ARNHGFSY 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	233	2 H82163	arginyl-trna-protein
2	40	69.0	555	2 T21028	hypothetical prote
3	39	67.2	350	2 S76212	hypothetical prote
4	39	67.2	470	2 H71667	glutamate--trna li
5	38	65.5	196	2 H64968	acetyl CoA acetyl
6	38	65.5	722	2 S64492	hypothetical prote
7	37	63.8	530	2 T01030	hypothetical prote
8	37	63.8	547	2 T48551	fructosidase-like
9	37	63.8	731	1 JC2464	probable copper-tr
10	37	63.8	849	2 E82038	GGDEF family prote
11	36	62.1	275	2 S75190	hypothetical prote
12	36	62.1	473	2 D70405	glutamate--trna li
13	36	62.1	548	1 B44511	fumarate hydratase
14	35	60.3	86	2 A81873	hypothetical prote
15	35	60.3	108	2 C72852	AcOrf-19 protein -
16	35	60.3	108	2 D44221	AcOrf-19 protein -
17	35	60.3	110	2 T41765	ACMNPV orf19 - Bom
18	35	60.3	113	2 S26468	Ig heavy chain V r
19	35	60.3	272	2 S27819	vitelline B1 precu
20	35	60.3	272	2 S27820	vitelline B2 precu
21	35	60.3	349	2 S15011	mbhl protein - mou
22	35	60.3	352	1 A39834	actin-capping prot
23	35	60.3	448	1 A60003	nucleocapsid prote
24	35	60.3	543	2 T27190	hypothetical prote
25	35	60.3	552	2 T27191	hypothetical prote
26	35	60.3	659	2 S30859	hypothetical prote
27	35	60.3	696	2 T48432	maturase-like prot
28	35	60.3	1466	2 T17138	Clf1AA protein - ra
29	35	60.3	1467	2 T18411	latrophilin-1, bra

30 35 60.3 1471 2 T17149
31 35 60.3 1472 2 T18413
32 35 60.3 1510 2 T17145
33 35 60.3 1515 2 T17156
34 35 60.3 2470 2 I50726
35 34.5 59.5 308 2 E81288
36 34 58.6 139 2 G29380
37 34 58.6 140 2 I37782
38 34 58.6 236 2 S16389
39 34 58.6 379 1 F64633
40 34 58.6 381 2 A71882
41 34 58.6 466 2 JC5897
42 34 58.6 467 2 T40348
43 34 58.6 604 2 S05447
44 34 58.6 813 2 A72203
45 34 58.6 1012 2 T23160

CLf1BA protein - ra
latrophilin-1, bra
Clf1AB protein - ra
Clf1BB protein - ra
cation-independent
hypothetical prote
Ig heavy chain pre
Ig variable region
sporamin - sweet p
site-specific DNA-
type II DNA modifi
killer cell inhibi
hypothetical prote
finger protein gla
cellobiose-phospho
hypothetical prote

arginyl-trna-protein transferase-related protein VC1736 [imported] - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: H82163
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequences of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833
A:Accession: H82163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <HEI>
A:Cross-references: GB:AE004251; GB:AE003852; MID:99656248; PIDN:AAF94886.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1736
A:Map position: 1

Query Match 72.4%; Score 42; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGFSY 9
||| ||| |
DB 117 ARRHGSMY 125

RESULT 2
T21028
hypothetical protein F16H6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21028
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19362
A:Accession: T21028
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <WIL>
A:Cross-references: EMBL:Z81506; PIDN:CAB04128.1; GSPDB:GN00023; CESP:F16H6.1
A:Experimental source: clone F16H6
C:Genetics:
A:Gene: CESP:F16H6.1
A:Map position: 5
A:Introns: 123/1; 318/3

ALIGNMENTS

Query Match 69.0%; Score 40; DB 2; Length 555;
 Best Local Similarity 87.5%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
 || |||||
 Db 314 HNHGSFYS 321

RESULT 3
 S76212
 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
 C:Species: *Synechocystis* sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S76212
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 S.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S76212
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <RAN>
 A:Cross-references: EMBL:D90914; GB:AB001339; NID:q1653477; PIDN:BAAL8471.1; PID:d101920
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 67.2%; Score 39; DB 2; Length 350;
 Best Local Similarity 71.4%; Pred. No. 13;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
 |||||:
 Db 247 HNHGNY 253

RESULT 4
 H71667
 glutamate--tRNA ligase (EC 6.1.1.17) (gltx2) RP623 - *Rickettsia prowazekii*
 C:Species: *Rickettsia prowazekii*
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 20-Jun-2000
 C:Accession: H71667
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499
 A:Accession: H71667
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-470 <RAN>
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:g386116
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: gltx2; RP623
 C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
 C:Keywords: aminocacyl-tRNA synthetase; ligase; protein biosynthesis
 F:4-281/Domain: glutamine--tRNA ligase homology <EGL>

Query Match 67.2%; Score 39; DB 2; Length 470;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNGSFY 9
 |||||:
 Db 31 ARHNGKFF 39

RESULT 5

H64968
 acetyl CoA acetyltransferase - *Escherichia coli*
 C:Species: *Escherichia coli*
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Jun-1999
 C:Accession: H64968; I69646; I69656
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: H64968
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-196 <BLAT>
 A:Cross-references: GB:AE000294; GB:U00096; NID:q1788338; PIDN:AACT5094.1; PID:g17883
 A:Experimental source: strain K-12, substrain MGL1655
 R:Yao, Z.; Valvano, M.A.
 J. Bacteriol. 176, 4133-4143, 1994
 A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r
 erotypes Y and 4a.
 A:Reference number: I55053; MUID:94292434
 A:Accession: I69646
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>
 A:Cross-references: EMBL:U03041; NID:q501028; PIDN:AACT31635.1; PID:g510256
 R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W.
 J. Bacteriol. 176, 4144-4156, 1994
 A:Title: Structure of the O antigen of *Escherichia coli* K-12 and the sequence of its
 A:Reference number: I55054; MUID:94292435
 A:Accession: I69656
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RE2>
 A:Cross-references: EMBL:U09876; NID:q508236; PID:g508245
 C:Genetics:
 A:Gene: yefH
 A:Map position: 45 min
 C:Superfamily: galactoside acetyltransferase

Query Match 65.5%; Score 38; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8
 |||||
 Db 105 HNHGSF 110

RESULT 6
 S64492
 hypothetical protein YGR178c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein G7139
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
 C:Accession: S64492
 R:Hebling, U.; Hofmann, B.; Delius, H.
 Submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64003
 A:Accession: S64492
 A:Molecule type: DNA
 A:Residues: 1-722 <HEB>
 A:Cross-references: EMBL:Z72963; NID:gi323314; PIDN:CAA97204.1; PID:g243559; PID:gi32
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:PPB1
 A:Cross-references: SGD:S0003410; MIPS:YGR178c
 A:Map position: 7R

Query Match 65.5%; Score 38; DB 2; Length 722;
 Best Local Similarity 75.0%; Pred. No. 40;

```

Matches      6;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  2  RHNGSFY  9
    1  |||||:
Db  474  RRNHGSFF  481

RESULT  7
T01030
hypothetical protein YUP8H12R.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
C:Accession: T01030
R:Theologis, A.; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwak,
Oefner, P.; Davis, R.W.
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A:Reference number: Z14227
A:Accession: T01030
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-530 <THE>
A:Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152559; GSPDB:GN000059; ATSP:YUP8H
C:Genetics:
A:Gene: ATSP:YUP8H12R.13
A:Map position: 1
A:Introns: 37/3; 77/1; 100/3; 219/3; 380/3; 451/3; 499/3

Query Match      63.8%;  Score 37;  DB 2;  Length 530;
Best Local Similarity 62.5%;  Pred. No. 44;
Matches      5;  Conservative  2;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  3  HNHSFYS  10
    1  ||| :||
Db  192  HNNHNYYS  199

RESULT  8
T48551
fructosidase-like protein - Arabidopsis thaliana
N:Alternate names: protein F14F18.90
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C:Accession: T48551
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24490
A:Accession: T48551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <BEV>
A:Cross-references: EMBL:AL163812
A:Experimental source: cultivar Columbia; BAC clone F14F18
C:Genetics:
A:Map position: 5
A:Introns: 31/1; 319/3; 373/3; 453/2; 483/3
A:Note: F14F18.90
C:Superfamily: beta-fructofuranosidase

Query Match      63.8%;  Score 37;  DB 2;  Length 547;
Best Local Similarity 55.6%;  Pred. No. 46;
Matches      5;  Conservative  4;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  2  RHNHGSFYS  10
    1  |||||:
Db  275  RYDHGTFYA  283

RESULT  9
JC2464
probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.

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C:Species: Enterobacteriaceae spp.
C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
C:Accession: JC2464
R:Trenor III., C.; Lin, W.; Andrews, N.C.
Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated se
A:Reference number: JC2464; MUID:95110304
A:Accession: JC2464
A:Molecule type: mRNA
A:Residues: 1-731 <TRE>
A:Cross-references: GB:U16658; NID:g643612; PID:AAA62113.1; PID:g643613
A:Experimental source: human small intestine cDNA library
A:Note: the source species is uncertain; the cloned sequence did not hybridize with h
C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-bindin
C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmem
F:7-92/Region: His-rich
F:135-477/Domain: ATPase transduction domain homology <APT>
F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
F:287/Active site: Glu #status predicted
F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match      63.8%;  Score 37;  DB 1;  Length 731;
Best Local Similarity 75.0%;  Pred. No. 61;
Matches      6;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  1  ARNHGGSF  8
    1  |||||
Db  88  AHHHGSF  95

RESULT  10
EGDEF
GGDEF family protein VC2750 [imported] - Vibrio cholerae (group O1 strain N16961)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: E82038
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: E82038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-849 <HEI>
A:Cross-references: GB:AE004340; GB:AE003852; NID:g9657344; PID:AAF95889.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2750
A:Map position: 1

Query Match      63.8%;  Score 37;  DB 2;  Length 849;
Best Local Similarity 70.0%;  Pred. No. 70;
Matches      7;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy  1  ARNHGGSFYS  10
    1  |||||
Db  572  AETHISFYS  581

RESULT  11
S75190
hypothetical protein slr2042 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75190
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996

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A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S75190
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <RAN>
 A:Cross-references: EMBL:D90903; GB:AB001339; NID:g1652127; PIDN:BAAL7104.1; PID:g165218
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 62.1%; Score 36; DB 2; Length 275;
 Best Local Similarity 62.5%; Pred. No. 35;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RHNHGSPY 9
 Db 253 OHNHGQLY 260
 ||||| |

RESULT 12
 D70405
 glutamate--trna ligase (EC 6.1.1.17) - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
 C:Accession: D70405
 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666
 A:Accession: D70405
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-473 <AQF>
 A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00065
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: gltX
 C:Superfamily: glutamate--trna ligase; glutamine--trna ligase homology
 C:Keywords: aminoacyl-trna synthetase; ligase; protein biosynthesis
 F:4-276/Domain: glutamine--trna ligase homology <EGL>

Query Match 62.1%; Score 36; DB 2; Length 473;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ARNHGGSF 8
 Db 31 ARNHNGGF 38
 ||||| |

RESULT 13
 B44511
 fumarate hydratase (EC 4.2.1.2) fumb, iron-dependent - Escherichia coli
 N:Alternate names: fumarase B
 C:Species: Escherichia coli
 C:Date: 03-Mar-1993 #sequence_revision 10-Oct-1997 #text_change 18-Jun-1999
 C:Accession: A65222; B44511; S56351
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: A65222
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-548 <BLAT>
 A:Cross-references: GB:U00096; NID:g1790563; PIDN:AAC77083.1; PID:g1790564;
 A:Experimental source: strain K-12, substrain MG1655
 R:Bell, P.J.; Andrews, S.C.; Sivak, M.N.; Guest, J.R.
 J. Bacteriol., 171, 3494-3503, 1989

A:Title: Nucleotide sequence of the FNR-regulated fumarase gene (fumb) of *Escherichia*
 A:Reference number: A44511; MUID:89255123
 A:Accession: B44511
 A:Molecule type: DNA
 A:Residues: 1-49, 'V', '51-548 <BEL>
 A:Cross-references: EMBL:M27058; NID:gl46046; PIDN:AAA23827.1; PID:gl46048
 R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 23, 2105-2119, 1995
 A:Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from
 A:Reference number: S56314; MUID:95334362
 A:Accession: S56351
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-49, 'X', '51-548 <BUR>
 A:Cross-references: EMBL:U14003; NID:gl263172; PIDN:AAA97022.1; PID:g536967
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 C:Comment: In *E. coli*, three fumarate hydratase genes (fuma, fumb, and fumC) have bee
 class I hydratase.
 C:Genetics:
 A:Gene: fumb
 A:Map position: 93.5 min
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the stereospecific interconversion of fumarate and L-malate
 A:Note: expressed at higher level under anaerobic conditions
 C:Superfamily: iron-dependent fumarate hydratase; iron-dependent tartrate dehydratase
 C:Keywords: 4Fe-4S; carbon-oxygen lyase; homodimer; hydro-lyase; iron-sulfur protein;
 F:2-548/Product: fumarate hydratase fumb, iron-dependent #status predicted <MAT>
 F:93-300/Domain: iron-dependent tartrate dehydratase alpha chain homology <TTDA>
 F:373-537/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>

Query Match 62.1%; Score 36; DB 1; Length 548;
 Best Local Similarity 66.7%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ARNHGGSF 9
 Db 473 ACHKHGGFY 481
 | | | | |

RESULT 14
 A81873
 hypothetical protein NMA1076 [imported] - Neisseria meningitidis (group A strain Z249
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 C:Accession: A81873
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491
 A:Reference number: A81775; MUID:20222556
 A:Accession: A81873
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-86 <PAR>
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84339.1; PID:g737
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1076

Query Match 60.3%; Score 35; DB 2; Length 86;
 Best Local Similarity 62.5%; Pred. No. 17;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNHGGSF 9
 Db 62 KHNGKGFY 69
 :||| |

RESULT 15
 C72852

AcOrf-19 protein - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, ACMNPV
A:Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-Jan-2000
C:Accession: C72852
R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A:Reference number: A72850; MUID:94303173
A:Accession: C72852
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <AYR>
A:Cross-references: GB:L22858; NID:g510708; PIDN:AAA66649.1; PID:g559088
C:Genetics:
A:Gene: AcOrf-19
C:Superfamily: ACMNPV hypothetical protein 19

Query Match 50.3%; Score 35; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
Db 25 ANRHSSFY 33

Search completed: March 28, 2001, 07:04:36
Job time: 1074 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:16 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGSPYS 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	67.2	470	1 SYE2_RICPR	Q9zct8 rickettsia
2	38	65.5	196	1 WBBJ_ECOLI	P37750 escherichia
3	38	65.5	722	1 PBPI_YEAST	P53297 saccharomyc
4	36	62.1	275	1 YK42_YEYN3	P73079 synechocyst
5	36	62.1	473	1 SYE_AQUAE	O67271 aquifex aeo
6	36	62.1	548	1 FUMB_ECOLI	P14407 escherichia
7	35	60.3	108	1 Y019_NPVAC	P41424 autographa
8	35	60.3	197	1 EGG5_FASHE	P07915 fasciola he
9	35	60.3	218	1 Y4VH_RHISN	Q53216 rhizobium s
10	35	60.3	352	1 CAPG_MOUSE	P24452 mus musculu
11	35	60.3	448	1 NCAP_CVHOC	P33469 human coron
12	35	60.3	567	1 CC45_XENLA	Q9yh26 xenopus lae
13	35	60.3	659	1 RA24_YEAST	P32641 saccharomyc
14	34	58.6	349	1 P16P_NOSPU	P48847 nostoc punc
15	34	58.6	435	1 PURA_SPICI	P52150 spiroplasma
16	34	58.6	604	1 LSP2_DROME	P13360 drosophila
17	34	58.6	718	1 IE18_PRVKA	Q24388 drosophila
18	34	58.6	1446	1 IE18_PRVKA	P33479 pseudorabie
19	34	58.6	1461	1 IE18_PRVKA	P11675 pseudorabie
20	33	56.9	81	1 YWR4_CAEEL	Q10927 caenorhabdi
21	33	56.9	225	1 CD9_MOUSE	P40240 mus musculu
22	33	56.9	284	1 YNB9_YEAST	P53975 saccharomyc
23	33	56.9	284	1 YND3_YEAST	P53964 saccharomyc
24	33	56.9	322	1 FATB_VIBAN	P11460 vibrio angu
25	33	56.9	347	1 UL33_HSV6U	P52380 herpes simp
26	33	56.9	394	1 IPOU_DROME	P24350 drosophila
27	33	56.9	480	1 SYE_HAETN	P43818 haemophilus
28	33	56.9	486	1 GATC_DROME	P91623 drosophila
29	33	56.9	502	1 KIR3_MOUSE	Q61288 mus musculu
30	33	56.9	503	1 KIR3_HUMAN	P37023 homo sapien
31	33	56.9	505	1 KIR3_RAT	P80203 rattus norv
32	33	56.9	596	1 GLMS_HELPJ	Q9zj94 h glucosami
33	33	56.9	596	1 GLMS_HELPY	O26060 h glucosami

34 33 56.9 692 1 AMO_PICAN P12807 pichia angu
35 33 56.9 767 1 AMDM_SCHPO P50998 schizosacch
36 33 56.9 783 1 FAND_ECOLI P12050 escherichia
37 33 56.9 798 1 YLFN_CAEEL Q20296 caenorhabdi
38 33 56.9 966 1 M172_HUMAN Q14596 homo sapien
39 33 56.9 1046 1 POL_FENV1 P31792 feline endo
40 33 56.9 1189 1 POL_BAEV1 P10272 baboon endo
41 32 55.2 117 1 GVPK_HALME Q02236 halobacteri
42 32 55.2 129 1 YP56_MYCTU Q50742 mycobacteri
43 32 55.2 166 1 YO21_BPHP1 P51723 bacterioph
44 32 55.2 174 1 YO30_BPHP1 P51734 bacterioph
45 32 55.2 190 1 SLVD_HAEIN P44830 haemophilus

ALIGNMENTS

RESULT 1
SYE2_RICPR ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria".
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
CC EMBL: AJ235272; CAA15066.1; -
CC HSSP; P27000; IGLN.
CC INTERPRO; IPR000924; -
CC INTERPRO; IPR001412; -
CC PFAM; PF00749; trna-synt_lc; 1.
CC PRINTS; PR00987; TRNASYNTHGLU.
CC PROSITE; PS00178; AA-TRNA-LIGASE-I; FALSE NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 67.2%; Score 39; DB 1; Length 470;
Best Local Similarity 66.7%; Pred. No. 4.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSPFY 9

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DB      11111111
      31 ARHNKGKF 39

RESULT 2
WBBJ_ECOLI
ID WBBJ_ECOLI STANDARD; PRT; 196 AA.
AC WBBJ50; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PUTATIVE LIPOPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ
DE (EC 2.3.1.-).
OS WBBJ.
GN Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a.";
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292435.
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
RA Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
RT of its rfb gene cluster.";
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292435.
RA Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
CC ON THE O ANTIGEN.
CC -!- PATHWAY: LIPOPOLYSACCHARIDE BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC -----
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CC -----
CC EMBL; U03041; AAC31635.1; -
CC EMBL; U09876; AAB88406.1; -
CC EMBL; AE000294; AAC75094.1; -
CC EMBL; D90841; CAB21803.1; -
CC EMBL; D90842; CAB21811.1; -
CC ECOGENE; EG11984; WBBJ.
CC INTERPRO; IPR001451; -
CC PFAM; PF00132; hexapep; 1.
CC PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1B1 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy, 3 HHGGSF 8
Db 105 HHGGSF 110

RESULT 3
PBPL_YEAST STANDARD; PRT; 722 AA.
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAB1-BINDING PROTEIN 1.
GN PBPI OR MRS16 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DBY747;
RA Mecklenbrauer I.;
RT "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns.";
RL Thesis (1996), Vienna Biocentre, Austria.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE; 99038243.
RA Mangus D.A., Amrani N., Jacobson A.;
RT "Pbpi, a factor interacting with Saccharomyces cerevisiae poly(A)-
RT binding protein, regulates polyadenylation.";
RL Mol. Cell. Biol. 18:7383-7396(1998).
CC -!- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
CC ABSENCE OF PBPI, THE 3' TERMINI OF PRE-MRNAs ARE PROPERLY CLEAVED
CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
CC -!- SUBUNIT: INTERACTS WITH PAB1.
CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -----
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CC -----
DR EMBL; 272963; CAA97204.1; -.
DR EMBL; 046931; AAB94294.1; -.
DR SGD; S0003410; PBPl.
KW Nuclear protein.
SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match 65.5%; Score 38; DB 1; Length 722;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFY 9
Db 474 RHNGSFF 481

RESULT 4
YK42_SYNY3
ID YK42_SYNY3 STANDARD; PRT; 275 AA.
AC P73079;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 31.9 KDA PROTEIN SLR2042.
GN SLR2042.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirotsawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SIMILARITY: TO E.COLI YEEL.
CC -----
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CC -----
DR EMBL; D90903; BAA17104.1; -.
KW Hypothetical protein.
SQ SEQUENCE 275 AA; 31929 MW; 3A46776EA239BD9E CRC64;

Query Match 62.1%; Score 36; DB 1; Length 275;
Best Local Similarity 62.5%; Pred. No. 9.9;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFY 9
Db 253 QHNGQLY 260

RESULT 5
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)

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DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujaay R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AE000729; AAC07230.1; -.
DR INTERPRO; IPR000924; -.
DR INTERPRO; IPR001412; -.
DR PFAM; PF00749; trna-synt_lc; 1.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA-TRNA-LIGASE-I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "RMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 62.1%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNHGSF 8
Db 31 ARHNGGF 38

RESULT 6
FUMB_ECOLI
ID FUMB_ECOLI STANDARD; PRT; 548 AA.
AC P14407; P78139;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FUMARATE HYDRATASE CLASS I, ANAEROBIC (EC 4.2.1.2) (FUMARASE).
GN FUMB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE; 89255123.
RA Bell P.J., Andrews S.C., Sivak M.N., Guest J.R.;
RT "Nucleotide sequence of the FNR-regulated fumarase gene (fumb) of
RT Escherichia coli K-12.";
RL J. Bacteriol. 171:3494-3503(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;

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RX MEDLINE; 95334362.
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
CC -!- FUNCTION: IT FUNCTIONS IN THE GENERATION OF FUMARATE FOR USE AS AN
CC ANAEROBIC ELECTRON ACCEPTOR.
CC -!- CATALYTIC ACTIVITY: L-MALATE = FUMARATE + H(2)O.
CC -!- COFACTOR: BINDS A 4FE-4S CLUSTER.
CC -!- ENZYME REGULATION: SUBJECT TO ANAEROBIC REPRESSION.
CC -!- PATHWAY: FERMENTATIVE PATHWAY THAT LEADS TO THE PRODUCTION OF
CC SUCCINATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: 79% IDENTITY WITH E.COLI FUM.
CC -!- SIMILARITY: TO OTHER THERMOLABILE CLASS I FUMARASES.
CC
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CC
CC EMBL; M27058; AAA23827.1; -.
CC DR EMBL; U14003; AAA97022.1; -.
CC DR EMBL; AE000485; AAC77083.1; -.
CC DR PIR; B44511; B44511.
CC DR ECOGENE; EGI0357; FUMB.
CC DR INTERPRO; IPR000362; -.
CC DR PFAM; PF00206; lyase_1; 1.
CC DR PROSITE; PS00163; FUMARATE LYASES; 1.
CC KW Lyase: Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S.
CC FT METAL 318 318 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC FT ACT-SITE 397 397 POTENTIAL.
CC FT BINDING 463 463 CARBOXYL GROUP (POTENTIAL).
CC FT CONFLICT 50 50 V -> L (IN AAC77083).
CC SQ SEQUENCE 548 AA; 60091 MW; 336854D8FA5551AB CRC64;

Query Match 62.1%; Score 36; DB 1; Length 548;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
DB 473 ACHKGGFY 481

RESULT 7
Y019_NPVAC STANDARD; PRT; 108 AA.
AC P41424;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 12.2 KDA PROTEIN IN EGT-TAP1 INTERGENIC REGION (ORF4).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE; 94303173.
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus";
RL Virology 202:586-605(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE; 93079853.

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RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
RA Summers M.D.;
RT "Sequence, genomic organization of the EcoRI-A fragment of Autographa
RT californica nuclear polyhedrosis virus, and identification of a
RT viral-encoded protein resembling the outer capsid protein VP8 of
RT rotavirus.";
RL Virology 191:1003-1008(1992).
CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
CC
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CC
CC EMBL; L22858; AAA66649.1; -.
CC DR EMBL; M96361; AAA66789.1; -.
CC DR PIR; D44221; D44221.
CC KW Hypothetical protein.
CC FT CONFLICT 6 6 A -> R (IN REF. 2).
CC SQ SEQUENCE 108 AA; 12162 MW; 8363B15DF72486A1 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
DB 25 ANRNHSFY 33

RESULT 8
EGGS_FASHE STANDARD; PRT; 197 AA.
AC P07915;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PUTATIVE EGGSHELL PROTEIN PRECURSOR.
OS Fasciola hepatica (liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87175670.
RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
RT "Cloning and characterization of a female genital complex cDNA from
RT the liver fluke Fasciola hepatica.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
CC
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CC
CC EMBL; M15871; AAA29138.1; -.
CC KW Eggshell; Signal.
CC FT SIGNAL 1 17
CC FT CHAIN 18 197 PUTATIVE EGGSHELL PROTEIN.
CC SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 8

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Db 17 ARHPGKF 24
      ||| |||
RESULT 9
Y4VH_RHISN
ID Y4VH_RHISN STANDARD; PRT; 218 AA.
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 24.6 KDA PROTEIN Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97305956.
RA Freiberg C.A., Fellay R., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96389014.
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase'; a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: NONE OBVIOUS.
CC
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CC
CC EMBL; Z68203; CAA92423.1; -
CC EMBL; AE00101; AAB91896.1; -
CC Hypothetical protein; plasmid.
KW SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;
Query Match 60.3%; Score 35; DB 1; Length 218;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ARHNHGSF 8
      || ||||
Db 68 ARDNHGSY 75
RESULT 10
CAPG_MOUSE
ID CAPG_MOUSE STANDARD; PRT; 352 AA.
AC P24452;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MACROPHAGE CAPPING PROTEIN (MYC BASIC MOTIF HOMOLOG-1) (ACTIN-CAPPING
DE PROTEIN GCAP39).
GN CAPG OR MBH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIH;
RX MEDLINE; 91184120.
RA Prendergast G.C., Ziff E.B.;
RT "Mb1: a novel gelsolin/severin-related protein which binds actin in
RT vitro and exhibits nuclear localization in vivo.";
RL EMBO J. 10:757-766(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE; 91075231.
RA Yu F.-X., Johnston P.A., Suedhof T.C., Yin H.L.;
RT "gCap39, a calcium ion- and polyphosphoinositide-regulated actin
RT capping protein.";
RL Science 250:1413-1415(1990).
RN [3]
RP PARTIAL SEQUENCE.
RX MEDLINE; 91009264.
RA Johnston P.A., Yu F.-X., Reynolds G.A., Yin H.L., Moomaw C.R.,
RA Slaughter C.A., Suedhof T.C.;
RT "Purification and expression of gCap39. An intracellular and secreted
RT Ca2(+)-dependent actin-binding protein enriched in mononuclear
RT phagocytes.";
RL J. Biol. Chem. 265:17946-17952(1990).
RN [4]
RP SUBCELLULAR LOCATION.
RX MEDLINE; 94123352.
RA Onoda K., Yu F.-X., Yin H.L.;
RT "gCap39 is a nuclear and cytoplasmic protein.";
RL Cell Motil. Cytoskeleton 26:227-238(1993).
CC -!- FUNCTION: CALCIUM-SENSITIVE PROTEIN WHICH REVERSIBLY BLOCKS THE
CC BARBED ENDS OF ACTIN FILAMENTS BUT DOES NOT SEVER PREFORMED ACTIN
CC FILAMENTS. MAY PLAY AN IMPORTANT ROLE IN MACROPHAGE FUNCTION. MAY
CC PLAY A ROLE IN REGULATING CYTOPLASMIC AND/OR NUCLEAR STRUCTURES
CC THROUGH POTENTIAL INTERACTIONS WITH ACTIN. MAY BIND DNA. UNCAPPING
CC OCCURS EITHER WHEN CA(2+) FALLS OR WHEN THE CONCENTRATION OF
CC POLYPHOSPHOINOSITIDE RISES, BOTH AT LOW AND HIGH CA(2+).
CC -!- SUBCELLULAR LOCATION: NUCLEAR, CYTOPLASMIC AND SECRETED. NUCLEAR
CC GCAP39 REDISTRIBUTES THROUGHOUT THE CYTOPLASM DURING MITOSIS AND
CC IS EXCLUDED FROM REGIONS CONTAINING CHROMOSOMES.
CC -!- TISSUE SPECIFICITY: PRESENT IN A LARGE VARIETY OF TISSUES AND IS
CC PARTICULARLY ABUNDANT IN KIDNEY AND LUNG.
CC -!- PTM: PHOSPHORYLATED. NUCLEAR GCAP39 IS MORE HIGHLY PHOSPHORYLATED
CC THAN CYTOPLASMIC GCAP39.
CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
CC -!- CAUTION: THIS PROTEIN WAS ORIGINALLY THOUGHT TO BE A DNA-BINDING
CC PROTEIN WITH A HELIX-LOOP-HELIX DOMAIN.
CC
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CC
CC EMBL; X54511; CAA38370.1; -
CC PIR; A39834; A39834.
CC PIR; S15011; S15011.
CC HSP; P10733; ISVO.
CC MGD; MGI:1098259; CAPG.
CC INTERPRO; IPR001974; -
CC PFAM; PF00626; Gelsolin; 3.
CC Nuclear protein; Actin-binding; Repeat; Phosphorylation.
CC DOMAIN 139 148 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC DOMAIN 32 310 3 X APPROXIMATE REPEATS.
CC REPEAT 32 78 1.
CC REPEAT 155 192 2.
CC REPEAT 267 312 3.
CC CONFLICT 32 32 V -> W (IN REF. 1).
CC CONFLICT 98 98 V -> L (IN REF. 1).
CC CONFLICT 117 117 MISSING (IN REF. 1).
CC CONFLICT 122 135 VESAFKHTSGARG -> GRVGISQDNLRATP (IN
CC REF. 1).
CC CONFLICT 156 156 P -> A (IN REF. 1).

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FT CONFLICT 245 248 O -> E (IN REF. 3).
FT CONFLICT 247 248 MISSING (IN REF. 1 AND 3).
FT CONFLICT 295 296 AQ -> GK (IN REF. 1).
FT CONFLICT 336 336 P -> R (IN REF. 1).
SQ SEQUENCE 352 AA; 39240 MW; 332CF78CD43B8057 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 352;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGFSFYS 10
DB 35 ARESHGIFFS 44

RESULT 11
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC NCAP_CVHOC
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RL coronavirus OC43".
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR INTERPRO; IPR001218;
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193ABIAE0D75626 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSF 8
DB 103 RHNRGSF 109

RESULT 12
CC45_XENLA STANDARD; PRT; 567 AA.
AC Q9YH26;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CDC45-RELATED PROTEIN.
GN CDC45.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98429493.
RA Mimura S., Takisawa H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RT chromatid under the control of S-phase Cdk.";
RL EMBO J. 17:5699-5707(1998).
CC -!- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.

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CC -!- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AF062494; AAC67520.1;
KW DNA replication; Cell cycle; Nuclear protein.
SQ SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 567;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGGS 7
DB 251 SRHNHGN 257

RESULT 13
RA24_YEAST STANDARD; PRT; 659 AA.
ID RA24_YEAST
AC P32641;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CHECKPOINT PROTEIN RAD24.
GN RAD24 OR YER173W OR SYGP-ORF60.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunkle-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Bolstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP IDENTIFICATION.
RX MEDLINE; 96112796.
RA Weinert T.;
RL Unpublished results, cited by:
RL Griffiths D.J.F., Barbet N.C., McCready S., Lehmann A.R.,
RL Carr A.M.;
RL EMBO J. 14:5812-5823(1995).
CC -!- FUNCTION: PARTICIPATES IN CHECKPOINT PATHWAYS ARREST OF THE CELL
CC CYCLE. A MECHANISM THAT ALLOWS THE DNA REPAIR PATHWAYS TO ACT TO
CC RESTORE THE INTEGRITY OF THE DNA PRIOR TO DNA SYNTHESIS OR
CC SEPARATION OF THE REPLICATED CHROMOSOMES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- SIMILARITY: TO S.POMBE RAD17 AND SOME SIMILARITY TO ACTIVATOR 1 36
CC TO 40 KDA SUBUNITS FAMILY.
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CC -----

DR EMBL; U18922; AAB64700.1; -
DR PIR; S30859; S30859.
DR SGD; S0000975; RAD24.
KW DNA damage; DNA repair; Nuclear protein; Cell cycle.
SQ SEQUENCE 659 AA; 75726 MW; 130FE54875CAA930 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 659;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NHGFSY 9
Db 436 NHGTVY 442
|||||

RESULT 14
F16P_NOSPU
ID F16P_NOSPU STANDARD; PRT; 349 AA.
AC P48847;

DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE
DE 1-PHOSPHOHYDROLASE) (FBPASE).
GN FBP.

OS Nostoc punctiforme.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29133 / PCC 73102;
RA Summers M.L., Wolf R.E. Jr., Chu S., Meeks J.C.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
CC -!- PATHWAY: KEY ENZYME OF THE REDUCTIVE CARBON DIOXIDE ASSIMILATION.
CC OR CALVIN CYCLE OF PHOTOSYNTHETIC CARBON DIOXIDE ASSIMILATION.
CC -!- SIMILARITY: BELONGS TO THE FBPAE FAMILY.

CC -----
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CC -----

DR EMBL; L32796; AAA50768.1; -
DR HSP; P0636; 3FBP.
DR INTERPRO; IPR000146; -
DR PFAM; PF00316; FBPAse; 1.
DR PRINTS; PR00115; FBPHPTASE.
DR PRINTS; PR00377; INFBBPHPTASE.
DR PROSITE; PS00124; FBPAse; 1.
KW Hydrolyase; Carbohydrate metabolism; Calvin cycle; Photosynthesis.
FT ACT_SITE 288 BY SIMILARITY.
SQ SEQUENCE 349 AA; 38618 MW; 6720CF7C8F38127E CRC64;

Query Match 58.6%; Score 34; DB 1; Length 349;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NHGFSY 10
Db 222 NHGSYS 228
|||||

RESULT 15:
PURA_SPICI

ID PURA_SPICI STANDARD; PRT; 435 AA.
AC P52150;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE)
DE (ADSS) (AMPSASE).
GN PURA.
OS Spiroplasma citri.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Spiroplasmataceae; Spiroplasma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R8A2HP;
RA Citti C., Saillard C., Bove J.M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE
CC NUCLEOTIDE BIOSYNTHESIS.
CC -!- CATALYTIC ACTIVITY: GTP + IMP + L-ASPARTATE = GDP + ORTHOPHOSPHATE
CC + ADENYLOSUCCINATE.
CC -!- PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE ADENYLOSUCCINATE SYNTHETASE FAMILY.
CC -----
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CC -----

DR EMBL; L22971; AAA26586.1; -
DR HSP; P12283; 1ADI.
DR INTERPRO; IPR001114; -
DR PFAM; PF00709; Adenylsucc_synth; 1.
DR PROSITE; PS00513; ADENYLOSUCCIN_SYN_2; 1.
DR PROSITE; PS01266; ADENYLOSUCCIN_SYN_1; 1.
KW Lyase; Purine biosynthesis; Ligase; GTP-binding.
FT NP_BIND 17 23 GTP (POTENTIAL).
FT ACT_SITE 146 146 BY SIMILARITY.
FT ACT_SITE 153 153 BY SIMILARITY.
SQ SEQUENCE 435 AA; 49609 MW; 74EB74E7B5A2091A CRC64;

Query Match 58.6%; Score 34; DB 1; Length 435;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNGSFY 9
Db 217 AIHNGKFY 225
|||||

Search completed: March 28, 2001, 07:35:18
Job time: 155 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:33 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42	72.4	233	2	Q9KRA6
2	40	69.0	555	5	Q9XV91
3	39	67.2	350	2	P74376
4	38	65.5	191	10	Q9W8I3
5	38	65.5	278	5	Q9VP63
6	38	65.5	839	10	Q9LIE5
7	37	63.8	326	2	Q9RJG3
8	37	63.8	530	10	O64526
9	37	63.8	547	10	Q9LYI1
10	37	63.8	573	10	Q9W0A8
11	37	63.8	583	5	Q9VHN8
12	37	63.8	731	2	O59369
13	37	63.8	849	2	Q9KNT8
14	36	62.1	227	5	Q9VNI9
15	36	62.1	339	2	Q9XDB5
16	36	62.1	463	5	O44923
17	36	62.1	627	10	O24474
18	35	60.3	86	2	Q9JU21
19	35	60.3	89	7	O19495

20	35	60.3	110	12	O92387
21	35	60.3	157	5	Q9VNB9
22	35	60.3	272	5	Q24950
23	35	60.3	272	5	Q24951
24	35	60.3	551	5	Q9UAG5
25	35	60.3	552	5	Q9XWG6
26	35	60.3	696	10	Q9LZA5
27	35	60.3	1008	5	Q9W345
28	35	60.3	1467	6	Q97830
29	35	60.3	1472	6	Q97831
30	35	60.3	1474	4	O94910
31	35	60.3	1515	11	O88917
32	35	60.3	2470	13	Q90681
33	34.5	59.5	308	2	Q9PMW8
34	34	58.6	137	12	Q9PY61
35	34	58.6	151	4	Q99702
36	34	58.6	181	5	Q9VDT4
37	34	58.6	236	10	Q40088
38	34	58.6	273	10	Q9LW98
39	34	58.6	371	5	Q94707
40	34	58.6	379	2	O25568
41	34	58.6	381	2	O9ZKT9
42	34	58.6	385	9	O64373
43	34	58.6	429	5	Q9VG09
44	34	58.6	449	5	Q9XYC7
45	34	58.6	450	3	O93934

ALIGNMENTS

RESULT 1

Q9KRA6
ID Q9KRA6 PRELIMINARY; PRT; 233 AA.
AC Q9KRA6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ARGINYL-TRNA-PROTEIN TRANSFERASE-RELATED PROTEIN.
GN VC1736.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae".
RL Nature 406:477-483(2000).
DR EMBL; AE004251; AAF94886.1;
DR TIGR; VC1736;
KW Transferase.
SQ SEQUENCE 233 AA; 27350 MW; AEB6E95905EC2C3C CRC64;

Query Match 72.4%; Score 42; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9

DB 117 ARRHGGSFY 125

RESULT 2

Q9XV91
ID Q9XV91 PRELIMINARY; PRT; 555 AA.
AC Q9XV91;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE F16H6.1 PROTEIN.
GN F16H6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=94150718; PubMed=7906398;
RX Matthews L.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=94150718; PubMed=7906398;
RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
DR EMBL; Z81506; CAB04128.1; -.
DR HSSP; P23807; 11XX.
DR INTERPRO; IPR000859; -.
DR INTERPRO; IPR001304; -.
DR PFAM; PF000059; lectin_c; 2.
DR PFAM; PF00431; CUB; 2.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 2.
SQ SEQUENCE 555 AA; 60401 MW; 00B58D22B2E14EDC CRC64;

Query Match 69.0%; Score 40; DB 5; Length 555;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFYS 10
||| |||||
Db 314 HHNGSFYS 321

RESULT 3
P74376
ID P74376 PRELIMINARY; PRT; 350 AA.
AC P74376;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 40.3 KDA PROTEIN.
GN SLL0428.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97061201; PubMed=8905231;
RX Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sugita M., Sasamoto S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90914; BAA18471.1; -.
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 40262 MW; 29E436C5B44839DC CRC64;

Query Match 67.2%; Score 39; DB 2; Length 350;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHNGSFYS 9
||| |||||
Db 247 HHNGNY 253

RESULT 4
Q9M813
ID Q9M813 PRELIMINARY; PRT; 191 AA.
AC Q9M813;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE TP1.6 PROTEIN.
GN TP1.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.D., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome I BAC T7P1 genomic sequence."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC018908; AAF27666.1; -.
SQ SEQUENCE 191 AA; 21501 MW; BF92CEBA22421D1 CRC64;

Query Match 65.5%; Score 38; DB 10; Length 191;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFYS 10
||| |||||
Db 56 HSHASFYS 63

RESULT 5
Q9VP63
ID Q9VP63 PRELIMINARY; PRT; 278 AA.
AC Q9VP63;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CG9391 PROTEIN.
GN CG9391.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;

MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003594; AAF51693.1; -;
DR HSSP: P29218; 2HWM.
DR FLYBASE: FBgn0037063; CG9391.
DR INTERPRO: IPR000760; -;
DR PFAM: PF00459; inositol_P; 1.
DR PRINTS: PR00378; INOSPHPTASE.
DR PROSITE: PS00629; IMP_1; 1.
DR PROSITE: PS00630; IMP_2; 1.
DR PROSITE: PS00630; IMP_2; 1.
SQ SEQUENCE 278 AA; 30626 MW; B5AEBC2445472D99 CRC64;

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Query Match      65.5%; Score 38; DB 5; Length 278;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 ARNHGSFYS 10
 || ||||:
 Db . 136 ARRGHAFYN 145

RESULT	6
Q9LIE5	
ID	PRELIMINARY; PRT; 839 AA.
AC	Q9LIE5
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE	FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE	PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC	Braassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxID=3702;

```

RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=COLUMBIA;
RA      Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=COLUMBIA;
RA      Nakamura Y.;
RT      *Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT      Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT      TAC and BAC clones.;
RL      DNA Res. 7:217-221 (2000).
DR      EMBL; AP001306; BAB03065.1; -.
SQ      SEQUENCE      839 AA; 95996 MW;  CBBF60DF8B6797F8  CRC64;
                                65.5%   Score 38;   DB 10;   Length 839.
Query Match

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Query Match	65.5%	Score 38	DB 10	Length 839
Best Local Similarity	75.0%	Pred. No. 60		
Matches	6	Conservative	2	Mismatches 0
				Indels 0
				Gaps 0

Qy	1	ARHNCSF	8
		: : :	
Db	274	SRHNYGSF	281

RESULT	7
Q9RJG3	
ID	Q9RJG3
PRELIMINARY;	
PRT;	326 AA.

Q2000, 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE PUTATIVE ARAC FAMILY TRANSCRIPTIONAL REGULATOR.
GN SCF76.11.
OS Streptomyces coelicolor

OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyceinae; Streptomycetaceae; Streptomyces.
NCBI TaxID=1902;

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RN      NCBI_FukuiD-15047,
RP      [1]
RC      SEQUENCE FROM N. A.
RC      STRAIN=A3(2);
RA      Murphy L., Harris D.;
RL      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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RN
 RN
 RP
 RC
 RA
 RI

submitted (SEP 1999) to the EMBL/GenBank/DDBJ databases.
 [2]
 SEQUENCE FROM N.A.
 STRAIN=A3(2);
 Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

KN	[3]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=A3(2);	
RC	Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,	
RA		
RA	Kinashi H., Hopwood D.A.;	
RT	"A set of ordered cosmids and a detailed genetic and physical map for	
RT	the 8 Mb Streptomyces coelicolor A3(2) chromosome.";	
RL	Mol. Microbiol. 21:77-96(1996).	
RL	EMBL: AL121600. CAB56731.1; -;	
DR	INTERPRO: IPR000005; -;	
DR	PFAM: PF001165; HTH_Arac; 1.	
SQ	SEQUENCE 326 AA; 34425 MW; 2FEF5346ACAC80D6 CRC64;	

Query Match	63.8%	Score 37:	DB 2:	Length 326:
Best Local Similarity	85.7%	Pred. No. 36:		
Matches	6:	Conservative	0:	Mismatches
			1:	Indels
				Caps 0:

Qy	2	RHNGSF	8
Db	85	RHNGSF	91

RESULT 8

064526 O64526 PRELIMINARY; PRT; 530 AA.
 AC 064526;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE YUP8H12R.13 PROTEIN.
 GN YUP8H12R.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A., Vysotskaia V.S., Osborne B.I., Schwartz J.R.,
 RA Federspiel N.A., Kwan A., Toriumi M., Yu G., Oji O., Araujo R.,
 RA Chung E., Dewar K., Dietrich F., Ecker J.R., Marziani A., Oefner P.,
 RA Davis R.W.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002986; AAC17040.1; -;
 DR MENDEL; 29344; Arath; 3318; 29344.
 DR INTERPRO; IPR001064; -;
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 SQ SEQUENCE 530 AA; 59679 MW; E326AA0A6958F910 CRC64;

Query Match 63.8%; Score 37; DB 10; Length 530;
 Best Local Similarity 62.5%; Pred. No. 58;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RHNGSFYS 10
 III :|||
 DB 192 HNHNYS 199

RESULT 9
 Q9LYI1 PRELIMINARY; PRT; 547 AA.
 AC Q9LYI1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE FRUCTOSIDASE-LIKE PROTEIN.
 GN FL4F18_90.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL163812; CAB87665.1; -;
 SQ SEQUENCE 547 AA; 61771 MW; 9616592D5D48AE74 CRC64;

Query Match 63.8%; Score 37; DB 10; Length 547;
 Best Local Similarity 55.6%; Pred. No. 60;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 I::|||:
 DB 275 RYDHGTFA 283

RESULT 10
 Q9MOA8 PRELIMINARY; PRT; 573 AA.
 ID Q9MOA8
 AC Q9MOA8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE RECEPTOR-LIKE KINASE HOMOLOG.
 GN AT4G30520.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL161577; CAB79770.1; -;
 KW Kinase.
 SQ SEQUENCE 573 AA; 62834 MW; E6F1CC9D0B3C0B66 CRC64;

Query Match 63.8%; Score 37; DB 10; Length 573;
 Best Local Similarity 66.7%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFY 9
 I::|||:
 DB 508 ASHNSHFY 516

RESULT 11
 Q9VHN8 PRELIMINARY; PRT; 583 AA.
 ID Q9VHN8
 AC Q9VHN8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CG8032 PROTEIN.
 GN CG8032.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003680; AAF54284.1; -
 DR FLYBASE; FBgn0037606; CG8032.
 DR INTERPRO; IPR00205; -
 DR INTERPRO; IPR002937; -
 DR PFAM; PF01593; Amino oxidase; 1.
 SQ SEQUENCE 583 AA; 64447 MW; BD75A2DA1973FF16 CRC64;

Query Match 63.8%; Score 37; DB 5; Length 583;
 Best Local Similarity 75.08; Pred. No. 64;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNHGSFYS 10
 I I I I I I
 Db 532 HTHSFSYS 539

RESULT 12
 Q59369
 ID Q59369 PRELIMINARY; PRT; 731 AA.
 AC Q59369;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE HISTIDINE RICH P TYPE ATPASE.
 GN HRA-1
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95110304; PubMed=7811248;
 RA Trenor C.C., Lin W., Andrews N.C.;
 RT "Novel bacterial P-type ATPases with histidine-rich heavy-metal-
 associated sequences.";
 RL Biochem. Biophys. Res. Commun. 205:1644-1650(1994).
 DR EMBL; U16558; AAA62113.1; -
 DR INTERPRO; IPR001757; -
 DR PFAM; PF00122; E1-E2_ATPase; 1.
 DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN.1.
 KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 731 AA; 78453 MW; 06237F155E151F0D CRC64;

Query Match 63.8%; Score 37; DB 2; Length 731;
 Best Local Similarity 75.08; Pred. No. 80;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ARNHGSF 8
 I I I I I I
 Db 88 AHHHGSF 95

RESULT 13
 Q9KN18
 ID Q9KN18 PRELIMINARY; PRT; 849 AA.
 AC Q9KN18;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE GGDEF FAMILY PROTEIN.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Omayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004340; AAF95889.1; -
 DR TIGR; VC2750; -
 SQ SEQUENCE 849 AA; 95053 MW; 2FF1438453FB998D CRC64;

Query Match 63.8%; Score 37; DB 2; Length 849;
 Best Local Similarity 70.08; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARNHGSFYS 10
 I I I I I I
 Db 572 AEHTHSFYS 581

RESULT 14
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 AC Q9VNI9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE CG2023 PROTEIN.
 GN CG2023
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003601; AAF51945.1;
 DR FLYBASE: FBgn0037383; CG2023.
 SQ SEQUENCE 227 AA; 25695 MW; 768718C22AE7C60E CRC64;

Query Match 62.1%; Score 36; DB 5; Length 227;
 Best Local Similarity 70.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFYS 10
 DB 126 ARHNGSLVS 135

RESULT 15
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 AC Q9XD85;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE SECRETED PROTEIN PRECURSOR.
 OS Corynebacterium diphtheriae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 OC Corynebacterium.
 OX NCBI_TaxID=1717;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C7(-);
 RA Drazek E.S., Schmitt M.P.;
 RT "Identification of Corynebacterium diphtheriae genes required for
 RT acquisition of iron from heme and hemoglobin that are homologous to
 RT ABC transporters.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF109162; AAD37497.1;
 KW Signal.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 339 SECRETED PROTEIN.
 SQ SEQUENCE 339 AA; 37116 MW; 4E0FCE7418685059 CRC64;

Query Match 62.1%; Score 36; DB 2; Length 339;

Best Local Similarity 85.7%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGGSFYS 10
 DB 120 HHGGSFYS 126

Search completed: March 28, 2001, 07:53:37
 Job time: 530 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:55 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-96

Perfect score: 58

Sequence: 1 ARNHGSPYS 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*

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19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19 W76038	LM609 grafted anti
2	52	89.7	10	19 W76040	LM609 grafted anti
3	49	84.5	10	19 W76037	LM609 grafted anti
4	48	82.8	10	19 W76039	LM609 grafted anti
5	48	82.8	10	19 W76023	LM609 grafted anti
6	47	81.0	10	19 W76020	LM609 grafted anti
7	43	74.1	10	19 W76024	LM609 grafted anti
8	41	70.7	10	19 W76022	LM609 grafted anti
9	41	70.7	10	19 W76025	LM609 grafted anti
10	41	70.7	10	19 W76026	LM609 grafted anti
11	41	70.7	10	19 W76027	LM609 grafted anti
12	41	70.7	10	19 W76028	LM609 grafted anti

13	41	70.7	10	19 W76029	LM609 grafted anti
14	41	70.7	10	19 W76030	LM609 grafted anti
15	41	70.7	10	19 W76010	LM609 grafted anti
16	41	70.7	117	19 W76001	Vitaxin antibody h
17	41	70.7	117	19 W76003	LM609 antibody hea
18	41	70.7	117	20 Y06381	Murine monoclonal
19	41	70.7	117	20 Y06387	Humanised LM609 an
20	41	70.7	118	20 Y06384	Humanised LM609 an
21	41	70.7	118	20 Y06385	Humanised LM609 an
22	41	70.7	118	20 Y06386	Humanised LM609 an
23	41	70.7	118	20 Y06383	Humanised LM609 an
24	41	70.7	130	20 Y06379	Murine monoclonal
25	38	65.5	10	19 W76021	LM609 grafted anti
26	36	62.1	627	20 W85700	Myrcene synthase o
27	36	62.1	627	20 W85710	Grand Fir monoterp
28	35	60.3	286	20 Y43477	Amino acid sequenc
29	35	60.3	352	15 Y53686	38KD HRI factor
30	35	60.3	353	15 R53687	38KD HR2 factor
31	35	60.3	659	18 W26662	Yeast checkpoint c
32	35	60.3	659	20 W73892	Yeast RAD24 protei
33	35	60.3	1466	20 Y41091	Rat latrophilin pr
34	35	60.3	1469	20 Y41097	Human lectomedin-2
35	35	60.3	1471	19 W74585	Calcium independen
36	35	60.3	1474	21 W77729	Human G protein-co
37	34	58.6	99	20 Y29137	Amino acid sequenc
38	34	58.6	204	19 W59609	DNA-binding/dimeri
39	34	58.6	229	21 W70509	Human BAG-4 protei
40	34	58.6	358	19 W98649	H. pylori GHP0 403
41	34	58.6	466	20 Y24317	Human dephosphoryl
42	34	58.6	483	19 W82550	Human Lir-pbmhh pr
43	34	58.6	514	19 W69235	Fcr-V protein sequ
44	33	56.9	18	21 Y98371	Alpha D peptide de
45	33	56.9	19	21 Y98381	Alpha D peptide de

ALIGNMENTS

RESULT 1

W76038
ID W76038 standard; Protein; 10 AA.

XX

AC W76038;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #14.

XX

Vitaxin; antibody; variable region; heavy chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.

XX

OS Mus sp.

XX

PN W09833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

WPI; 1998-437472/37.

DR N-PSDB; V49875.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 43; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10
 |||||

DB 1 arhnhsfys 10

RESULT 2

ID W76040 standard; Protein; 10 AA.

XX W76040;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #16.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49877.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

XX LM609, also related nucleic acid, used to treat, prevent or diagnose

XX angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 89.7%; Score 52; DB 19; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.0017;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10

|||||

DB 1 arhnysfys 10

RESULT 3

ID W76037 standard; Protein; 10 AA.

XX W76037;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #13.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49874.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 XX LM609, also related nucleic acid, used to treat, prevent or diagnose
 XX angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

XX LM609 heavy and light chain variable region. LM609 and the antibody

XX vitaxin bind selectively to integrin alphavbeta3 and can be used to

XX inhibit binding of alphavbeta3 to a ligand and thus block

XX integrin-mediated signal transduction. This is useful in the treatment,

XX prevention and diagnosis of alphavbeta3-mediated disease, specifically

XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 84.5%; Score 49; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. NO. 0.0059;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNHGSFYS 10
 Db 1 arnhnhsfys 10
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RESULT 4

ID W76039 standard; Protein; 10 AA.

XX AC W76039;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #15.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49876.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 82.8%; Score 48; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 0.0089;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSFY 9
 Db 1 arhnysfy 9
 |||||

RESULT 5

ID W76023 standard; Protein; 10 AA.

XX AC W76023;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #5.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49860.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 82.8%; Score 48; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. NO. 0.0089;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSFY 9
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Db      1 arhnygsfy 9

RESULT      6
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ID W76020 standard; Protein; 10 AA.
AC W76020;
XX
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #2.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX WO9833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX N-PSDB; V49857.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 10 AA;

Query Match      81.0%; Score 47; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARHNHGSF 8
Db      1 arhnygsf 8
|||||

RESULT      7
W76024
ID W76024 standard; Protein; 10 AA.
XX

AC W76024;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #6.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
XX Mus sp.
OS
XX
XX WO9833919-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
PA
XX
XX Glaser SM, Huse WD;
PI
XX
XX WPI; 1998-437472/37.
DR
XX
XX N-PSDB; V49861.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 10 AA;

Query Match      74.1%; Score 43; DB 19; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.068;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ARHNHGSFYS 10
Db      1 arhnygsfas 10
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RESULT      8
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ID W76022 standard; Protein; 10 AA.
XX
XX
XX AC W76022;
XX
XX 02-NOV-1998 (first entry)
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #4.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

```

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 XX WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX N-PSDB; V49859.
 DR Humanised antibody, vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 PS W76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX SQ Sequence 10 AA;
 Query Match 70.7%; Score 41; DB 19; Length 10;
 Best Local Similarity 87.5%; Pred. NO. 0.15;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNHGSF 8
 Db ||||:||||
 1 arhnygsf 8
 RESULT 9
 ID W76025 standard; Protein; 10 AA.
 XX W76025;
 AC 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #7.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX OS Mus sp.

XX WO9833919-A2.
 PN 06-AUG-1998.
 PD 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 XX N-PSDB; V49862.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 XX integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 PS W76007-W76040 are protein fragments of the grafted monoclonal antibody
 XX LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX SQ Sequence 10 AA;
 Query Match 70.7%; Score 41; DB 19; Length 10;
 Best Local Similarity 87.5%; Pred. NO. 0.15;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ARHNHGSF 8
 Db ||||:||||
 1 arhnygsf 8
 RESULT 10
 ID W76026 standard; Protein; 10 AA.
 XX W76026;
 AC 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #8.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX OS Mus sp.
 XX WO9833919-A2.
 PD 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 DR N-PSDB; V49863.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ Query Match 70.7%; Score 41; DB 19; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.15; Length 10;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSGF 8
 Db ||||:|
 1 arhnygsf 8
 RESULT 11
 W76027 ID W76027 standard; Protein; 10 AA.
 XX AC W76027;
 XX 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #9..
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS WO9833919-A2.
 XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX WPI: 1998-437472/37.

DR N-PSDB; V49864.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 62; Page 41; 129pp; English.
 XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX Sequence 10 AA;
 SQ Query Match 70.7%; Score 41; DB 19; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.15; Length 10;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSGF 8
 Db ||||:|
 1 arhnygsf 8
 RESULT 12
 W76028 ID W76028 standard; Protein; 10 AA.
 XX AC W76028;
 XX 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #10.
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS WO9833919-A2.
 XX 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01826.
 XX 30-JAN-1997; 97US-0791391.
 XX (IXSY-) IXSYS INC.
 PA Glaser SM, Huse WD;
 XX WPI: 1998-437472/37.
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX WPI: 1998-437472/37.

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

XX

SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 19; Length 10;

Best Local Similarity 87.5%; Pred. No. 0.15;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSF 8

||||:||||

Db 1 arhnygsf 8

RESULT 13

W76029

ID W76029 standard; Protein; 10 AA.

XX

AC W76029;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI: 1998-437472/37.

XX

DR N-PSDB; V49866.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 62; Page 41; 129pp; English.

XX

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

CC

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

XX

SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 19; Length 10;

Best Local Similarity 87.5%; Pred. No. 0.15;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGSF 8

||||:||||

Db 1 arhnygsf 8

RESULT 14

W76030

ID W76030 standard; Protein; 10 AA.

XX

AC W76030;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #12.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI: 1998-437472/37.

XX

DR N-PSDB; V49867.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 62; Page 41; 129pp; English.

XX

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

CC

XX SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 19; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSF 8
| | | | : | | |
Db 1 arhnygsf 8

RESULT 15

W76010
ID W76010 standard; Protein; 10 AA.

XX AC W76010;

XX DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #1.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-Y) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI: 1998-437472/37.

XX DR N-PSDB; V49847.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match

Best Local Similarity 70.7%; Score 41; DB 19; Length 10;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSF 8

Db 1 arhnygsf 8

Search completed: March 28, 2001, 06:59:55
Job time: 1391 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:02:00 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-96

Perfect score: 58

Sequence: 1 ARNHGFSFY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgnl_7/ptodata/1/iaa/PTCUS_COMB.pep:*

5: /cgnl_7/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	35	60.3	659	2	US-08-870-693-13
3	34	58.6	204	1	US-08-591-989-4
4	33	56.9	94	3	US-09-147-550-14
5	33	56.9	94	3	US-09-147-550-45
6	33	56.9	94	3	US-09-147-550-48
7	33	56.9	94	3	US-09-147-550-77
8	33	56.9	94	3	US-09-147-550-84
9	33	56.9	94	3	US-09-147-550-90
10	33	56.9	94	3	US-09-147-550-101
11	33	56.9	318	3	US-08-816-977-6
12	33	56.9	326	3	US-08-816-977-25
13	33	56.9	329	3	US-08-816-977-39
14	33	56.9	503	2	US-08-481-337A-2
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21	32	55.2	213	2	US-08-655-821-16
22	32	55.2	271	1	US-07-914-282D-4
23	32	55.2	271	1	US-08-276-887A-4
24	32	55.2	271	4	PCT-US93-02460-4
25	32	55.2	291	1	US-07-593-657-5
26	32	55.2	443	1	US-07-940-245-2
27	32	55.2	443	1	US-08-226-486-2
28	32	55.2	661	1	US-08-232-538-12

29 32 55.2 661 2 US-08-786-164-12 Sequence 12, Appli
30 32 55.2 687 1 US-08-232-538-6 Sequence 6, Appli
31 32 55.2 687 2 US-08-786-164-6 Sequence 6, Appli
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33 32 55.2 758 3 US-08-643-839-1 Sequence 1, Appli
34 32 55.2 780 1 US-08-232-538-14 Sequence 14, Appli
35 32 55.2 780 2 US-08-786-164-14 Sequence 14, Appli
36 32 55.2 907 3 US-08-938-830-26 Sequence 26, Appli
37 32 55.2 907 3 US-09-020-222-26 Sequence 26, Appli
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ALIGNMENTS

RESULT 1
US-08-198-446B-13
; Sequence 13, Application US/08198446B
; Patent No. 5674996
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Pion, Sharon E.
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/198,446B
; FILING DATE: 18-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCRI7537
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Yeast RAD24 protein
US-08-198-446B-13

Query Match 60.3%; Score 35; DB 1; Length 659;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGFSFY 9

|||||

DB 436 HNHGTVY 442

RESULT 2
US-08-870-693-13
; Sequence 13, Application US/08870693
; Patent No. 5866338
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Plon, Sharon E.
; APPLICANT: Groudine, Mark T.
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,693
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,446
; FILING DATE: February 18, 1994
; APPLICATION NUMBER: PCT/US93/04458
; FILING DATE: May 12, 1993
; APPLICATION NUMBER: US 07/884,426
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: US 07/882,051
; FILING DATE: May 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCRL10798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: yeast RAD24 protein
US-08-870-693-13

Query Match 60.3%; Score 35; DB 2; Length 659;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHGGSFY 9
|||||
DB 436 HHGCTVY 442

RESULT 3
US-08-591-989-4
; Sequence 4, Application US/08591989
; Patent No. 5795721
; GENERAL INFORMATION:
; APPLICANT: Ross S. Rabin, Sumedha Jayasena
; APPLICANT: and Larry Gold
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
; MOLECULE TYPE: ACID LIGANDS OF ICP4

; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,989
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX 49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-591-989-4

Query Match 58.6%; Score 34; DB 1; Length 204;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
|||||
DB 137 APHGGSF 144

RESULT 4
US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/Jp97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-14

Query Match 56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFYS 10
 |||:| | |
 Db 80 RHNGVFES 88

RESULT 5

US-09-147-550-45
 ; Sequence 45, Application US/09147550.
 ; Patent No. 6090540

; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 45

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-45

Query Match 56.9%; Score 33; DB 3; Length 94;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 2 RHNGSFYS 10
 |||:| | |
 Db 80 RHNGVFES 88

RESULT 6

US-09-147-550-48

; Sequence 48, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 48

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-48

Query Match 56.9%; Score 33; DB 3; Length 94;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 2 RHNGSFYS 10
 |||:| | |
 Db 80 RHNGVFES 88

RESULT 7

US-09-147-550-77

; Sequence 77, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 77

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-77

Query Match 56.9%; Score 33; DB 3; Length 94;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 2 RHNGSFYS 10
 |||:| | |
 Db 80 RHNGVFES 88

RESULT 8

US-09-147-550-84

; Sequence 84, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 84

; LENGTH: 94

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-84

Query Match 56.9%; Score 33; DB 3; Length 94;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 2 RHNGSFYS 10
 |||:| | |
 Db 80 RHNGVFES 88

RESULT 9

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US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-90

Query Match          56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNGSFYS 10
    |||:| | |
Db   80 RHNGVFES 88

RESULT 10
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match          56.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNGSFYS 10
    |||:| | |
Db   80 RHNGVFES 88

RESULT 11
US-08-816-977-6
; Sequence 6, Application US/08816977
; Patent No. 6080400

```

```

; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-977-6

Query Match          56.9%; Score 33; DB 3; Length 318;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  3 HNHGSFYS 10
    | | | | : :
Db   65 HTHGSIFA 72

RESULT 12
US-08-816-977-25
; Sequence 25, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977

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;; FILING DATE: 13-MAR-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MacKnight, Kamrin T.
;; REGISTRATION NUMBER: 38,230
;; REFERENCE/DOCKET NUMBER: OPND-02450
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 326 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-816-977-25

Query Match 56.9%; Score 33; DB 3; Length 326;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
| |||:::
DB 65 HTHGSYFA 72

RESULT 13
US-08-816-977-39
; Sequence 39, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrne, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,977
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPND-02450
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-977-39

Query Match 56.9%; Score 33; DB 3; Length 329;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
| |||:::
DB 76 HTHGSYFA 83

RESULT 14
US-08-481-337A-2
; Sequence 2, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: SAMPATH, Kuber T.
; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
; TITLE OF INVENTION: Surface Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,337A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-097CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-481-337A-2

Query Match 56.9%; Score 33; DB 2; Length 503;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFYS 9
| ||| |
DB 280 HEHGSLY 286

RESULT 15
US-08-696-268B-2
; Sequence 2, Application US/08696268B
; Patent No. 5968752
; GENERAL INFORMATION:
; APPLICANT: ICHIGO, Hidenori
; APPLICANT: NISHITOH, Hideki
; APPLICANT: SAMPATH, Kuber T.
; TITLE OF INVENTION: NOVEL SIGNALING RECEPTOR FOR
; TITLE OF INVENTION: MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.

;
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,268B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-696-268B-2

Query Match 56.9%; Score 33; DB 2; Length 503;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSEY 9
| | | | |
Db 280 HERGSLY 286

Search completed: March 28, 2001, 07:02:01
Job time: 1340 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:36 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFY 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	67.2	113	2 S26468	Ig heavy chain V r
2	38	65.5	275	2 G75130	translation initia
3	38	65.5	275	2 D71087	probable translati
4	38	65.5	402	2 T25001	hypothetical prote
5	37	63.8	134	2 B72651	hypothetical prote
6	37	63.8	386	2 S51436	probable membrane
7	37	63.8	388	1 JCS461	cellulase (EC 3.2.
8	37	63.8	388	1 S43920	cellulase (EC 3.2.
9	37	63.8	405	2 F81273	hypothetical prote
10	37	63.8	2288	2 T29999	hypothetical prote
11	36	62.1	82	2 I51106	Major Histocompati
12	36	62.1	89	2 S38688	MHC class II histo
13	36	62.1	89	2 S38683	MHC class II histo
14	36	62.1	89	2 S38684	MHC class II histo
15	36	62.1	225	2 I47095	MHC class II OVAR
16	36	62.1	233	2 H82163	arginyl-tRNA-prote
17	36	62.1	446	2 T19625	hypothetical prote
18	36	62.1	470	2 H71667	glutamate--tRNA li
19	36	62.1	723	2 F83173	outer membrane pro
20	36	62.1	786	2 S37031	probable succinogl
21	35	60.3	9	2 S36850	Ig heavy chain V r
22	35	60.3	167	2 T16454	hypothetical prote
23	35	60.3	210	1 B69265	conserved hypothet
24	35	60.3	230	2 S46332	homeotic protein G
25	35	60.3	255	2 B71273	probable methionin
26	35	60.3	326	2 H65118	hypothetical adeni
27	35	60.3	326	2 S47248	site-specific DNA-
28	35	60.3	378	2 T11713	probable alpha-1,2
29	35	60.3	555	2 T47604	oligopeptide trans

30	35	60.3	555	2 T21028	hypothetical prote
31	35	60.3	575	2 T12094	beta-fructofuranos
32	35	60.3	583	2 S56680	beta-fructofuranos
33	35	60.3	592	2 JQ0991	beta-fructofuranos
34	35	60.3	592	2 S56681	beta-fructofuranos
35	35	60.3	592	2 S61503	beta-fructofuranos
36	35	60.3	593	2 T01575	beta-fructofuranos
37	35	60.3	686	2 D71292	probable DNA recom
38	35	60.3	790	2 S67803	probable membrane
39	34	58.6	80	2 S25050	Ig heavy chain V r
40	34	58.6	86	2 A81873	hypothetical prote
41	34	58.6	102	2 S25025	Ig heavy chain - m
42	34	58.6	106	2 S25036	Ig heavy chain V r
43	34	58.6	107	2 PL0080	Ig kappa chain V r
44	34	58.6	108	2 C72852	AcOrf-19 protein -
45	34	58.6	108	2 D44221	orf4 protein - Aut

ALIGNMENTS

RESULT 1

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ARHNYGSFY 9
||| |||:|
Db 93 ARHPYGNYY 101

RESULT 2

G75130
translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75130
R:anonymous; Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A:Reference number: A75001
A:Accession: G75130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:g545
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: aif2A; PAB0568
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 65.5%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY      3 HNYGSFYE 10
      |||||
Db      23 HNYGAFLE 30

RESULT  3
D71087
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: D71087
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137
A:Accession: D71087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:g3257375
A:Experimental source: strain OR3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0961
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match      65.5%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HNYGSFYE 10
      |||||
Db      23 HNYGAFLE 30

RESULT  4
T25001
Hypothetical protein T19C9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25001
R:Matthews, L.
Submitted to the EMBL Data Library, March 1997
A:Reference number: Z19967
A:Accession: T25001
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-402 <WIL>
A:Cross-references: EMBL:T292972; PIDN:CAB07486.1; GSPDB:GN00023; CESP:T19C9.8
A:Experimental source: clone T19C9
C:Genetics:
A:Gene: CESP:T19C9.8
A:Map position: 5
A:Introns: 54/1, 229/2; 337/2

Query Match      65.5%; Score 38; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HNYGSFYE 10
      |||||
Db      261 HDYNSFYE 268

RESULT  5
B72651
Hypothetical protein APE0639 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: B72651
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: B72651
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <KAW>
A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79610.1; PID:dl043396; PID:g
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0639

Query Match      63.8%; Score 37; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HNYGSFYE 10
      |||||
Db      26 HVGNFYE 33

RESULT  6
S51436
probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein I9470.1
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998
C:Accession: S51436
R:Wohldmann, P.
Submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 9470.
A:Reference number: S51414
A:Accession: S51436
A:Molecule type: DNA
A:Residues: 1-386 <WOH>
A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w
C:Genetics:
A:Gene: SGD:PEX13
A:Cross-references: SGD:S0004181; MIPS:YLR191w
A:Map position: 12R
C:Superfamily: SH3 homology
C:Keywords: transmembrane protein
F:264-280/Domain: transmembrane #status predicted <TMM>
F:313-367/Domain: SH3 homology <SH3>

Query Match      63.8%; Score 37; DB 2; Length 386;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 HNYGSFY 9
      |||||
Db      117 NNYGSFY 123

RESULT  7
JC5461
cellulase (EC 3.2.1.4) precursor - imperfect fungus (Humicola grisea)
N:Alternate names: endo-1,4-beta-glucanase; endoglucanase
C:Species: Humicola grisea var. thermolidea
C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 16-Jun-2000
C:Accession: JC5461
R:Takashima, S.; Nakamura, A.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 61, 245-250, 1997
A:Title: Cloning, sequencing, and expression of a thermostable cellulase gene of Humi
A:Reference number: JC5461
A:Accession: JC5461
A:Molecule type: DNA
A:Residues: 1-388 <TAK>

```

A:Cross-references: DDBJ:D84470; NID:G1304101; PIDN:BAAL2676.1; PID:gl304102
A:Experimental source: strain IF09854

C:Genetics:

A:Gene: egl2

A:Introns: 120/3; 369/1

C:Function:

A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cellulose

A:Pathway: cellulose degradation

C:Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-388/Product: cellulase #status predicted <MAT>

F:21-52/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 63.8%; Score 37; DB 1; Length 388;

Best Local Similarity 62.5%; Pred. No. 28;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFYE 10

||| |||

Db 175 HNFGRYYE 182

RESULT 8

S43920

cellulase (EC 3.2.1.4) precursor - imperfect fungus (Humicola insolens)

N:Alternate names: endo-1,4-beta-glucanase; endoglucanase

C:Species: Humicola insolens

C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 18-Jun-1999

C:Accession: S43920

R:Daiboge, H.; Heidt-Hansen, H. P.

Mol. Gen. Genet. 243, 253-260, 1994

A:Title: A novel method for efficient expression cloning of fungal enzyme genes.

A:Reference number: S43919; MUID:94247364

A:Accession: S43920

A:Molecule type: mRNA

A:Residues: 1-388 <DAL>

A:Cross-references: EMBL:X76046; NID:g505194; PIDN:CAA53631.1; PID:g505195

C:Genetics:

A:Gene: CMC3

C:Function:

A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cellulose

A:Pathway: cellulose degradation

C:Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-388/Product: cellulase #status predicted <MAT>

F:21-52/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 63.8%; Score 37; DB 1; Length 388;

Best Local Similarity 62.5%; Pred. No. 28;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFYE 10

||| |||

Db 175 HNFGRYYE 182

RESULT 9

F81273

hypothetical protein Cjl305c [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 20-Jun-2000

C:Accession: F81273

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: AB1250; MUID:20150912

A:Accession: F81273

A>Status: preliminary

A:Status: preliminary

A:Status: preliminary

A:Status: preliminary

A:Status: preliminary

A:Status: preliminary

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <PAR>

A:Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73732.1; PID:g696

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cjl305c

C:Superfamily: Campylobacter jejuni hypothetical protein Cjl306c

Query Match 63.8%; Score 37; DB 2; Length 405;

Best Local Similarity 62.5%; Pred. No. 29;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFYE 10

||| |||

Db 238 HSYGDYVE 245

RESULT 10

T29999

hypothetical protein ZC8.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T29999

R:Latrelle, P.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid ZC8.

A:Reference number: Z20719

A:Accession: T29999

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-2288 <LAT>

A:Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4

A:Experimental source: strain Bristol N2; clone ZC8

C:Genetics:

A:Gene: CESP:ZC8.4

A:Map position: X

A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 16

Query Match 63.8%; Score 37; DB 2; Length 2288;

Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSPY 9

.| ||| ||

Db 34 SRSNYGEFY 42

RESULT 11

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 9;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 12

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the HLA-DRB gene
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. NO. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 13

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the HLA-DRB gene
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. NO. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 14

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
C:Species: Galago senegalensis (northern lesser bushbaby)
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the HLA-DRB gene
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 15

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: I47095
R:Tabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility antigen (MHC) class II genes
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. NO. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 68 RHNYGVF 74

Search completed: March 28, 2001, 07:04:37
Job time: 1075 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:18 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNGSFYE 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	65.5	275	1 IF2A_PYRAB	Q9V0E4 pyrococcus
2	38	65.5	275	1 IF2A_PYRHO	O58655 pyrococcus
3	37	63.8	386	1 PEXD_YEAST	P06667 saccharomyc
4	36	62.1	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
5	36	62.1	786	1 EXOP_RHIME	P33698 rhizobium m
6	35	60.3	255	1 AMPM_TREPA	O83814 treponema p
7	35	60.3	294	1 YHDJ_ECOLI	P28638 escherichia
8	35	60.3	367	1 LHX4_MOUSE	P53776 mus musculus
9	35	60.3	583	1 INV3_DAUCA	Q39693 daucus caro
10	35	60.3	592	1 INV2_DAUCA	P26792 daucus caro
11	35	60.3	592	1 RECQ_TREPA	Q39692 daucus caro
12	35	60.3	686	1 Y019_NPVAC	P96130 treponema p
13	34	58.6	108	1 IPYR_PICPA	P41424 autographa
14	34	58.6	284	1 IPYR_KLJOLA	O13505 pichia past
15	34	58.6	286	1 IPYR_KLJOLA	P13998 kluyveromyc
16	34	58.6	286	1 IPYR_YEAST	P00817 saccharomyc
17	34	58.6	564	1 LDHD_HAETN	P45295 haemophilus
18	34	58.6	718	1 LSP2_DROME	Q24388 drosophila
19	34	58.6	887	1 QVAL_DROME	Q23989 drosophila
20	33	56.9	89	1 CFA_CITFR	P45509 citrobacter
21	33	56.9	347	1 UL33_HSV6U	P52380 herpes simp
22	33	56.9	364	1 SUCC_METJA	Q57663 methanococc
23	33	56.9	448	1 NCAP_CVHOC	P33469 human coron
24	33	56.9	473	1 SYE_AQUAE	O67271 aquifex aeo
25	33	56.9	494	1 RNHI_CRIFA	Q07762 crithidia f
26	33	56.9	512	1 PNTA_HAETN	P43842 haemophilus
27	33	56.9	514	1 LIM_HALRO	Q25132 halocynthia
28	33	56.9	572	1 NH25_CAEEL	Q19345 caenorhabdi
29	33	56.9	713	1 HS90_EIMTE	O44001 elmeria ten
30	33	56.9	715	1 ADSP_BOVIN	Q28046 bos taurus
31	33	56.9	725	1 ADSP_BOVIN	Q96412 dianthus ca
32	33	56.9	826	1 VILI_CHICK	P02640 gallus gall
33	33	56.9	1386	1 RPOD_MARPO	P06274 marchantia

ALIGNMENTS

RESULT 1

ID IF2A_PYRAB STANDARD; PRT; 275 AA.
AC Q9V0E4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN EIF2A OR PAB0568.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN
RP SEQUENCE FROM N.A.
RC STRAIN-ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.

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EMBL; AJ248285; CAB49760.1; -
INTERPRO; IPR003029; -
DR PFAM; PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis; RNA-binding.
FT DOMAIN 8 83 SI MOTIF.
SQ SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match 65.5%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
|||:|
Db 23 HNYGAFLE 30

RESULT 2

ID IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN EIF2A OR PH0961.
 OS PYROCoccus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE: 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuwa H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
 CC
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 CC
 CC EMBL: AP000004; BAA30058.1; -
 DR INTERPRO: IPR003029; -
 DR PFAM: PF00575; SI; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 83 SI MOTIF.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FB436 CRC64;

 Query Match 65.5%; Score 38; DB 1; Length 275;
 Best Local Similarity 75.0%; Pred. No. 3.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 3 HNYGSFYE 10
 Db 23 HNYGAFLE 30

 RESULT 3
 PEXD_YEAST
 ID PEXD_YEAST STANDARD; PRT; 386 AA.
 AC P80667;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).
 GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97011156.
 RA Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
 RA Tabak H.F., Distel B.;
 RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
 RT protein pex13p functions as a docking site for Pex5p, a mobile
 RT receptor for the import pex1-containing proteins.";
 RL J. Cell Biol. 135:97-109(1996).

RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneses S.,
 RA Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L.,
 RA Taich A., Trevaskis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=S288C;
 RX MEDLINE: 97011157.
 RA Erdmann R., Blobel G.;
 RT "Identification of Pex13p a peroxisomal membrane receptor for the
 RT PTS1 recognition factor.";
 RL J. Cell Biol. 135:111-121(1996).
 CC -1- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
 CC WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
 CC (PAS10/PEX5).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC
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 CC
 CC EMBL: S82571; AAB46885.1; -
 DR EMBL: U37420; AAB79308.1; -
 DR EMBL: U17246; AAB67453.1; -
 DR EMBL: U14913; AAB67448.1; -
 DR HSSP: Q06187; IAWW.
 DR SGD: S0004181; PEX13.
 DR INTERPRO: IPR001452; -
 DR PFAM: PF00018; SH3; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS00002; SH3; 1.
 KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
 FT DOMAIN 1 263 LUMENAL (POTENTIAL).
 FT TRANSMEM 264 280 POTENTIAL.
 FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 306 372 SH3.
 SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;

 Query Match 63.8%; Score 37; DB 1; Length 386;
 Best Local Similarity 85.7%; Pred. No. 8.6;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 HNYGSFY 9
 Db 117 HNYGSFY 123

 RESULT 4
 SYE2_RICPR
 ID SYE2_RICPR STANDARD; PRT; 470 AA.
 AC Q9ZCT8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
 DE (GLURS 2).
 GN GLTX2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsia.

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL; AJ235272; CAAL5066.1; -
CC HSSP; P27000; IGLN.
CC DR INTERPRO; IPR000924; -
CC DR INTERPRO; IPR001412; -
CC DR PFAM; PF00749; tRNA-synt_lc; 1.
CC DR PRINTS; PRO0987; TRNASYNTHGLU.
CC DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 62.1%; Score 36; DB 1; Length 470;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
   |||||
Db 31 ARHNNKGF 39

RESULT 5
EXOP_RHIME STANDARD; PRT; 786 AA.
AC P33698;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUCCINOGLYCAN BIOSYNTHESIS TRANSPORT PROTEIN EXOP.
GN EXOP.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSym (megaplasmid 2).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE; 94042869.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Family of glycosyl transferases needed for the synthesis of
RT succinoglycan by Rhizobium meliloti.";
RL J. Bacteriol. 175:7033-7044(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE; 94042870.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;

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```

RT "Genes needed for the modification, polymerization, export, and
RT processing of succinoglycan by Rhizobium meliloti: a model for
RT succinoglycan biosynthesis.";
RL J. Bacteriol. 175:7045-7055(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RX MEDLINE; 94067019.
RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes
RT involved in exopolysaccharide biosynthesis and mapping of promoters
RT located on the exoKLAMONP fragment.";
RL Mol. Gen. Genet. 241:367-379(1993).
CC -1- PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: SOME, TO B.SOLANACEARUM EPSB.
CC
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CC
CC EMBL; L20758; AAA16042.1; -
CC DR EMBL; 222636; CAA80349.1; -
CC DR PIR; B49349; B49349.
CC DR PIR; S37031; S37031.
CC DR PIR; S39960; S39960.
CC KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding;
CC Plasmid.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 66 POTENTIAL.
FT DOMAIN 67 889 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 690 711 POTENTIAL.
FT DOMAIN 712 786 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 583 590 ATP (POTENTIAL).
SQ SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Match 62.1%; Score 36; DB 1; Length 786;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
   |||||
Db 768 RHRYGKY 775

RESULT 6
AMPM_TREPA STANDARD; PRT; 255 AA.
AC O83814;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE METHIONINE AMINOPEPTIDASE (EC 3.4.11.18) (MAP) (PEPTIDASE M).
GN MAP OR TP0842.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE; 98332770.
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis

```


RT spirochete.;
 RL Science 281:375-388(1998).
 CC -!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
 CC PROTEINS.
 CC -!- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)O = L-METHIONINE +
 CC PEPTIDE.
 CC -!- COFACTOR: COBALT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24A; ALSO KNOWN AS THE
 CC MAP FAMILY 1.
 CC -----
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 CC -----
 DR EMBL; A6001255; AAC65810.1;
 DR TIGR; TP0842;
 DR INTERPRO: IPR000994;
 DR INTERPRO: IPR001714;
 DR INTERPRO: IPR002467;
 DR PFAM; PF00557; Peptidase_M24; 1.
 DR PRINTS; PR00599; MAPEPTIDASE.
 DR PROSITE; PS00680; MAP_1; 1.
 KW Amino-peptidase; Hydrolase; Cobalt.
 FT METAL 93 93 COBALT (BY SIMILARITY).
 FT METAL 104 104 COBALT (BY SIMILARITY).
 FT METAL 174 174 COBALT (BY SIMILARITY).
 FT METAL 201 201 COBALT (BY SIMILARITY).
 FT METAL 233 233 COBALT (BY SIMILARITY).
 SQ SEQUENCE 255 AA; 27316 MW; 4EDE582C67F3526A CRC64;

 Query Match 60.3%; Score 35; DB 1; Length 255;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ARHNYGSFYE 10
 III : I II
 DB 154 ARHFGVWVE 163

 RESULT 7
 ID YHDL_ECOLI STANDARD; PRT; 294 AA.
 AC P28638;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HYPOTHETICAL ADENINE-SPECIFIC METHYLASE IN FIS-ENVIR INTERGENIC REGION
 DE (EC 2.1.1.72) (ORF2).
 GN YHDL.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE OF 1-98 FROM N.A.
 RX MEDLINE; 93094136.
 RA Ball C.A., Osuna R., Ferguson K.C., Johnson R.C.;
 RT "Dramatic changes in Fis levels upon nutrient upshift in Escherichia
 RT coli.";

RL J. Bacteriol. 174:8043-8056(1992).
 RP [3]
 RN SEQUENCE OF 1-11 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE; 88217925.
 RA Johnson R.C., Ball C.A., Pfeiffer D., Simon M.I.;
 RT "Isolation of the gene encoding the Hin recombinational enhancer
 RT binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3484-3488(1988).
 CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE =
 CC S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPURINE.
 CC -!- SIMILARITY: BELONGS TO THE N-6 ADENINE-SPECIFIC DNA METHYLASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; U18997; AAA58066.1; ALT_INIT.
 DR EMBL; AE000405; AAC76294.1; ALT_INIT.
 DR EMBL; M95784; AAA23784.1; ALT_INIT.
 DR EMBL; J03245; AAA83857.1;
 DR PIR; D47043; D47043.
 DR HSP; P11409; IBOO.
 DR ECGENE; EG11498; YHDL.
 DR INTERPRO: IPR001091;
 DR INTERPRO: IPR002052;
 DR INTERPRO: IPR002295;
 DR INTERPRO: IPR002941;
 DR PFAM; PF01555; N6_M4_Mtase; 1.
 DR PRINTS; PR00506; D21N6MTFRASE.
 DR PRINTS; PR00508; S21N4MTFRASE.
 DR PROSITE; PS00092; N6_MTFASE; 1.
 KW Hypothetical protein; Transferase; Methyltransferase.
 FT CONFLICT 28 28 K -> N (IN REF 2).
 SQ SEQUENCE 294 AA; 33397 MW; 6BCC49D9A571884B CRC64;

 Query Match 60.3%; Score 35; DB 1; Length 294;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ARHNYGSFYE 10
 I : III II
 DB 119 AKKHYSWYE 128

 RESULT 8
 ID LHX4_MOUSE STANDARD; PRT; 367 AA.
 AC P53776; O08916; O9R280;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE LIM/HOMEOBOX PROTEIN LHX4.
 GN LHX4 OR GSH4 OR GSH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sakai T., Kawaguchi A., Nagashima M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 7-196 FROM N.A.
 RC STRAIN-FVB/N; TISSUE=EMBRYO;
 RX MEDLINE; 97432832.
 RA Yamashita T., Moriyama K., Sheng H.Z., Westphal H.;
 RT "Lhx4, a LIM homeobox gene.";

Genomics 44:144-146(1997).

[3] SEQUENCE OF 136-367 FROM N.A.

RL MEDLINE; 94298779.

RA Li H., Witte D.P., Branford W.W., Aronow B.J., Weinstein M., Kaur S.,

RA Wert S., Singh G., Schreiner C.M., Whitsett J.A., Scott W.J. Jr.,

RA Potter S.S.

RT "Gsh-4 encodes a LIM-type homeodomain, is expressed in the developing

RT central nervous system and is required for early postnatal

RT survival."

RL EMOB J. 13:2876-2885(1994).

CC -!- FUNCTION: MAY PLAY A CRITICAL ROLE IN THE DEVELOPMENT OF

CC RESPIRATORY CONTROL MECHANISMS AND IN THE NORMAL GROWTH AND

CC MATURATION OF THE LUNG.

CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

CC -!- TISSUE SPECIFICITY: TRANSIENT EXPRESSION IN VENTROLATERAL REGIONS

CC OF THE DEVELOPING NEURAL TUBE AND HINDRAIN.

CC -!- SIMILARITY: TO OTHER HOMEODOMAIN DOMAINS. BELONGS TO THE LIM

CC SUBFAMILY.

CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC

CC IONS.

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CC -----

DR EMBL; AF135415; AAC30125.1; -

DR EMBL; U89343; AAC53336.1; -

DR EMBL; S71659; AAB31260.1; -

DR HSSP; P02836; 1HDD.

DR MCD; MGI:101776; LHX4.

DR INTERPRO; IPR001356; -

DR INTERPRO; IPR001781; -

DR PFAM; PF00412; LIM; 2.

DR PFAM; PF00046; homeobox; 1.

DR PROSITE; PS00478; LIM_DOMAIN_1; 2.

DR PROSITE; PS50023; LIM_DOMAIN_2; 2.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS50071; HOMEBOX_2; 1.

KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM motif;

KW Metal-binding; Zinc; Transcription regulation.

FT DOMAIN 7 57 LIM.

FT DOMAIN 66 120 LIM.

FT DNA_BIND 134 193 HOMEBOX.

FT SEQUENCE 367 AA; 40811 MW; 86553C7014A0E27C CRC64;

Query Match 60.3%; Score 35; DB 1; Length 367;

Best Local Similarity 55.6%; Pred. No. 20;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10

Db 198 RHRWGQFYK 206

||:|:|:

RESULT 9

INV3_DAUCA STANDARD; PRT; 583 AA.

AC Q39693;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3 PRECURSOR (EC 3.2.1.26)

DE (SUCROSE-6-PHOSPHATASE, INSOLUBLE ISOENZYME 3) (CELL WALL BETA-FRUCTOSIDASE 3).

GN INV3.

OS Daucus carota (Carrot).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

[1] SEQUENCE FROM N.A.

RC STRAIN=CV. QUEEN ANNE'S LACE;

RX MEDLINE; 95306787

RA Lorenz K., Lienhard S., Sturm A.

RT "Structural organization and differential expression of carrot beta-fructofuranosidase genes: identification of a gene coding for a flower bud-specific isozyme."

RT Plant Mol. Biol. 28:189-194(1995).

RL -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.

CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.

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CC -----

DR EMBL; X78423; CAA55188.1; -

DR INTERPRO; IPR001362; -

DR PFAM; PF00251; Glyco_hydro_32; 1.

DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.

KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.

FT SIGNAL 1 ? POTENTIAL.

FT PROPEP ? ?

FT CHAIN ? 583 BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3.

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 60.3%; Score 35; DB 1; Length 583;

Best Local Similarity 62.5%; Pred. No. 32;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9

Db 313 RYDYGNYF 320

||:|:|:

RESULT 10

INV1_DAUCA STANDARD; PRT; 592 AA.

AC P26792.

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 PRECURSOR (EC 3.2.1.26)

DE (SUCROSE-6-PHOSPHATASE, INSOLUBLE ISOENZYME 1) (CELL WALL BETA-FRUCTOSIDASE 1).

GN INV1.

OS Daucus carota (Carrot).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

[1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=CV. QUEEN ANNE'S LACE;

RX MEDLINE; 93005650.

RA Sturm A., Chrispeels M.J.;

RT "cDNA cloning of carrot extracellular beta-fructosidase and its

RT expression in response to wounding and bacterial infection.";

RL Plant Cell 2:1107-1119(1990).

RN [2]

RA SEQUENCE FROM N.A.

RX MEDLINE; 94035200.

RY Ramloch-Lorenz K., Knudsen S., Sturm A.;

RA "Molecular characterization of the gene for carrot cell wall beta-fructofuranosidase.";

RT Plant J. 4:545-554(1993).

RL -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.

CC -1- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.

CC -1- INDUCTION: IN RESPONSE TO WOUNDING AND BACTERIAL INFECTION.

CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.

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CC EMBL; M58362; AAA03516.1; -.

DR EMBL; X69321; CAA49162.1; -.

DR PIR; J00991; J00991.

DR INTERPRO; IPR001362; -.

DR PFAM; PF00251; Glyco_hydro_32; 1.

DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.

KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.

FT SIGNAL 1 31 OR 39 (POTENTIAL).

FT PROPEP 32 48 OR 40 (POTENTIAL).

FT CHAIN 49 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1.

FT ACT_SITE 74 74 BY SIMILARITY.

FT CARBOHYD 170 170 N-LINKED (GLCNAC. .) (COMPLEX).

FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (COMPLEX).

FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (HIGH MANNOSE).

FT CARBOHYD 570 570 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 133 133 R -> W (IN REF. 2).

FT CONFLICT 487 487 A -> V (IN REF. 2).

SQ SEQUENCE 592 AA; 66813 MW; E3DF85355D277D0C CRC64;

Query Match 60.3%; Score 35; DB 1; Length 592;

Best Local Similarity 62.5%; Pred. No. 33;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9

DB 321 RYDYGNYF 328

RESULT 11

INV2_DAUCA

ID INV2_DAUCA STANDARD; PRT; 592 AA.

AC Q39692;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2 (CELL WALL BETA-FRUCTOSIDASE 2).

DE (SUCROSE-6-PHOSPHATE HYDROLASE 2) (INVERTASE 2)

GN INV2

OS Daucus carota (Carrot).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. QUEEN ANNE'S LACE;

RX MEDLINE; 95306787.

RA Lorenz K., Lienhard S., Sturm A.;

RT "Structural organization and differential expression of carrot beta-fructofuranosidase genes: identification of a gene coding for a flower bud-specific isozyme.";

RL Plant Mol. Biol. 28:189-194(1995).

CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.

CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.

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CC EMBL; X78424; CAA55189.1; -.

DR INTERPRO; IPR001362; -.

DR PFAM; PF00251; Glyco_hydro_32; 1.

DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.

KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.

FT SIGNAL 1 ? POTENTIAL.

FT PROPEP ? ? POTENTIAL.

FT CHAIN ? 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2.

FT ACT_SITE 75 75 BY SIMILARITY.

FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 310 310 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 568 568 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 592 AA; 67397 MW; 2734603836709133 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 592;

Best Local Similarity 62.5%; Pred. No. 33;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9

DB 320 RYDYGNYF 327

RESULT 12

RECG_TREPA

ID RECG_TREPA STANDARD; PRT; 686 AA.

AC P96130;

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1.1);

GN RECG OR TP0687.

OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-NICHOLS;

RA Stamm L.V., Barnes N.Y.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-NICHOLS;

RX MEDLINE; 98332770.

RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,

RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 CC -1- FUNCTION: CRITICAL ROLE IN RECOMBINATION AND DNA REPAIR. HELP
 CC PROCESS HOLLIDAY JUNCTION INTERMEDIATES TO MATURE PRODUCTS BY
 CC CATALYSING BRANCH MIGRATION. HAS A DNA UNWINDING ACTIVITY
 CC CHARACTERISTIC OF A DNA HELICASE WITH A 3' TO 5' POLARITY. RECG
 CC UNWIND BRANCHED DUPLEX DNA (Y-DNA) (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RECG SUBFAMILY OF HELICASES.
 CC
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 CC
 DR EMBL; U70661; AAB38707.1; -;
 DR EMBL; AE001243; AAC65656.1; -;
 DR TIGR; TP0687; -;
 DR INTERPRO; IPR001410; -;
 DR INTERPRO; IPR001650; -;
 DR PFAM; PF00270; DEAD; 1;
 DR PFAM; PF00271; helicase_C; 1;
 KW Helicase; DNA repair; ATP-binding; DNA recombination; DNA-binding.
 FT NP_BIND 298 305 ATP (POTENTIAL).
 FT SITE 399 402 DEQ BOX.
 SQ SEQUENCE 686 AA; 77196 MW; B05AFCDG6FA046B0 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 686;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YGSFYE 10
 Db 116 YGSFYE 121

RESULT 13
 Y019_NPVAC
 ID Y019_NPVAC STANDARD; PRT; 108 AA.
 AC P41424;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 12.2 KDA PROTEIN IN EGT-IP1 INTERGENIC REGION (ORF4).
 OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 RN [1]
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 CC
 DR EMBL; AJ001000; CAA04453.1; -;
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -;
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolyase; Magnesium.
 FT INIT_MET 0
 FT ACT_SITE 56 56
 FT BINDING 78 78
 FT BY SIMILARITY.
 FT PROBABLE.
 FT INORGANIC PYROPHOSPHATE (BY SIMILARITY).

RL Virology 191:1003-1008(1992).
 CC -1- SIMILARITY: TO CORRESPONDING ORF IN OPMPV.
 CC
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 CC
 DR EMBL; L22858; AAA66649.1; -;
 DR EMBL; M96361; AAA66789.1; -;
 DR PIR; D44221; D44221.
 KW Hypothetical protein.
 FT CONFLICT 6 A -> R (IN REF. 2).
 SQ SEQUENCE 108 AA; 12162 MW; 8363B15DF72486A1 CRC64;
 Query Match 58.6%; Score 34; DB 1; Length 108;
 Best Local Similarity 60.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ARHNYGSFYE 10
 Db 25 ANRHSSEFYE 34
 RESULT 14
 IPYR_PICPA
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 CC SEQUENCE FROM N.A.
 RC STRAIN-NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -1- MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AJ001000; CAA04453.1; -;
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -;
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolyase; Magnesium.
 FT INIT_MET 0
 FT ACT_SITE 56 56
 FT BINDING 78 78
 FT BY SIMILARITY.
 FT PROBABLE.
 FT INORGANIC PYROPHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNYGSF 8
Db 91 HNYGAF 96

OY 3 HNYGSF 8
Db 91 HNYGAF 96

Search completed: March 28, 2001, 07:35:19
Job time: 156 sec

RESULT 15

IPYR_KLULA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1 OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E. COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X14230; CAA32446.1; -
DR FIR; S07894; PWKL.
DR HSSP; P00817; LWGI.
DR INTERPRO; IPR001596; -
DR PFAM; PF00719; Pyrophosphatase; 1.
DR PROSITE; PS00387; PPASE; 1.
KW Hydrolase; Magnesium.
FT INIT_MET 0 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 58.6%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:37 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFYE 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	74.1	839	10	Q9LIE5 arabidopsis
2	38	65.5	89	7	Q19495
3	38	65.5	402	5	O45792 caenorhabdi
4	37	63.8	134	1	O45792 caenorhabdi
5	37	63.8	149	2	Q9YED6 aeropyrum p
6	37	63.8	388	3	Q9ZBB5 streptococ
7	37	63.8	388	3	Q12620 humicola gr
8	37	63.8	405	2	Q12624 humicola in
9	37	63.8	483	10	Q9PMZ4 campylobact
10	37	63.8	2288	5	O22861 arabidopsis
11	36	62.1	39	7	Q23081 caenorhabdi
12	36	62.1	39	7	P79474 cervus elap
13	36	62.1	39	7	P79477 cervus elap
14	36	62.1	39	7	P79478 cervus elap
15	36	62.1	39	7	P79479 cervus elap
16	36	62.1	74	6	Q9TTM4 bos taurus
17	36	62.1	76	7	Q9TFC2 macaca mula
18	36	62.1	78	6	O97835 ovis aries
19	36	62.1	78	6	O97839 ovis aries
					O97844 ovis aries

20	36	62.1	78	6	O97968	O97968 ovis aries
21	36	62.1	78	7	O9MWT6	O9MWT6 leopardus p
22	36	62.1	78	7	O9MWT5	O9MWT5 leopardus p
23	36	62.1	78	7	O9MWT4	O9MWT4 leopardus p
24	36	62.1	79	7	O19191	O19191 prionailuru
25	36	62.1	79	7	O19192	O19192 prionailuru
26	36	62.1	79	7	O19380	O19380 felis silve
27	36	62.1	79	7	O19381	O19381 felis silve
28	36	62.1	79	7	O19382	O19382 felis silve
29	36	62.1	79	7	O19396	O19396 felis silve
30	36	62.1	79	7	O19397	O19397 felis silve
31	36	62.1	79	7	O19405	O19405 felis silve
32	36	62.1	79	7	O19406	O19406 felis silve
33	36	62.1	79	7	O19407	O19407 felis silve
34	36	62.1	79	7	O19408	O19408 felis silve
35	36	62.1	79	7	O19435	O19435 felis silve
36	36	62.1	79	7	O9MX19	O9MX19 leopardus p
37	36	62.1	79	7	O9MX13	O9MX13 leopardus p
38	36	62.1	79	7	O9MX03	O9MX03 leopardus p
39	36	62.1	79	7	O9MX00	O9MX00 leopardus p
40	36	62.1	79	7	O9MW29	O9MW29 leopardus p
41	36	62.1	79	7	O9MW28	O9MW28 leopardus p
42	36	62.1	79	7	O9MW27	O9MW27 leopardus p
43	36	62.1	79	7	O9MWY9	O9MWY9 leopardus p
44	36	62.1	79	7	O9MWY8	O9MWY8 leopardus p
45	36	62.1	79	7	O9MWY6	O9MWY6 leopardus p

ALIGNMENTS

RESULT 1
Q9LIE5 PRELIMINARY; PRT; 839 AA.
AC Q9LIE5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE
DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones".
RL DNA Res. 7:217-221(2000).
DR EMBL; AP001306; BAB03065.1; -.
SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 74.1%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSF 8
Db 274 SRHNYGSF 281

RESULT 2
O19495

```

ID 019495 PRELIMINARY; PRT; 89 AA.
AC 019495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR INTERPRO; IPR000353; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;

Query Match 65.5%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHYGSF 8
DB 75 RHYGDF 81
|||||

RESULT 3
O45792 PRELIMINARY; PRT; 402 AA.
AC O45792;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE T19C9.8 PROTEIN.
GN T19C9.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL Nature 368:32-38(1994).
DR EMBL; Z92972; CAB07486.1; -.
SQ SEQUENCE 402 AA; 45029 MW; 072C5F89A4DE0C89 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 402;

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Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
DB 261 HDYNSFYE 268
|||||

RESULT 4
Q9YED6 PRELIMINARY; PRT; 134 AA.
ID Q9YED6;
AC Q9YED6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HYPOTHETICAL 14.8 KDA PROTEIN APE0639.
GN APE0639.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI;
RX MEDLINE=99310339; PubMed=10382966;
RA Kwarabavasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S., Anka A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K., Kubota K., Nakamura Y.,
RA Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000060; BAA79610.1; -.
KW Hypothetical protein.
SQ SEQUENCE 134 AA; 14845 MW; 57942011F9A404C4 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
DB 26 HVGNFYE 33
|||||

RESULT 5
Q9ZBB5 PRELIMINARY; PRT; 149 AA.
ID Q9ZBB5;
AC Q9ZBB5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE HYPOTHETICAL 17.5 KDA PROTEIN.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPI000; TRANSPOSON=TN5252;
RX MEDLINE=98154299; PubMed=9473447;
RA Sampath J., Vijayakumar M.N.;
RT "Identification of a DNA cytosine methyltransferase gene in
RT conjugative transposon Tn5252.";
RL Plasmid 39:63-76(1998).
DR EMBL; L29323; AAC98423.1; -.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 17465 MW; 5DEFCFBAB306B131 CRC64;

```

Query/Match 63.8%; Score 37; DB 2; Length 149;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
: : : : :
Db 52 KHNYPLFYE 60

RESULT 6
Q12620 Q12620 PRELIMINARY; PRT; 388 AA.
AC Q12620;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CELLULASE (EC 3.2.1.4) (ENDOGLUCANASE) (ENDO-1,4-BETA-GLUCANASE)
DE (CARBOXYMETHYL CELLULOSE).
OS Humicola grisea.
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Humicola.
OX NCBI_TaxID=5527;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IFO9854;
RA Takashima S., Nakamura A., Masaki H., Uozumi T.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
LINKAGES IN CELLULOSE.
CD EMBL; D84470; BAA12676.1; -;
DR HSP; P00725; IAZ6.
DR INTERPRO; IPR000254; -;
DR INTERPRO; IPR001547; -;
DR PFAM; PF00150; cellulase; 1.
DR PFAM; PF00734; CBD.1; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PRODOM; PD001821; -; 1.
KW Hydrolase; Glycosidase.
SQ SEQUENCE 388 AA; 42606 MW; D103247F0E9FCF50 CRC64;

Query Match 63.8%; Score 37; DB 3; Length 388;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
: : : : :
Db 175 HNFGRYIE 182

RESULT 7
Q12624 Q12624 PRELIMINARY; PRT; 388 AA.
AC Q12624;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CELLULASE PRECURSOR (EC 3.2.1.4) (ENDOGLUCANASE) (ENDO-1,4-BETA-
GLUCANASE) (CARBOXYMETHYL CELLULOSE).
GN CMC3.
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Humicola.
OX NCBI_TaxID=34413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94247364; PubMed=8190078;
RA Dalboeue H., Hansen H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
genes.";
RL Mol. Gen. Genet. 243:253-260(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
LINKAGES IN CELLULOSE.
CD EMBL; X76046; CAA53631.1; -;
DR HSP; P00725; IAZ6.

DR INTERPRO; IPR000254; -;
DR INTERPRO; IPR001547; -;
DR PFAM; PF00150; cellulase; 1.
DR PFAM; PF00734; CBD.1; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PRODOM; PD001821; -; 1.
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 16 POTENTIAL.
SQ SEQUENCE 388 AA; 42563 MW; C7CF349DACC10690 CRC64;

Query Match 63.8%; Score 37; DB 3; Length 388;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
: : : : :
Db 175 HNFGRYIE 182

RESULT 8
Q9PMZ4 Q9PMZ4 PRELIMINARY; PRT; 405 AA.
AC Q9PMZ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHETICAL PROTEIN CJI305C.
GN CJI305C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karleyshev A., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139078; CAB73732.1; -;
KW Hypothetical protein.
SQ SEQUENCE 405 AA; 47315 MW; D96641B34301DF0A CRC64;

Query Match 63.8%; Score 37; DB 2; Length 405;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
: : : : :
Db 238 HSYGDYIE 245

RESULT 9
O22861 O22861 PRELIMINARY; PRT; 483 AA.
AC O22861;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HYPOTHETICAL PROTEIN.
GN T01024.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;


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RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Tschudy M.M., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002335; AAB64341.1;
DR INTERPRO; IPR001005;
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
SQ SEQUENCE 483 AA; 54491 MW; C665DCA7ELE4BAFB CRC64;

Query Match 63.8%; Score 37; DB 10; Length 483;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
DB 288 HQYASYE 295

RESULT 10
Q23081 ID Q23081 PRELIMINARY; PRT; 2288 AA.
AC Q23081;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK33H8.3.
GN ZC8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonnenhammer E., Staden K., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).

[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RA Latreille P., Bradshaw H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

[3]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

[4]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64862; AAB52624.1;
SQ SEQUENCE 2288 AA; 262172 MW; 06D1700A0F4ACD2F CRC64;

Query Match 63.8%; Score 37; DB 5; Length 2288;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;

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Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
DB 34 SRSNYGEFY 42

RESULT 11
P79474 ID P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;

[1]
RN SEQUENCE FROM N.A.
RP Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1;
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 62.1%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 25 RHNYGVF 31

RESULT 12
P79477 ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;

[1]
RN SEQUENCE FROM N.A.
RP Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1;
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 62.1%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 25 RHNYGVF 31

```

RESULT 13

P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 62.1%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 6.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 I I I I I I
 DB 25 RHNYGVF 31

RESULT 14

P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swabrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 62.1%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 6.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 I I I I I I
 DB 25 RHNYGVF 31

RESULT 15

Q9TTM4 PRELIMINARY; PRT; 74 AA.
 AC Q9TTM4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE MHC(BOLA) CLASS II DR-BETA CHAIN (FRAGMENT).

GN BOLA-DRB3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE BLACK;
 RA Takeshima S., Ikegami M., Morita M., Nakai Y., Aida Y.;
 RT "Identification of BOLA-DRB3 exon 2 of Japanese black cattle.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033388; BAA85470.1; -;
 DR INTERPRO; IPR000353; -;
 DR PFAM; PF00969; MHC_II_beta; 1.
 FT NON_TER 1 1
 FT NON_TER 74 74
 SQ SEQUENCE 74 AA; 9132 MW; C5834842F0E38BA6 CRC64;

Query Match 62.1%; Score 36; DB 6; Length 74;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 I I I I I I
 DB 68 RHNYGVF 74

Search completed: March 28, 2001, 07:53:38
 Job time: 531 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:55 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNGSFYE 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36.*

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5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
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21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	19	W76039
2	53	91.4	10	19	W76040
3	53	91.4	10	19	W76023
4	49	84.5	10	19	W76027
5	48	82.8	10	19	W76038
6	46	79.3	10	19	W76022
7	46	79.3	10	19	W76024
8	46	79.3	10	19	W76025
9	46	79.3	10	19	W76026
10	46	79.3	10	19	W76028
11	46	79.3	10	19	W76029
12	46	79.3	10	19	W76030
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti
					LM609 grafted anti

13	46	79.3	10	19	W76010	LM609 grafted anti
14	46	79.3	117	19	W76001	Vitaxin antibody h
15	46	79.3	117	19	W76003	LM609 antibody hea
16	46	79.3	117	20	Y06381	Murine monoclonal
17	46	79.3	117	20	Y06387	Humanised LM609 an
18	46	79.3	118	20	Y06384	Humanised LM609 an
19	46	79.3	118	20	Y06385	Humanised LM609 an
20	46	79.3	118	20	Y06386	Humanised LM609 an
21	46	79.3	118	20	Y06383	Humanised LM609 an
22	46	79.3	130	20	Y06379	Murine monoclonal
23	43	74.1	10	19	W76021	LM609 grafted anti
24	41	70.7	10	19	W76037	LM609 grafted anti
25	41	70.7	10	19	W76020	LM609 grafted anti
26	38	65.5	110	20	W84099	Vitronectin alpha-
27	38	65.5	117	20	W84093	Murine vitronectin
28	38	65.5	117	20	W84097	Humanised anti-alp
29	37	63.8	8	20	Y06371	Murine monoclonal
30	37	63.8	86	19	W60938	Streptococcus pneu
31	37	63.8	119	19	Y86109	S. pneumoniae derl
32	36	62.1	117	16	R79157	Human IgE receptor
33	36	62.1	117	16	R79155	Human IgE receptor
34	36	62.1	117	18	W27357	Heavy chain variab
35	36	62.1	117	18	W27526	Heavy chain variab
36	36	62.1	117	18	W27354	Heavy chain variab
37	36	62.1	239	20	W73874	Human antiFc epsil
38	36	62.1	242	20	W73876	Human antiFc epsil
39	34	58.6	30	21	Y81870	Yeast IPPI protein
40	34	58.6	36	21	Y76271	Fragment of human
41	34	58.6	256	13	R22568	SCFVB18 construct
42	34	58.6	256	13	R22583	SCFVB18 construct
43	34	58.6	256	13	R22584	SCFVB18 construct
44	34	58.6	256	13	R22585	SCFVB18 construct
45	34	58.6	256	13	R22586	SCFVB18 construct

ALIGNMENTS

```
RESULT 1
W76039
ID W76039 standard; Protein; 10 AA.
XX
AC W76039;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarily determining region.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
N-PSDB; V49876.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
```

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 43; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC angiogenesis and restenosis of alphavbeta3-mediated disease, specifically
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYE 10
 |||||
 Db 1 arhnygsfye 10

RESULT 2

ID W76040 standard; Protein; 10 AA.

XX W76040;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #16.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49877.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC angiogenesis and restenosis of alphavbeta3-mediated disease, specifically
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 91.4%; Score 53; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0025;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9

|||||

Db 1 arhnygsfy 9

RESULT 3

ID W76023 standard; Protein; 10 AA.

XX W76023;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #5.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49860.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC angiogenesis and restenosis of alphavbeta3-mediated disease, specifically
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 91.4%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
 Db 1 arhnygsfy 9
 |||||

RESULT 4

ID W76027 standard; Protein; 10 AA.

XX AC

XX AC

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX OS

XX OS

XX PN

XX PD

XX PD

XX PF

XX PR

XX PA

XX PI

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

Query Match 84.5%; Score 49; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
 Db 1 arhnygsfy 10
 |||||

RESULT 5

ID W76038 standard; Protein; 10 AA.

XX AC

XX AC

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #14.

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX OS

XX OS

XX PN

XX PD

XX PD

XX PF

XX PR

XX PA

XX PI

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 macular degeneration; osteoporosis; primer; V-H region; CDR;
 complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49875.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

XX LM609, also related nucleic acid, used to treat, prevent or diagnose

XX angiogenesis or restenosis

XX Claim 62; Page 43; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

XX LM609 heavy and light chain variable region. LM609 and the antibody

XX vitaxin bind selectively to integrin alphavbeta3 and can be used to

XX inhibit binding of alphavbeta3 to a ligand and thus block

XX integrin-mediated signal transduction. This is useful in the treatment,

XX prevention and diagnosis of alphavbeta3-mediated disease, specifically,

XX angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

XX diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

XX arthritis, macular degeneration, osteoporosis etc.). The antibodies

XX contain non-murine framework regions so are suitable for use in humans.

XX Enhanced types of LM609 have affinity more than 90 times greater than

XX that of parent the parent antibody.

XX Sequence 10 AA;

Qy 1 ARHNYGSFY 9

Db 1 arhnygsfy 9

|||

Query Match 82.8%; Score 48; DB 19; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.018;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
 Db 1 arhnygsfy 9
 |||

Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 macular degeneration; osteoporosis; primer; V-H region; CDR;
 complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis

Claim 62; Page 43; 129pp; English.

W76007-W76040 are protein fragments of the grafted monoclonal antibody

LM609 heavy and light chain variable region. LM609 and the antibody

vitaxin bind selectively to integrin alphavbeta3 and can be used to

inhibit binding of alphavbeta3 to a ligand and thus block
 integrin-mediated signal transduction. This is useful in the treatment,
 prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 arthritis, macular degeneration, osteoporosis etc.). The antibodies
 contain non-murine framework regions so are suitable for use in humans.
 Enhanced types of LM609 have affinity more than 90 times greater than
 that of parent the parent antibody.

Sequence 10 AA;

Qy 1 ARHNYGSFY 9

Db 1 arhnygsfy 9

|||

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region.
 XX Mus sp.
 XX OS
 XX WO9833919-A2.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX
 XX Glaser SM, Huse WD;
 PI
 XX
 XX WPI; 1998-437472/37.
 DR
 DR N-PSDB; V49862.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

 Query Match 79.3%; Score 46; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSF 8
 Db |||||
 1 arhnygsf 8

 RESULT 9
 W76026
 ID W76026 standard; Protein; 10 AA.
 XX
 AC W76026;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region.
 XX Mus sp.

XX WO9833919-A2.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX
 XX (IXSY-) IXSYS INC.
 PA
 XX
 XX Glaser SM, Huse WD;
 PI
 XX
 XX WPI; 1998-437472/37.
 DR
 DR N-PSDB; V49863.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 62; Page 41; 129pp; English.
 XX
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 XX
 SQ Sequence 10 AA;

 Query Match 79.3%; Score 46; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ARHNYGSF 8
 Db |||||
 1 arhnygsf 8

 RESULT 10
 W76028
 ID W76028 standard; Protein; 10 AA.
 XX
 AC W76028;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX
 DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 XX complementarity determining region.
 XX Mus sp.
 XX WO9833919-A2.
 PN
 XX
 XX 06-AUG-1998.
 PD
 XX
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

XX

SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.039;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8

Db 1 arhnygsf 8

|||||||

RESULT 13

W76010

ID W76010 standard; Protein; 10 AA.

AC W76010;

XX

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #1.

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX

PD 06-AUG-1998.

XX

XX 30-JAN-1998; 98WO-US01826.

XX

XX 30-JAN-1997; 97US-0791391.

XX

XX (IXSY-) IXSYS INC.

PA

XX

XX Glaser SM, Huse WD;

PI

XX

XX WPI: 1998-437472/37.

DR

XX

XX N-PSDB; V49847.

DR

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Disclosure; Page 40; 129pp; English.

XX

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

XX

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

XX

SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.039;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8

Db 1 arhnygsf 8

|||||||

RESULT 14

W76001

ID W76001 standard; Protein; 117 AA.

XX

AC W76001;

XX

XX

DT 02-NOV-1998 (first entry)

XX

DE Vitaxin antibody heavy chain variable region protein fragment.

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX

PD 06-AUG-1998.

XX

XX 30-JAN-1998; 98WO-US01826.

XX

XX 30-JAN-1997; 97US-0791391.

XX

XX (IXSY-) IXSYS INC.

PA

XX

XX Glaser SM, Huse WD;

PI

XX

XX WPI: 1998-437472/37.

DR

XX

XX N-PSDB; V49820.

DR

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 1; Fig 1a; 129pp; English.

XX

XX This sequence represents a fragment of the vitaxin antibody variable

XX heavy chain region. Vitaxin and the antibody LM609 bind selectively to

CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3

CC to a ligand and thus block integrin-mediated signal transduction. This is

CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,

CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,

CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 79.3%; Score 46; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSF 8
 |||||
 Db 97 arhnygsf 104

RESULT 15
 W76003
 ID W76003 standard; Protein; 117 AA.
 XX
 AC W76003;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody heavy chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; V49822.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 43; Fig 2a; 129pp; English.
 XX
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 79.3%; Score 46; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSF 8
 |||||
 Db 97 arhnygsf 104

Search completed: March 28, 2001, 06:59:56
 Job time: 1392 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:02:01 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-98

Perfect score: 58

Sequence: 1 ARHNYGSFYE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*

1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*

2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*

3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*

4: /cgnl_7/ptodata/1/iaa/PCTUS.COMB.pep.*

5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	62.1	94	3	US-09-147-550-14
2	36	62.1	94	3	US-09-147-550-45
3	36	62.1	94	3	US-09-147-550-48
4	36	62.1	94	3	US-09-147-550-77
5	36	62.1	94	3	US-09-147-550-84
6	36	62.1	94	3	US-09-147-550-90
7	36	62.1	94	3	US-09-147-550-101
8	34	58.6	286	2	US-08-809-267-3
9	34	58.6	286	4	PCT-US95-13662A-3
10	34	58.6	287	2	US-08-741-437-5
11	34	58.6	287	2	US-09-134-593-5
12	33	56.9	270	2	US-08-484-938-47
13	33	56.9	270	2	US-08-484-1588-47
14	33	56.9	270	2	US-08-484-596A-47
15	33	56.9	270	2	US-08-480-150A-47
16	33	56.9	270	3	US-08-458-731-47
17	33	56.9	270	3	US-08-149-223A-47
18	33	56.9	566	2	US-08-484-938-41
19	33	56.9	566	2	US-08-484-1588-41
20	33	56.9	566	2	US-08-484-596A-41
21	33	56.9	566	2	US-08-480-150A-41
22	33	56.9	566	3	US-08-458-731-41
23	33	56.9	566	3	US-08-149-223A-41
24	33	56.9	715	3	US-08-669-286-5
25	32	55.2	15	1	US-08-618-464-7
26	32	55.2	15	3	US-09-107-615-7
27	32	55.2	25	2	US-08-480-190-44
28	32	55.2	25	2	US-08-488-379-44

29	32	55.2	25	4	PCT-US93-07545-44	Sequence 44, Appl
30	32	55.2	36	1	US-08-053-131-84	Sequence 84, Appl
31	32	55.2	36	1	US-08-645-641-84	Sequence 84, Appl
32	32	55.2	36	1	US-07-853-408B-84	Sequence 84, Appl
33	32	55.2	36	2	US-08-096-762-84	Sequence 84, Appl
34	32	55.2	36	2	US-08-308-865-84	Sequence 84, Appl
35	32	55.2	36	4	PCT-US92-10983-84	Sequence 84, Appl
36	32	55.2	80	1	US-08-264-250A-1	Sequence 1, Appl
37	32	55.2	89	1	US-08-025-038-30	Sequence 30, Appl
38	32	55.2	89	1	US-08-039-137-17	Sequence 17, Appl
39	32	55.2	90	2	US-08-485-133-23	Sequence 23, Appl
40	32	55.2	94	3	US-09-147-550-12	Sequence 12, Appl
41	32	55.2	94	3	US-09-147-550-13	Sequence 13, Appl
42	32	55.2	94	3	US-09-147-550-15	Sequence 15, Appl
43	32	55.2	94	3	US-09-147-550-16	Sequence 16, Appl
44	32	55.2	94	3	US-09-147-550-17	Sequence 17, Appl
45	32	55.2	94	3	US-09-147-550-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14

; Sequence 14, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; TYPE: PRT

; ORGANISM: BOVINE

US-09-147-550-14

Query Match 62.1%; Score 36; DB 3; Length 94;

Best Local Similarity 85.7%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 80 RHNYGVF 86

RESULT 2

US-09-147-550-45

; Sequence 45, Application US/09147550

; Patent No. 6090540

; GENERAL INFORMATION:

; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550

; CURRENT APPLICATION NUMBER: US/09/147,550

; CURRENT FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: PCT/JP97/02485

; EARLIER FILING DATE: 1997-07-17

; EARLIER APPLICATION NUMBER: JP 8-190933

; EARLIER FILING DATE: 1996-07-19

; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 3

US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 4

US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 5

US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 6

US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT

ORGANISM: BOVINE
US-09-147-550-90

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

DB 80 RHNYGVF 86

RESULT 7

US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 62.1%; Score 36; DB 3; Length 94;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

DB 80 RHNYGVF 86

RESULT 8

US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,267
FILING DATE: 12-MAR-1997
CLASSIFICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662
FILING DATE:
APPLICATION NUMBER: US 08/329,721
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-809-267-3

Query Match 58.6%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
|||||

DB 91 HNYGAF 96

RESULT 9

PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/329,721
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-13662A-3

Query Match 58.6%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 10
US-08-741-437-5
Sequence 5, Application US/08741437
Patent No. 5843665
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,437
FILING DATE: Filed herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199

US-08-741-437-5
Query Match 58.6%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 11
US-09-134-593-5
Sequence 5, Application US/09134593
Patent No. 5981232
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,593
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/741,437
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0148 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 4199

US-09-134-593-5
Query Match 58.6%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 92 HNYGAF 97

RESULT 12
US-08-484-993B-47
Sequence 47, Application US/08484993B
Patent No. 5837497
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,993B
; FILING DATE: 09-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-993B-47

Query Match 56.9%; Score 33; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NYGSPY 9
Db 58 NYGSYY 63

RESULT 13
US-08-484-158B-47
; Sequence 47, Application US/08484158B
; Patent No. 5976545
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; TITLE OF INVENTION: Pharmaceutical Compositions for
; TITLE OF INVENTION: Immunocontraception
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,158B
; FILING DATE: 07-JUNE-95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,223
; FILING DATE: 09-NOV-93
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 32794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-158B-47

Query Match 56.9%; Score 33; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NYGSPY 9
Db 58 NYGSYY 63

RESULT 14
US-08-484-596A-47
; Sequence 47, Application US/08484596A
; Patent No. 5981228
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,596A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,223
; FILING DATE: 11-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
```

; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-596A-47

Query Match 56.9%; Score 33; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFY 9
Db 58 NYGSYY 63

RESULT 15
US-08-480-150A-47
; Sequence 47, Application US/08480150A
; Patent No. 5989550
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,150A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,223
; FILING DATE: 09-NOV-1993
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-150A-47

Query Match 56.9%; Score 33; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFY 9
Db 58 NYGSYY 63

Db 58 NYGSYY 63

Search completed: March 28, 2001, 07:02:01
Job time: 1340 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:04:37 ; Search time 130.08 Seconds
(without alignments)
5.220 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	70.2	113	2 S26468	Ig heavy chain V r
2	39	68.4	555	2 T21028	hypothetical prote
3	38	66.7	89	2 S38688	MHC class II histo
4	38	66.7	89	2 S38683	MHC class II histo
5	38	66.7	89	2 S38684	MHC class II histo
6	38	66.7	225	2 S38684	MHC class II OVAR-
7	37	64.9	386	2 S51436	probable membrane
8	37	64.9	479	1 F70039	probable iron-sulf
9	37	64.9	2288	2 T29999	hypothetical prote
10	36	63.2	82	2 T51106	Major Histocompati
11	36	63.2	233	2 H82163	arginyl-tRNA-prote
12	36	63.2	446	2 T19625	hypothetical prote
13	36	63.2	470	2 H71667	glutamate-tRNA li
14	36	63.2	575	2 T12094	beta-fructofuranos
15	36	63.2	583	2 S56680	beta-fructofuranos
16	36	63.2	592	2 J00991	beta-fructofuranos
17	36	63.2	592	2 S56681	beta-fructofuranos
18	36	63.2	592	2 S61503	beta-fructofuranos
19	36	63.2	593	2 T01575	beta-fructofuranos
20	36	63.2	786	2 S37031	probable succinogl
21	35	61.4	9	2 S36850	Ig heavy chain V r
22	35	61.4	83	2 S21593	Ig heavy chain V r
23	35	61.4	167	2 T16454	hypothetical prote
24	35	61.4	568	2 T28876	hypothetical prote
25	35	61.4	584	2 T06163	beta-fructofuranos
26	35	61.4	660	2 S71276	beta-fructofuranos
27	35	61.4	1024	2 T46016	hypothetical prote
28	35	61.4	2295	2 B71621	probable membrane
29	34	59.6	65	2 S17441	hypothetical prote

30	34	59.6	85	2 I59634	MHC class II DR-be
31	34	59.6	86	2 A81873	hypothetical prote
32	34	59.6	89	2 S38676	MHC class II histo
33	34	59.6	89	2 S38680	MHC class II histo
34	34	59.6	89	2 S57512	MHC class II histo
35	34	59.6	98	1 WMBP72	gene 7 protein - p
36	34	59.6	98	1 WMBP72	gene 7 protein - p
37	34	59.6	107	2 PL0080	Ig kappa chain V r
38	34	59.6	123	2 C25239	MHC class II histo
39	34	59.6	200	2 D32526	class II histocomp
40	34	59.6	210	1 B69265	conserved hypothet
41	34	59.6	221	2 I45939	MHC cell surface g
42	34	59.6	230	2 S46332	homeotic protein G
43	34	59.6	237	2 C27060	class II histocomp
44	34	59.6	248	2 T14547	beta-fructofuranos
45	34	59.6	266	2 I54287	gene HLA-DRB1 prot

ALIGNMENTS

RESULT 1

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R.Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <RAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAAM1833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IM>

Query Match 70.2%; Score 40; DB 2; Length 113;
Best Local Similarity 60.0%; Pred. No. 2.1;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10

Db 93 ARHPYGNYYA 102

RESULT 2

T21028

hypothetical protein F16H6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21028

R.Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19362

A:Accession: T21028

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-555 <MIL>

A:Cross-references: EMBL:Z81506; PIDN:CAB04128.1; GSPDB:GN00023; CESP:F16H6.1

A:Experimental source: clone F16H6

C:Genetics:

A:Gene: CESP:F16H6.1

A:Map position: 5

A:Introns: 123/1; 318/3

Query Match 68.4%; Score 39; DB 2; Length 555;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
 II IIIII
 Db 314 HNSGSFYS 321

RESULT 3

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38688

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 3.9;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

IIIII I I

Db 75 RHNYGVFES 83

RESULT 4

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38683

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;

Best Local Similarity 77.8%; Pred. No. 3.9;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

IIIII I I

Db 75 RHNYGVFES 83

RESULT 5

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - northern lesser bushbaby
 C:Species: Galago senegalensis (northern lesser bushbaby)

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: S38684

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:227154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;
 Best Local Similarity 77.8%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

IIIII I I

Db 75 RHNYGVFES 83

RESULT 6

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000

C:Accession: I47095

R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

Anim. Genet. 24, 249-255, 1993

A:Title: Isolation, characterization and evolution of ovine major histocompatibility

A:Reference number: I47075; MUID:94057592

A:Accession: I47095

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-225 <FAB>

A:Cross-references: GB:L04790; NID:9458880; PIDN:AAAL6562.1; PID:9458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

F:98-163/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 38; DB 2; Length 225;

Best Local Similarity 77.8%; Pred. No. 9.9;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

IIIII I I

Db 68 RHNYGVFES 76

RESULT 7

S51436

probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L9470.1

C:Species: Saccharomyces cerevisiae

C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998

C:Accession: S51436

R:Wohldmann, P.

submitted to the EMBL Data Library, November 1994

A:Description: The sequence of S. cerevisiae cosmid 9470.

A:Reference number: S51414

A:Accession: S51436

A:Molecule type: DNA

A:Residues: 1-386 <WOH>

A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w

C:Genetics:

A:Gene: SGD:PEX13

A:Cross-references: SGD:S0004181; MIPS:YLR191w

A:Map position: 12R

C:Superfamily: SH3 homology

C:Keywords: transmembrane protein

F:264-280/Domain: transmembrane #status predicted <TMM>

F:313-367/Domain: SH3 homology <SH3>

Query Match 64.9%; Score 37; DB 2; Length 386;

Best Local Similarity 85.7%; Pred. No. 26;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9

:IIIIII

Db 117 NNYGSFY 123

```

Qy 1 ARHNYGSFY 9
   :| ||| ||
Db 34 SRSNYGEFY 42

RESULT 10
IS1106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: IS1106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: IS1103; MUID:94245280
A:Accession: IS1106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 63.2%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
   ||||| |
Db 75 RHNYGVF 81

RESULT 11
H82163
argInyl-tRNA-protein transferase-related protein VC1736 [imported] - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: H82163
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.;
  chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
  I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: H82163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <HEI>
A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94886.1; GSPDB:GN
  C:Genetics:
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
A:Gene: VC1736
A:Map position: 1

Query Match 63.2%; Score 36; DB 2; Length 233;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
   ||| :|| |
Db 117 ARHRGSMY 125

RESULT 12
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997

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A:Reference number: Z19153

A:Accession: T19625

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C3IH5.6

A:Experimental source: clone C3IH5

C:Genetics:

A:Gene: CESP:C3IH5.6

A:Map position: 1

A:Introns: 49/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

C:Superfamily: Caenorhabditis elegans hypothetical protein W03D8.8

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 446;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7

Db 51 RHNYGS 56

RESULT 13

H71667

glutamate--tRNA ligase (EC 6.1.1.17) (gltX2) RP623 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 20-Jun-2000

C:Accession: H71667

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499

A:Accession: H71667

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-470 <AND>

A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:g386116

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: gltX2; RP623

C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

F:4-281/Domain: glutamine--tRNA ligase homology <EGL>

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 470;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

Db 31 ARHNNKFF 39

RESULT 14

T12094

beta-fructofuranosidase (EC 3.2.1.26) - fava bean

C:Species: Vicia faba (fava bean)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T12094

R:Weber, H.; Borisjuk, L.; Helm, U.; Buchner, P.; Wobus, U.

Plant Cell 7, 1835-1846, 1995

A:Title: Seed coat-associated invertases of Fava bean control both unloading and storage

A:Reference number: Z17416; MUID:96093423

A:Accession: T12094

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-575 <WEB>

A:Cross-references: EMBL:Z35162; NID:g861154; PIDN:CAA84526.1; PID:g861155

A:Experimental source: cv. Fribo, seed coat

C:Genetics:

A:Gene: CWINV1

C:Superfamily: beta-fructofuranosidase

C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 575;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

Db 308 RYDYGNEYA 316

RESULT 15

S56680

beta-fructofuranosidase (EC 3.2.1.26) 3 precursor, cell wall - carrot

N:Alternate names: invertase

C:Species: Daucus carota (carrot)

C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999

C:Accession: S56680

R:Lorenz, K.; Lienhard, S.; Sturm, A.

Plant Mol. Biol. 28, 189-194, 1995

A:Title: Structural organization and differential expression of carrot beta-fructofur

A:Reference number: S56680; MUID:95306787

A:Accession: S56680

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-583 <LOR>

A:Cross-references: EMBL:X78423; NID:g468534; PIDN:CAA55188.1; PID:gl020102

C:Genetics:

A:Gene: inv3

A:Introns: 68/1; 71/1; 357/3; 410/3; 493/2; 523/3

C:Superfamily: beta-fructofuranosidase

C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

F:1-42/Domain: signal sequence and propeptide #status predicted <SIG>

F:43-583/Product: beta-fructofuranosidase 3, cell wall #status predicted <MAT>

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 583;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

Db 313 RYDYGNEYA 321

Search completed: March 28, 2001, 07:04:38

Job time: 1076 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:35:19 ; Search time 72.95 Seconds
(without alignments)
4.379 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues.

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	64.9	386	1 PEXD_YEAST	P80667 saccharomyc
2	36	63.2	470	1 SYE2_RICPR	Q9zct8 rickettsia
3	36	63.2	583	1 INV1_DAUCA	Q39693 daucus caro
4	36	63.2	592	1 INV1_DAUCA	Q36792 daucus caro
5	36	63.2	592	1 INV2_DAUCA	Q39692 daucus caro
6	36	63.2	786	1 EXOP_RHIME	P33698 rhizobium m
7	34	59.6	65	1 CCOSA_PEA	P31172 pisum sativ
8	34	59.6	98	1 VG7_BPPH2	P13848 bacterioph
9	34	59.6	98	1 VG7_BPPZA	P07533 bacterioph
10	34	59.6	275	1 IF2A_PYRAB	Q9v0e4 pyrococcus
11	34	59.6	275	1 IF2A_PYRHO	Q38655 pyrococcus
12	34	59.6	284	1 IPYR_PICPA	O13505 pichia past
13	34	59.6	286	1 IPYR_KLULA	P13998 kluyveromyc
14	34	59.6	286	1 IPYR_YEAST	P00817 saccharomyc
15	34	59.6	328	1 CCOSA_ARATH	P56770 arabidopsis
16	34	59.6	367	1 LHX4_MOUSE	P53776 mus musculu
17	34	59.6	512	1 PNTA_HAEIN	P43842 haemophilus
18	34	59.6	683	1 SPPI_YEAST	P32432 saccharomyc
19	34	59.6	1386	1 RPOD_MARPO	P06274 marchantia
20	33	57.9	245	1 GSC_CHICK	P33545 gallus gall
21	33	57.9	313	1 CCOSA_TOBAC	P12216 nicotiana t
22	33	57.9	316	1 Y025_NPVAC	P41430 autographa
23	33	57.9	347	1 UL33_HSV6U	P52380 herpes simp
24	33	57.9	371	1 MNCP_OXYFA	P15798 oxytricha f
25	33	57.9	371	1 MNCP_OXYTR	Q27151 oxytricha t
26	33	57.9	448	1 NCAP_CVHOC	P33469 human coron
27	33	57.9	473	1 SYE_AQUAE	O67271 aquifex aeo
28	33	57.9	494	1 RNHL_CRIFA	Q07762 crithidia f
29	33	57.9	514	1 LIM_HALRO	Q25132 halocynthia
30	33	57.9	590	1 INVA_MAIZE	P49174 zea mays (m
31	33	57.9	642	1 INVA_VICFA	Q43857 vicia faba
32	33	57.9	649	1 INVA_PHAUU	P29001 phaseolus a
33	33	57.9	651	1 INVA_PHAVU	Q24509 phaseolus v

34 33 57.9 715 1 ADSV_BOVIN
35 33 57.9 802 1 YGN9_YEAST
36 33 57.9 1196 1 XPG_XENLA
37 33 57.9 1790 1 VIT_ANTGR
38 33 57.9 2184 1 RRPL_CDVO
39 32 56.1 65 1 CCSA_OENBE
40 32 56.1 194 1 PTH_SALTI
41 32 56.1 196 1 WBBJ_ECOLI
42 32 56.1 198 1 HB2G_HUMAN
43 32 56.1 266 1 HB2A_HUMAN
44 32 56.1 266 1 HB2B_HUMAN
45 32 56.1 266 1 HB2C_HUMAN

ALIGNMENTS

RESULT 1

ID PEXD_YEAST STANDARD; PRT; 386 AA.
AC P80667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).
GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97011156.
RA Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
RA Tabak H.F., Distel B.;
RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
protein Pex13p functions as a docking site for Pex5p, a mobile
receptor for the import PTS1-containing proteins.";
RT J. Cell Biol. 135:97-109(1996).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Talc A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN-S288C;
RA Erdmann R., Blobel G.;
RX MEDLINE; 97011157.
RT "Identification of Pex13p a peroxisomal membrane receptor for the
PTS1 recognition factor.";
RT J. Cell Biol. 135:111-121(1996).
RL [4]
CC -!- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
(PAS10/PEX5).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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DR EMBL; S82971; AAB46895.1;
DR EMBL; U37420; AAB79308.1;

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DR EMBL: U17246; AAB67453.1; -.
DR EMBL: U14913; AAB67448.1; -.
DR HSPF: Q06187; IAWW.
DR SGD: S0004181; PEX13.
DR INTERPRO: IPR001452; -.
DR PFAM: PF00018; SH3.1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS00002; SH3.1.
KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
FT DOMAIN 1 263 LUMENAL (POTENTIAL).
FT TRANSMEM 264 280 POTENTIAL.
FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 372 SH3.
SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 386;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
DB 117 NNYGSFY 123

RESULT 2
SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E.
RX MEDLINE; 95039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria".
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL: AJ235272; CAA15066.1; -.
CC HSPF: P27000; 1GLN.
CC INTERPRO: IPR000924; -.
CC PFAM: PF00749; TRNA-synt_lc; 1.
CC PRINTS: PR00987; TRNA-synt_lc; 1.
CC PROSITE: PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING * 242 242 ATP (BY SIMILARITY).

SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 63.2%; Score 36; DB 1; Length 470;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
DB 31 ARHNGKFF 39

RESULT 3
INV3_DAUCA STANDARD; PRT; 583 AA.
ID INV3_DAUCA
AC Q39693;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3 PRECURSOR (EC 3.2.1.26).
DE (SUCROSE-6-PHOSPHATE HYDROLASE 3) (INVERTASE 3) (CELL WALL BETA-
DE FRUCTOSIDASE 3).
GN INV3.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
OC euasterids II; Apiales; Apiaceae; Daucus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. QUEEN ANNE'S LACE;
RX MEDLINE; 95306787.
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-
RT fructofuranosidase genes: identification of a gene coding for a
RT flower bud-specific isozyme".
RL Plant Mol. Biol. 28:189-194(1995).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
CC STRESS RESPONSE.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL: X78423; CAA55188.1; -.
CC INTERPRO: IPR001362; -.
CC PFAM: PF00251; Glyco_hydro_32; 1.
CC PROSITE: PS00609; GLYCOSYL_HYDROL_F32; 1.
CC KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; zymogen; Signal.
CC SIGNAL 1 ? POTENTIAL.
CC PROPEP ? ? POTENTIAL.
CC CHAIN ? 583 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
CC ISOENZYME 3.
CC CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 280 280 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 561 561 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 63.2%; Score 36; DB 1; Length 583;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

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Db 313 RYDYGNEYA 321
 ::|||::

RESULT 4
 INV1_DAUC
 ID INV1_DAUC STANDARD; PRT; 592 AA.
 AC P26792;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 (EC 3.2.1.26)
 DE (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL BETA-
 DE FRUCTOSIDASE 1).
 GN INV1.
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 OC euasterids II; Apiales; Apiaceae; Daucus.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=CV, QUEEN ANNE'S LACE;
 RX MEDLINE; 93005650.
 RA Sturm A., Chrispeels M.J.;
 RT "cDNA cloning of carrot extracellular beta-fructosidase and its
 RT expression in response to wounding and bacterial infection.";
 RL Plant Cell 2:1107-1119(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94035200.
 RA Ramloch-Lorenz K., Knudsen S., Sturm A.;
 RT "Molecular characterization of the gene for carrot cell wall beta-
 RT fructosidase.";
 RL Plant J. 4:545-554(1993).
 CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
 CC STRESS RESPONSE.
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
 CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
 CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
 CC -!- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.
 CC -!- INDUCTION: IN RESPONSE TO WOUNDING AND BACTERIAL INFECTION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL: M58362; AAA03516.1; -
 CC DR EMBL; X69321; CAA49162.1; -
 CC DR PIR; JQ0991; JQ0991.
 CC DR INTERPRO: IPR001362; -
 CC DR PFAM: PF00251; Glyco_hydro_32; 1.
 CC DR PROSITE; PS00609; Glycoprotein; Cell wall; Zymogen; Signal.
 CC KW Hydrolyase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 CC FT SIGNAL 1 31 OR 39 (POTENTIAL).
 CC FT PROPEP 32 48 OR 40 (POTENTIAL).
 CC FT CHAIN 49 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 CC FT ACT_SITE 74 74 BY SIMILARITY.
 CC FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (COMPLEX).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (COMPLEX).
 CC FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
 CC FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CONFLICT 133 133 R -> W (IN REF. 2).
 CC FT CONFLICT 487 487 A -> V (IN REF. 2).
 CC SQ SEQUENCE 592 AA; 66813 MW; E3DF85355D277D0C CRC64;

Query Match 63.2%; Score 36; DB 1; Length 592;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 ::|||::
 DB 321 RYDYGNEYA 329

RESULT 5
 INV2_DAUC
 ID INV2_DAUC STANDARD; PRT; 592 AA.
 AC Q39692;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2 (EC 3.2.1.26)
 DE (SUCROSE-6-PHOSPHATE HYDROLASE 2) (INVERTASE 2) (CELL WALL BETA-
 DE FRUCTOSIDASE 2).
 GN INV2.
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 OC euasterids II; Apiales; Apiaceae; Daucus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, QUEEN ANNE'S LACE;
 RX MEDLINE; 95306787.
 RA Lorenz K., Lienhard S., Sturm A.;
 RT "Structural organization and differential expression of carrot beta-
 RT fructofuranosidase genes: identification of a gene coding for a
 RT flower bud-specific isozyme.";
 RL Plant Mol. Biol. 28:189-194(1995).
 CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
 CC STRESS RESPONSE.
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
 CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
 CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
 CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL: X78424; CAA55189.1; -
 CC DR INTERPRO: IPR001362; -
 CC DR PFAM: PF00251; Glyco_hydro_32; 1.
 CC DR PROSITE; PS00609; Glycoprotein; Cell wall; Zymogen; Signal.
 CC KW Hydrolyase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 CC FT SIGNAL 1 31 POTENTIAL.
 CC FT PROPEP 32 48 POTENTIAL.
 CC FT CHAIN 49 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 CC FT ACT_SITE 75 75 BY SIMILARITY.
 CC FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 592 AA; 67397 MW; 2734603836709133 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 592;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 ::|||::
 DB 320 RYDYGNEYA 328

RESULT 6
EXP_RHIME STANDARD; PRT; 786 AA.
AC P33698;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUCCINOGLYCAN BIOSYNTHESIS TRANSPORT PROTEIN EXP.
GN EXP.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE; 94042869.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Family of glycosyl transferases needed for the synthesis of
succinoglycan by Rhizobium meliloti";
RL J. Bacteriol. 175:7033-7044(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE; 94042870.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Genes needed for the modification, polymerization, export, and
processing of succinoglycan by Rhizobium meliloti: a model for
succinoglycan biosynthesis";
RL J. Bacteriol. 175:7045-7053(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RX MEDLINE; 94067019.
RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes
involved in exopolysaccharide biosynthesis and mapping of promoters
located on the exoHKLAMONP fragment";
RL Mol. Gen. Genet. 241:367-379(1993).
CC -!- PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -!- SIMILARITY: SOME, TO B.SOLANACEARUM EPSB.
CC -----
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CC -----
DR EMBL; L20758; AAA16042.1; -
DR EMBL; Z22636; CAA80349.1; -
DR PIR; B49349; B49349.
DR PIR; S37031; S37031.
DR PIR; S39960; S39960.
KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding;
KW Plasmid.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 66 POTENTIAL.
FT DOMAIN 67 689 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 690 711 POTENTIAL.
FT DOMAIN 712 786 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 583 590 ATP (POTENTIAL).
FT SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Watch 63.2%; Score 36; DB 1; Length 786;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYVGSFY 9
Db 768 RHYGKYI 775
RESULT 7
CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE; 91355950.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
in pea chloroplasts";
RL Plant Mol. Biol. 17:541-545(1991).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE COMP/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; X59015; CAA41754.1; -
DR PIR; S17441; S17441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1 1
FT SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;
Query Match 59.6%; Score 34; DB 1; Length 65;
Best Local Similarity 75.0%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFYS 10
Db 57 HSYGSFYS 64
RESULT 8
VG7_BPPH2 STANDARD; PRT; 98 AA.
AC P13848;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN 7.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87106857.
RA Vilek C., Paces V.;
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
completes the 19,285-bp sequence of phi 29 genome. Comparison with
the homologous sequence of phage PZA.";


```

RL  Gene 46:215-225(1986).
RN  SEQUENCE FROM N.A.
RX  MEDLINE; 87016351.
RA  Innis C.A., Garvey K.J., Ito J.;
RT  "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
RL  spacer between the major early and late genes.";
RL  Nucleic Acids Res. 14:7129-7129(1986).
CC  -----
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CC  -----
DR  EMBL; M14782; AAA32279.1; -.
DR  EMBL; X04386; CAA27974.1; -.
DR  PIR; A28923; WMBPF9.
KW  Late protein.
SQ  SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;

Query Match          59.6%; Score 34; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSPYS 10
Db  | | | | | |
    33 RVNYGSPVS 41

RESULT 9
VG7_BPPZA          STANDARD;          PRT;          98 AA.
AC  P07533;
DT  01-APR-1988 (Rel. 07, Created)
DT  01-APR-1988 (Rel. 07, Last sequence update)
DT  01-FEB-1991 (Rel. 17, Last annotation update)
DE  HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN  7.
OS  Bacteriophage PZA.
OC  Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 87031573.
RA  Paces V., Vicek C., Urbanek P.;
RT  "Nucleotide sequence of the late region of Bacillus subtilis phage
RL  PZA, a close relative of phi 29.";
RL  Gene 44:107-114(1986).
CC  -----
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CC  -----
DR  EMBL; M11813; AAA98483.1; -.
DR  PIR; A24831; WMBP72.
KW  Late protein.
SQ  SEQUENCE 98 AA; 11281 MW; 444408C39B606A25 CRC64;

Query Match          59.6%; Score 34; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSPYS 10
Db  | | | | | |
    33 RVNYGSPVS 41

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RESULT 10
IF2A_PYRAB
ID  IF2A_PYRAB          STANDARD;          PRT;          275 AA.
AC  Q9W0E4;
DT  01-OCT-2000 (Rel. 40, Created)
DT  01-OCT-2000 (Rel. 40, Last sequence update)
DT  01-OCT-2000 (Rel. 40, Last annotation update)
DE  PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN  EIF2A OR PAB0568.
OS  Pyrococcus abyssi.
OC  Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-ORSAY;
RA  Hellig R.;
RT  "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RL  structure and evolution.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC  BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC  (BY SIMILARITY).
CC  -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC  CHAIN (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
CC  -!- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.
CC  -----
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CC  -----
DR  EMBL; AJ248285; CAB49760.1; -.
DR  INTERPRO; IPR003029; -.
DR  PFAM; PF00575; SI; 1.
KW  Initiation factor; Protein biosynthesis; RNA-binding.
FT  DOMAIN 8 83 SI MOTIF.
SQ  SEQUENCE 275 AA; 31912 MW; B2659F3A49879B4F CRC64;

Query Match          59.6%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  3 HNYGSF 8
Db  | | | | |
    23 HNYGAF 28

RESULT 11
IF2A_PYRHO
ID  IF2A_PYRHO          STANDARD;          PRT;          275 AA.
AC  O58655;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  01-OCT-2000 (Rel. 40, Last annotation update)
DE  PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN  EIF2A OR PH0961.
OS  Pyrococcus horikoshii.
OC  Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-ORS3;
RX  MEDLINE; 98344137.
RA  Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA  Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA  Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA  Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA  Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

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RA Masuchi Y., Shizuwa H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OF3.";
 RL DNA Res. 5:55-76(1998).
 CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: HETERODIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
 CC
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 CC
 CC EMBL; AP000004; BAA30038.1; -
 DR INTERPRO; IPR003029; -
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding.
 FT DOMAIN 8 S1 MOTIF; 6AADI5F10FPB436 CRC64;
 SQ SEQUENCE 275 AA; 31980 MW; 6AADI5F10FPB436 CRC64;
 Query Match 59.6%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 Db 23 HNYGAF 28
 ||||:|
 RESULT 12
 IPYR_PICPA STANDARD; PRT; 284 AA.
 ID IPYR_PICPA
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NREL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC
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 CC

DR EMBL; AJ001000; CAA04453.1; -
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;
 Query Match 59.6%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 Db 91 HNYGAF 96
 ||||:|
 RESULT 13
 IPYR_KLUULA STANDARD; PRT; 286 AA.
 ID IPYR_KLUULA
 AC F13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E.COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC
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 CC
 CC EMBL; X14230; CAA32446.1; -
 DR PIR; S07894; PWVKL.
 DR HSSP; P00817; IWGI.
 DR INTERPRO; IPR001596; -
 DR PFAM; PF00719; Pyrophosphatase; 1.
 DR PROSITE; PS00387; PPASE; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT

FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 59.68; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 ||||:|
 Db 91 HNYGAF 96

RESULT 14
 IPYR_YEAST
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (ppa) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Botes E., Miosga T., Schaeff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN=S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database";
 RL Electrophoresis 15:1466-1486(1994).
 [5]
 RP SEQUENCE OF 239-249.
 RC STRAIN=ATCC 38531 / Y41;
 RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT *Saccharomyces cerevisiae*.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 [6]
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 [7]

RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohn W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of *Saccharomyces cerevisiae*
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E. COLI AND K. LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -!- MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
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 CC -----
 CC EMBL; X13253; CAA31629.1; -
 CC EMBL; 235880; CAA84949.1; -
 CC PIR; S45864; PWB. -
 CC PDB; 1PVP; 15-OCT-91.
 CC PDB; 1YPP; 07-DEC-96.
 CC PDB; 1WGI; 19-NOV-97.
 CC PDB; 1WGI; 19-NOV-97.
 CC PDB; 1HUK; 08-APR-98.
 CC PDB; 1HUK; 08-APR-98.
 CC PDB; 117E; 23-DEC-98.
 CC PDB; 8PRK; 23-DEC-98.
 CC SWISS-2DPAGE; P00817; YEAST.
 CC YEPD; 7305; -
 CC SGD; S0000215; IPP1.
 CC INTERPRO: IPR001596;
 CC PFAM: PF00719; Pyrophosphatase; 1.
 CC PROSITE: PS00387; PPASE; 1.
 KW Hydrolase; Magnesium; 3D-structure.
 FT INIT_MET 0
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
 FT CONFLICT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 71 71 D -> N (IN REF. 3).

FT CONFLICT 74 MISSING (IN REF. 3).
FT CONFLICT 123 E -> Q (IN REF. 3).
FT CONFLICT 136 Q -> E (IN REF. 3).
FT CONFLICT 186 N -> D (IN REF. 3).
FT CONFLICT 224 D -> N (IN REF. 3).
FT CONFLICT 266 L -> P (IN REF. 2).
FT STRAND 4
FT STRAND 16
FT STRAND 25
FT STRAND 28
FT STRAND 30
FT STRAND 38
FT STRAND 41
FT STRAND 45
FT STRAND 55
FT STRAND 79
FT STRAND 97
FT STRAND 111
FT STRAND 112
FT STRAND 121
FT STRAND 123
FT STRAND 131
FT STRAND 132
FT STRAND 135
FT STRAND 138
FT STRAND 146
FT STRAND 151
FT STRAND 158
FT STRAND 160
FT STRAND 161
FT STRAND 165
FT STRAND 167
FT STRAND 172
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FT STRAND 176
FT STRAND 177
FT STRAND 179
FT STRAND 180
FT STRAND 182
FT STRAND 197
FT STRAND 203
FT STRAND 205
FT STRAND 207
FT STRAND 210
FT STRAND 212
FT STRAND 230
FT STRAND 231
FT STRAND 245
FT STRAND 246
FT STRAND 249
FT STRAND 251
FT STRAND 252
FT STRAND 255
FT STRAND 260
FT STRAND 274
FT STRAND 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
| | | | |
Db 91 HNYGAF 96

RESULT 15
CCSA_ARATH
ID CCSA_ARATH STANDARD; PRT; 328 AA.
AC P56770;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HERE ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.

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CC -----

DR EMBL; AF000423; BAA84436.1; -
DR INTERPRO; IPR002541; -
DR PFAM; PF01578; CYTC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 328 AA; 37732 MW; C88D1508H2924D6F CRC64;

Query Match 59.6%; Score 34; DB 1; Length 328;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
| : | | | | |
Db 320 HSYGSFYS 327

Search completed: March 28, 2001, 07:35:20
Job time: 157 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:59:56 ; Search time 154.19 Seconds
(without alignments)
2.218 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	19	W76040 LM609 grafted anti
2	53	93.0	10	19	W76039 LM609 grafted anti
3	53	93.0	10	19	W76023 LM609 grafted anti
4	52	91.2	10	19	W76038 LM609 grafted anti
5	48	84.2	10	19	W76024 LM609 grafted anti
6	46	80.7	10	19	W76022 LM609 grafted anti
7	46	80.7	10	19	W76025 LM609 grafted anti
8	46	80.7	10	19	W76026 LM609 grafted anti
9	46	80.7	10	19	W76027 LM609 grafted anti
10	46	80.7	10	19	W76028 LM609 grafted anti
11	46	80.7	10	19	W76029 LM609 grafted anti
12	46	80.7	10	19	W76030 LM609 grafted anti

13	46	80.7	10	19	W76010 LM609 grafted anti
14	46	80.7	117	19	W76001 Vitaxin antibody h
15	46	80.7	117	19	W76003 LM609 antibody hea
16	46	80.7	117	20	Y06381 Murine monoclonal
17	46	80.7	117	20	Y06387 Humanised LM609 an
18	46	80.7	118	20	Y06384 Humanised LM609 an
19	46	80.7	118	20	Y06385 Humanised LM609 an
20	46	80.7	118	20	Y06386 Humanised LM609 an
21	46	80.7	118	20	Y06383 Humanised LM609 an
22	46	80.7	130	20	Y06379 Murine monoclonal
23	43	75.4	10	19	W76037 LM609 grafted anti
24	43	75.4	10	19	W76021 LM609 grafted anti
25	41	71.9	10	19	W76020 LM609 grafted anti
26	38	66.7	110	20	W84099 Vitronectin alpha-
27	38	66.7	117	20	W84093 Murine vitronectin
28	38	66.7	117	20	W84097 Humanised anti-alp
29	37	64.9	8	20	Y06371 Murine monoclonal
30	37	64.9	119	19	Y86109 S. pneumoniae deri
31	36	63.2	117	16	R79157 Human IgE receptor
32	36	63.2	117	16	R79155 Human IgE receptor
33	36	63.2	117	18	W27357 Heavy chain variab
34	36	63.2	117	18	W27356 Heavy chain variab
35	36	63.2	117	18	W27354 Heavy chain variab
36	36	63.2	239	20	W73874 Human antilepsil
37	36	63.2	242	20	W73876 Human antilepsil
38	35	61.4	615	20	Y57299 A33 1-SST enzyme.
39	35	61.4	640	20	Y57301 C33 enzyme. Cicho
40	34	59.6	30	21	Y81870 Yeast IPPI protein
41	34	59.6	89	17	Y14338 Protein encoded by
42	34	59.6	89	17	Y14306 Protein encoded by
43	34	59.6	89	17	Y14307 Protein encoded by
44	34	59.6	256	13	R22568 ScFvB18 construct.
45	34	59.6	256	13	R22583 ScFvB18 construct

ALIGNMENTS

RESULT 1

W76040
ID W76040 standard; Protein; 10 AA.

XX W76040;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #16.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.

OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49877.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 57; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFYS 10
Db 1 arhnygsfys 10
RESULT 2
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #15.
XX Vitaxin: antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX Mus sp.
OS W09833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01826.
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; V49876.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX Claim 62; Page 43; 129pp; English.
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX SQ Sequence 10 AA;
Query Match 93.0%; Score 53; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFY 9
Db 1 arhnygsfy 9
RESULT 3
W76023
ID W76023 standard; Protein; 10 AA.
XX AC W76023;
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #5.
XX Vitaxin: antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX Mus sp.
OS W09833919-A2.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01826.
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; V49860.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX Claim 62; Page 41; 129pp; English.
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 93.0%; Score 53; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 Db 1 arhnygsfy 9
 |||||

RESULT 4
 W76038 ID W76038 standard; Protein; 10 AA.
 AC W76038;
 XX
 XX DT 02-NOV-1998 (first entry)
 XX LM609 grafted antibody V-H region CDR3 protein fragment #14.
 DE
 DE

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US01826.
 XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49875.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 43; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 91.2%; Score 52; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.006;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10
 Db 1 arhngsfys 10
 |||||

RESULT 5
 W76024 ID W76024 standard; Protein; 10 AA.
 XX AC W76024;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; V49861.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 84.2%; Score 48; DB 19; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.028;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFYS 10
 |||||

Db 1 arhnygsfas 10

RESULT 6
W76022
ID W76022 standard; Protein; 10 AA.
XX AC
XX W76022;
XX
DT 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #4.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; V49859.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 10 AA;
Query Match 80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSF 8
Db 1 arhnygsf 8
RESULT 7
W76025
ID W76025 standard; Protein; 10 AA.
XX

AC W76025;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; V49862.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 62; Page 41; 129pp; English.
XX
XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
XX
XX Sequence 10 AA;
Query Match 80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSF 8
Db 1 arhnygsf 8
RESULT 8
W76026
ID W76026 standard; Protein; 10 AA.
XX
XX W76026;
XX
XX 02-NOV-1998 (first entry)
XX LM609 grafted antibody V-H region CDR3 protein fragment #8.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX MUS SP.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49863.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 80.7%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.059;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSF 8

|||||||

Db 1 arhnygsf 8

RESULT 9

W76027

ID W76027 standard; Protein; 10 AA.

XX W76027;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #9.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX MUS SP.

XX

PN WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; V49864.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.

XX Sequence 10 AA;

Query Match 80.7%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.059;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSF 8

|||||||

Db 1 arhnygsf 8

RESULT 10

W76028

ID W76028 standard; Protein; 10 AA.

XX W76028;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 protein fragment #10.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

XX MUS SP.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.
XX
PA {IXSY-) IXSY'S INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR N-PSDB; V49865.

XX	Humanised antibody. Vitaxin, that binds selectively to alphavbeta3
PT	integrin - and related grafted antibodies based on murine monoclonal
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
PT	angiogenesis or restenosis
XX	
XX	Claim 62; Page 41; 129pp; English.
XX	
CC	W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC	LM609 heavy and light chain variable region. LM609 and the antibody
CC	LM609 bind selectively to integrin alphavbeta3 and can be used to
CC	inhibit binding of alphavbeta3 to a ligand and thus block
CC	integrin-mediated signal transduction. This is useful in the treatment,
CC	prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC	angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC	diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC	arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC	contain non-murine framework regions so are suitable for use in humans.
CC	Enhanced types of LM609 have affinity more than 90 times greater
CC	that of parent the parent antibody.
XX	
XX	Sequence 10 AA; SQ

```
Query Match      80.7%; Score 46; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	ARHNYGSF	8
Db	1	arhnyqsf	8

RESULT 11
W76029
ID W76029 standard: Proteinp: 10 AA:

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.

Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 macular degeneration; osteoporosis; primer; V-H region; CDR;
 complementarity determining region.

DR N-PSDB; V49866.

Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal Lm609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

W76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

Query Match	80.7%;	Score 46;	DB 19;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 0.059;		
Matches	8;	Conservative	0;	Mismatches 0;
				Indels

Qy 1 ARHNYGSF 8
| | | | | | | |
Db 1 arhnyqsf 8

RESULT 12
W76030
ID W76030 standard: Protein: 10 AA:

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #12.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.

AA	Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT	integrin - and related grafted antibodies based on murine monoclonal
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
PT	angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 80.7%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. NO. 0.059;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

Db | | | | | | | |

1 arhnygsf 8

RESULT 13

W76010

ID W76010 standard; Protein; 10 AA.

AC

XX W76010;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-H region CDR3 protein fragment #1.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; V49847.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Disclosure; Page 40; 129pp; English.

XX

XX W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 80.7%; Score 46; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. NO. 0.059;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8

Db | | | | | | | |

1 arhnygsf 8

RESULT 14

W76001

ID W76001 standard; Protein; 117 AA.

XX

AC W76001;

XX

DT 02-NOV-1998 (first entry)

XX

DE Vitaxin antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; V49820.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 1; Fig 1a; 129pp; English.

XX

XX This sequence represents a fragment of the vitaxin antibody variable

CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to

CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3

CC to a ligand and thus block integrin-mediated signal transduction. This is

CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,

CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,

CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 117 AA;

Search completed: March 28, 2001, 06:59:56
Job time: 1392 sec

Query Match 80.7%; Score 46; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db 97 arhnygsf 104

RESULT 15
W76003
ID W76003 standard; Protein; 117 AA.
XX W76003;
XX AC
XX AC
XX AC
DT 02-NOV-1998 (first entry)
XX LM609 antibody heavy chain variable region protein fragment.
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
XX Mus sp.
XX OS
XX PN W098333919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX WPI: 1998-437472/37.
XX N-PSDB; V49822.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX Claim 43; Fig 2a; 129pp; English.
XX This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX Sequence 117 AA;
SQ

Query Match 80.7%; Score 46; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db 97 arhnygsf 104

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:02:01 ; Search time 113.49 Seconds
(without alignments)
1.582 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6_COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	66.7	94	3	US-09-147-550-14
2	38	66.7	94	3	US-09-147-550-45
3	38	66.7	94	3	US-09-147-550-48
4	38	66.7	94	3	US-09-147-550-77
5	38	66.7	94	3	US-09-147-550-84
6	38	66.7	94	3	US-09-147-550-90
7	38	66.7	94	3	US-09-147-550-101
8	34	59.6	94	3	US-09-147-550-39
9	34	59.6	94	3	US-09-147-550-59
10	34	59.6	94	3	US-09-147-550-63
11	34	59.6	286	2	US-08-809-267-3
12	34	59.6	286	4	PCT-US95-13662A-3
13	34	59.6	287	2	US-08-741-437-5
14	34	59.6	287	2	US-09-134-593-5
15	33	57.9	94	3	US-09-147-550-55
16	33	57.9	94	3	US-09-147-550-62
17	33	57.9	94	3	US-09-147-550-87
18	33	57.9	94	3	US-09-147-550-108
19	33	57.9	270	2	US-08-484-993B-47
20	33	57.9	270	2	US-08-484-158B-47
21	33	57.9	270	2	US-08-484-596A-47
22	33	57.9	270	2	US-08-480-150A-47
23	33	57.9	270	3	US-08-458-731-47
24	33	57.9	270	3	US-08-149-223A-47
25	33	57.9	527	2	US-08-823-516-144
26	33	57.9	566	2	US-08-484-993B-41
27	33	57.9	566	2	US-08-484-158B-41
28	33	57.9	566	2	US-08-484-596A-41

29 33 57.9 566 2 US-08-480-150A-41 Sequence 41, Appl
30 33 57.9 566 3 US-08-458-731-41 Sequence 41, Appl
31 33 57.9 566 3 US-08-149-223A-41 Sequence 41, Appl
32 33 57.9 715 3 US-08-669-286-5 Sequence 5, Appl
33 32 56.1 13 3 US-08-881-037-93 Sequence 93, Appl
34 32 56.1 15 1 US-08-618-464-7 Sequence 7, Appl
35 32 56.1 15 3 US-09-107-615-7 Sequence 7, Appl
36 32 56.1 25 2 US-08-480-190-44 Sequence 44, Appl
37 32 56.1 25 2 US-08-488-379-44 Sequence 44, Appl
38 32 56.1 25 4 PCT-US93-07545-44 Sequence 44, Appl
39 32 56.1 36 1 US-08-053-131-84 Sequence 84, Appl
40 32 56.1 36 1 US-08-645-641-84 Sequence 84, Appl
41 32 56.1 36 1 US-07-853-408B-84 Sequence 84, Appl
42 32 56.1 36 2 US-08-096-762-84 Sequence 84, Appl
43 32 56.1 36 2 US-08-308-865-84 Sequence 84, Appl
44 32 56.1 36 4 PCT-US92-10983-84 Sequence 84, Appl
45 32 56.1 80 1 US-08-264-250A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-147-550-14
; Sequence 14, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aiga, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
; US-09-147-550-14

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
Db 80 RHNYGVFES 88
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RESULT 2

US-09-147-550-45
; Sequence 45, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aiga, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979

; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-45

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
DB 80 RHNYGVFES 88

RESULT 3
US-09-147-550-48
; Sequence 48, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-48

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
DB 80 RHNYGVFES 88

RESULT 4
US-09-147-550-77
; Sequence 77, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-77

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
DB 80 RHNYGVFES 88

RESULT 5
US-09-147-550-84
; Sequence 84, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-84

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | | | |
DB 80 RHNYGVFES 88

RESULT 6
US-09-147-550-90
; Sequence 90, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT

; ORGANISM: BOVINE
US-09-147-550-90

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 |||||
Db 80 RHNYGVFES 88

RESULT 7
US-09-147-550-101
; Sequence 101, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-101

Query Match 66.7%; Score 38; DB 3; Length 94;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 |||||
Db 80 RHNYGVFES 88

RESULT 8
US-09-147-550-39
; Sequence 39, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-39

Query Match 59.6%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 |||||
Db 80 RHNYGMES 88

RESULT 9
US-09-147-550-59
; Sequence 59, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-59

Query Match 59.6%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
 |||||
Db 80 RHNYGMES 88

RESULT 10
US-09-147-550-63
; Sequence 63, Application US/09147550
; Patent No. 6090540
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: SEQUENCE LISTING FOR 09/147,550
; CURRENT APPLICATION NUMBER: US/09/147,550
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: PCT/JP97/02485
; EARLIER FILING DATE: 1997-07-17
; EARLIER APPLICATION NUMBER: JP 8-190933
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: JP 9-77979
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-147-550-63

Query Match 59.6%; Score 34; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
|||||
Db 80 RHNYGGMES 88

RESULT 11

US-08-809-267-3
; Sequence 3, Application US/08809267
; Patent No. 5861296
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.
; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/809,267
; APPLICATION NUMBER: US/08/809,267
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 433
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662

; FILING DATE:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein

US-08-809-267-3

Query Match 59.6%; Score 34; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
|||||
Db 91 HNYGAF 96

RESULT 12

PCT-US95-13662A-3
; Sequence 3, Application PC/TUS9513662A
; GENERAL INFORMATION:
; APPLICANT: LENNOX, Tricia L.
; APPLICANT: SLATKO, Barton E.
; APPLICANT: SEARS, Lauren E.

; TITLE OF INVENTION: PURIFIED THERMOSTABLE INORGANIC
; TITLE OF INVENTION: PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
; TITLE OF INVENTION: LITORALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13662A
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,721
; FILING DATE: 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-105-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; PCT-US95-13662A-3

Query Match 59.6%; Score 34; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
|||||
Db 91 HNYGAF 96

RESULT 13

US-08-741-437-5
; Sequence 5, Application US/08741437
; Patent No. 5843665
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,437
; FILING DATE: Filed Herewith

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0148 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 855-0555
;; TELEFAX: (415) 845-4166
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 287 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 4199
;; US-08-741-437-5

Query Match 59.6%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
| | | | |
DB 92 HNYGAF 97

RESULT 14
US-09-134-593-5
;; Sequence 5, Application US/09134593
;; Patent No. 5981232
;; GENERAL INFORMATION:
;; APPLICANT: Hawkins, Phillip R.
;; APPLICANT: Hillman, Jennifer L.
;; TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/134,593
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/741,437
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0148 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 855-0555
;; TELEFAX: (415) 845-4166
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 287 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide

;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 4199
;; US-09-134-593-5

Query Match 59.6%; Score 34; DB 2; Length 287;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
| | | | |
DB 92 HNYGAF 97

RESULT 15
US-09-147-550-55
;; Sequence 55, Application US/09147550
;; Patent No. 6090540
;; GENERAL INFORMATION:
;; APPLICANT: Aida, Yoko
;; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
;; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
;; CURRENT APPLICATION NUMBER: US/09/147,550
;; CURRENT FILING DATE: 1999-04-23
;; EARLIER APPLICATION NUMBER: PCT/JP97/02485
;; EARLIER FILING DATE: 1997-07-17
;; EARLIER APPLICATION NUMBER: JP 8-190933
;; EARLIER FILING DATE: 1996-07-19
;; EARLIER APPLICATION NUMBER: JP 9-77979
;; EARLIER FILING DATE: 1997-03-28
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 55
;; LENGTH: 94
;; TYPE: PRT
;; ORGANISM: BOVINE
;; US-09-147-550-55

Query Match 57.9%; Score 33; DB 3; Length 94;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
| | | | |
DB 80 RHNYGGVES 88

Search completed: March 28, 2001, 07:02:02
Job time: 1341 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:53:38 ; Search time 443.95 Seconds
(without alignments)
2.640 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNYGSFYS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	839	09LIE5	Q9LIE5 arabidopsis
2	40	70.2	89	019495	019495 gallus gall
3	39	68.4	555	Q9XV91	Q9XV91 caenorhabdi
4	39	68.4	611	Q9X5S2	Q9X5S2 streptomyce
5	38	66.7	39	P79474	P79474 cervus elap
6	38	66.7	39	P79477	P79477 cervus elap
7	38	66.7	39	P79478	P79478 cervus elap
8	38	66.7	39	P79479	P79479 cervus elap
9	38	66.7	76	Q9TPC2	Q9TPC2 macaca mula
10	38	66.7	82	Q30606	Q30606 macaca mula
11	38	66.7	82	Q30608	Q30608 macaca mula
12	38	66.7	82	Q30637	Q30637 macaca mula
13	38	66.7	82	Q30638	Q30638 macaca mula
14	38	66.7	82	Q30658	Q30658 macaca mula
15	38	66.7	82	Q30659	Q30659 macaca mula
16	38	66.7	82	Q30666	Q30666 macaca mula
17	38	66.7	82	Q30667	Q30667 macaca mula
18	38	66.7	82	Q30668	Q30668 macaca mula
19	38	66.7	82	019287	019287 macaca mula

20	38	66.7	82	7	019288	019288 macaca mula
21	38	66.7	82	7	Q9TPC9	Q9TPC9 callicebus
22	38	66.7	82	7	Q9MXN1	Q9MXN1 macaca mula
23	38	66.7	83	6	Q9TSS5	Q9TSS5 bos indicus
24	38	66.7	83	7	Q98002	Q98002 ovis aries
25	38	66.7	85	7	Q30796	Q30796 ovis aries
26	38	66.7	85	7	Q30800	Q30800 ovis aries
27	38	66.7	85	7	Q30803	Q30803 ovis aries
28	38	66.7	85	7	Q30812	Q30812 ovis aries
29	38	66.7	85	7	P79966	P79966 capra aegag
30	38	66.7	85	7	P79967	P79967 capra aegag
31	38	66.7	85	7	P79968	P79968 capra aegag
32	38	66.7	86	7	Q30326	Q30326 bos taurus
33	38	66.7	89	7	019210	019210 capra hircu
34	38	66.7	89	7	019212	019212 capra hircu
35	38	66.7	89	7	Q30521	Q30521 galago sene
36	38	66.7	89	7	Q30522	Q30522 galago sene
37	38	66.7	89	7	Q30526	Q30526 galago sene
38	38	66.7	89	7	Q30217	Q30217 homo sapien
39	38	66.7	89	7	Q9MXW8	Q9MXW8 aotus nancy
40	38	66.7	89	7	Q9MXW4	Q9MXW4 aotus nancy
41	38	66.7	89	7	Q9MXW3	Q9MXW3 aotus nancy
42	38	66.7	89	7	Q9MXV8	Q9MXV8 aotus nancy
43	38	66.7	89	7	Q9MXV7	Q9MXV7 aotus nancy
44	38	66.7	89	7	Q9MXV5	Q9MXV5 aotus nancy
45	38	66.7	89	7	Q9MXU6	Q9MXU6 aotus nancy

ALIGNMENTS

RESULT 1

Q9LIE5 PRELIMINARY: PRT: 839 AA.

ID Q9LIE5

AC Q9LIE5

DT 01-OCT-2000 (TREMBlrel..15, Created)

DT 01-OCT-2000 (TREMBlrel..15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel..15, Last annotation update)

DE FAR-RED IMPAIRED RESPONSE PROTEIN, MUTATOR-LIKE TRANSPOSASE-LIKE

DE PROTEIN, PHYTOCHROME A SIGNALING PROTEIN-LIKE.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.

RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,

RL DNA Res. 7:217-221(2000).

DR EMBL; AP001306; BAB03065.1;

SQ SEQUENCE 839 AA; 95996 MW; CBBF60DF8B6797F8 CRC64;

Query Match 75.4%; Score 43; DB 10; Length 839;
Best Local Similarity 87.5%; Pred. NO. 7.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 1 ARHNYGSF 8

Db 274 SRHNYGSF 281

RESULT 2

019495

ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA Pharr G.T., Dodgson J.B., Hunt H.D., Bacon L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL: U91532; AAC15813.1; -;
DR INTERPRO: IPR000353;
DR PFAM: PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; BC7D558B6AEB1379 CRC64;
Query Match 70.2%; Score 40; DB 7; Length 89;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFYS 10
|||||
DB 75 RHNYGDFES 83
RESULT 3
Q9XV91 PRELIMINARY; PRT; 555 AA.
AC Q9XV91;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE F166.1 PROTEIN.
GN F166.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Matthews L.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smalton N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Wellstock L., Wilkinson-Spoat J., Wellman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z81506; CAB04128.1; -;
DR HSSP: P23807; I1XX.

DR INTERPRO: IPR000859;
DR INTERPRO: IPR001304;
DR PFAM: PF00059; Lectin_C; 2.
DR PFAM: PF00431; CUB; 2.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 2.
SQ SEQUENCE 555 AA; 60401 MW; 00B58D22B2E14EDC CRC64;
Query Match 68.4%; Score 39; DB 5; Length 555;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNYGSFYS 10
|||||
DB 314 HNSGSFYS 321
RESULT 4
Q9X5S2 PRELIMINARY; PRT; 611 AA.
AC Q9X5S2;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MMCD.
GN MMCD.
OS Streptomyces lavendulae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1914;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NRRL 2564;
RX MEDLINE=99201491; PubMed=10099135;
RA Mao Y.Q., Varoglu M., Sherman D.H.;
RT "Molecular characterization and analysis of the biosynthetic gene
RT cluster for the antitumor antibiotic mitomycin C from Streptomyces
RT lavendulae NRRL 2564.";
RL Chem. Biol. 6:251-263(1999).
DR EMBL: AF127374; AAD32727.1; -;
SQ SEQUENCE 611 AA; 68499 MW; 350B189E5D19EC64 CRC64;
Query Match 68.4%; Score 39; DB 2; Length 611;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFYS 10
|||||
DB 524 RHNYGFFMS 532
RESULT 5
P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Swarbrick P.A., Crawford A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL: U63077; AAB37777.1; -;
KW MHC.

FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; CAF3680999733D1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DB 25 RHNYGVFES 33
 IIIII I I

RESULT 6

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 ID P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478;
 DB 25 RHNYGVFES 33
 IIIII I I

RESULT 7

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 2.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 ID P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DB 25 RHNYGVFES 33
 IIIII I I

RESULT 8

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swarbrick P.A., Crawford A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; C2188A16752A3C1D CRC64;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 ID P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DB 25 RHNYGVFES 33
 IIIII I I

RESULT 9

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MHC CLASS II ANTIGEN (FRAGMENT).
 GN MAMU-DRB1
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saueremann U., Khazand M., Nagy M., Peiberg C.;
 RL "Mhc-DO-DRB-haplotype analysis in the rhesus macaque: evidence for a
 number of different haplotypes displaying a low allelic
 polymorphism"; 0:0-0(1999).
 RL Tissue Antigens 0:0-0(1999).
 DR EMBL; AF175315; AAF07040.1; -.
 DR INTERPRO; IPR000353; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 76 76
 SQ SEQUENCE 76 AA; 9315 MW; 1DC073E1B87A9AD0 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 76;
 Best Local Similarity 77.8%; Pred. No. 5.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 RHNYGSFYS 10
Db 67 RHNYGVFES 75

RESULT 10
Q30606
ID Q30606 PRELIMINARY; PRT; 82 AA.
AC Q30606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
GN MHC-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152405; PubMed=8995183;
RA Knapp L.A., Cadavid L.F., Eberle M.E., Knechtle S.J., Bontrop R.E.,
RA Watkins D.I.;
RT "Identification of new mamu-DRB alleles using DGGE and direct
RT sequencing.";
RL Immunogenetics 45:171-179(1997).
DR EMBL: U57948; AAC50981.1; -
DR INTERPRO: IPR000353; -
DR PFAM: PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9921 MW; CC75FCF5EE35EEC2 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 73 RHNYGVFES 81

RESULT 11
Q30608
ID Q30608 PRELIMINARY; PRT; 82 AA.
AC Q30608;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
GN MHC-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152405; PubMed=8995183;
RA Knapp L.A., Cadavid L.F., Eberle M.E., Knechtle S.J., Bontrop R.E.,
RA Watkins D.I.;
RT "Identification of new mamu-DRB alleles using DGGE and direct
RT sequencing.";
RL Immunogenetics 45:171-179(1997).
DR EMBL: U57950; AAC50983.1; -
DR INTERPRO: IPR000353; -
DR PFAM: PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 10024 MW; FAAB1152D09CD306 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 73 RHNYGVFES 81

RESULT 12
Q30637
ID Q30637 PRELIMINARY; PRT; 82 AA.
AC Q30637;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IKM; TISSUE=BLOOD;
RX MEDLINE=93123123; PubMed=1478892;
RA Slienderdregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
RA Bontrop R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
RT complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=IKM; TISSUE=BLOOD;
RX MEDLINE=93123123; PubMed=1478892;
RA Slienderdregt B.L.;
RA Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z26140; CAAB1141.1; -
DR INTERPRO: IPR000353; -
DR PFAM: PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 10024 MW; FAAB1152D09CD306 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 73 RHNYGVFES 81

RESULT 13
Q30638
ID Q30638 PRELIMINARY; PRT; 82 AA.
AC Q30638;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1KL; TISSUE=BLOOD;
RX  MEDLINE=93123123; PubMed=1478892;
RA  Slierendregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
RA  Bontrop R.E.;
RT  "Evolutionary stability of transspecies major histocompatibility
RL  complex class II DRB lineages in humans and rhesus monkeys.";
RL  Hum. Immunol. 35:29-39(1992).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1KL; TISSUE=BLOOD;
RA  Slierendregt B.L.;
RL  Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z26141; CAA81162.1; -
DR  INTERPRO; IPR000353; -
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER 1
FT  NON_TER 82
SQ  SEQUENCE 82 AA; 9953 MW; FB1B03E5209CD316 CRC64;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSFYS 10
Db  73 RHNYGVFES 81

RESULT 14
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AC  Q30658;
DT  01-NOV-1996 (TREMBlrel. 01, Created)
DT  01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT  01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE  MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN  MHC DR-BETA 5.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC  Cercopitheciinae; Macaca.
OX  NCBI_TaxID=9544;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1KL; TISSUE=BLOOD;
RA  Slierendregt B.L.;
RL  Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z26162; CAA81163.1; -
DR  INTERPRO; IPR000353; -
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER 1
FT  NON_TER 82
SQ  SEQUENCE 82 AA; 9964 MW; 8AF2C663B1B4D4ED CRC64;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RN  [1]
RP  SEQUENCE FROM N.A.
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RX  MEDLINE=93123123; PubMed=1478892;
RA  Slierendregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
RA  Bontrop R.E.;
RT  "Evolutionary stability of transspecies major histocompatibility
RL  complex class II DRB lineages in humans and rhesus monkeys.";
RL  Hum. Immunol. 35:29-39(1992).
RN  [2]
RP  SEQUENCE FROM N.A.
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RA  Slierendregt B.L.;
RL  Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z26161; CAA81162.1; -
DR  INTERPRO; IPR000353; -
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER 1
FT  NON_TER 82
SQ  SEQUENCE 82 AA; 9964 MW; 8AF2C663B1B4D4ED CRC64;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY  2 RHNYGSFYS 10
Db  73 RHNYGVFES 81

RESULT 15
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AC  Q30659;
DT  01-NOV-1996 (TREMBlrel. 01, Created)
DT  01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT  01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE  MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN  MHC DR-BETA 5.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC  Cercopitheciinae; Macaca.
OX  NCBI_TaxID=9544;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1ME; TISSUE=BLOOD;
RX  MEDLINE=93123123; PubMed=1478892;
RA  Slierendregt B.L., van Noort J.T., Bakas R.M., Otting N., Jonker M.,
RA  Bontrop R.E.;
RT  "Evolutionary stability of transspecies major histocompatibility
RL  complex class II DRB lineages in humans and rhesus monkeys.";
RL  Hum. Immunol. 35:29-39(1992).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1ME; TISSUE=BLOOD;
RA  Slierendregt B.L.;
RL  Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z26162; CAA81163.1; -
DR  INTERPRO; IPR000353; -
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER 1
FT  NON_TER 82
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Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSFYS 10
Db  73 RHNYGVFES 81

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Search completed: March 28, 2001, 07:53:38
Job time: 531 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:25 ; Search time 828.17 Seconds
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Title: US-09-016-061-88
Perfect score: 54
Sequence: 1 QQSTSWPHT 9

Scoring table:
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Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	100.0	9	14	US-09-016-061-88
2	54	100.0	9	17	US-09-339-922A-88
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4	49	90.7	9	13	US-08-986-016-2
5	49	90.7	9	14	US-09-016-061-86
6	49	90.7	9	17	US-09-339-922A-86
7	49	90.7	107	8	US-08-484-537-62
8	49	90.7	107	8	US-08-484-537-63
9	49	90.7	107	8	US-08-484-537-87
10	49	90.7	107	17	US-09-325-000-21
11	49	90.7	107	17	US-09-325-000-22

12	49	90.7	109	1	PCT-US98-25828-45	Sequence 45, Appl
13	49	90.7	109	1	PCT-US98-25828-49	Sequence 49, Appl
14	49	90.7	109	1	PCT-US98-25828-55	Sequence 55, Appl
15	49	90.7	109	13	US-08-986-016-45	Sequence 45, Appl
16	49	90.7	109	13	US-08-986-016-49	Sequence 49, Appl
17	49	90.7	109	13	US-08-986-016-55	Sequence 55, Appl
18	49	90.7	127	8	US-08-484-537-83	Sequence 83, Appl
19	47	87.0	9	14	US-09-016-061-46	Sequence 46, Appl
20	47	87.0	9	17	US-09-339-922A-46	Sequence 46, Appl
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22	47	87.0	107	11	US-08-790-540-8	Sequence 8, Appl
23	47	87.0	107	11	US-08-790-540A-4	Sequence 4, Appl
24	47	87.0	107	11	US-08-790-540A-8	Sequence 8, Appl
25	47	87.0	107	11	US-08-791-391-4	Sequence 4, Appl
26	47	87.0	107	11	US-08-791-391-8	Sequence 8, Appl
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28	47	87.0	107	11	US-08-791-391A-8	Sequence 8, Appl
29	47	87.0	107	11	US-08-791-391A-32	Sequence 32, Appl
30	47	87.0	107	11	US-09-016-061-4	Sequence 4, Appl
31	47	87.0	107	14	US-09-016-061-8	Sequence 8, Appl
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33	47	87.0	107	14	US-09-339-922A-4	Sequence 4, Appl
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35	47	87.0	107	17	US-09-339-922A-32	Sequence 32, Appl
36	47	87.0	107	17	US-09-339-922A-8	Sequence 8, Appl
37	44	81.5	259	18	US-09-419-788-29	Sequence 29, Appl
38	44	81.5	1194	22	US-60-167-217-15793	Sequence 15793, A
39	44	81.5	1194	22	US-60-173-464-12947	Sequence 12947, A
40	44	81.5	1194	22	US-60-191-637-15791	Sequence 15791, A
41	44	81.5	1194	22	US-60-191-681-12515	Sequence 12515, A
42	43	79.6	33	7	US-08-307-868-12	Sequence 12, Appl
43	43	79.6	33	9	US-08-525-539-12	Sequence 12, Appl
44	43	79.6	33	9	US-08-525-539A-12	Sequence 12, Appl
45	43	79.6	107	3	US-07-804-464A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-88
; Sequence 88, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-88

Query Match 100.0%; Score 54; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 1 QOSTSWPHT 9

RESULT 2

US-09-339-922A-88
; Sequence 88, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-88

Query Match 100.0%; Score 54; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 1 QOSTSWPHT 9

RESULT 3

PCT-US98-25828-2
; Sequence 2, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-2

Query Match 90.7%; Score 49; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QOSTSWPHT 9
Db 1 QOSTSWPHT 9

RESULT 4

US-08-986-016-2
; Sequence 2, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsri 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-2

Query Match 90.7%; Score 49; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 1 QOSTSWPHT 9

RESULT 5

US-09-016-061-86
; Sequence 86, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 86:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-86

Query Match 90.7%; Score 49; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
||| |||||
DB 1 QOQNSWPHT 9

RESULT 6
US-09-339-922A-86
; Sequence 86, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-86

Query Match 90.7%; Score 49; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
||| |||||
DB 1 QOQNSWPHT 9

RESULT 7
US-08-484-537-62
; Sequence 62, Application US/08484537
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US/07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-537-62

Query Match 90.7%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSTSWPHT 9
||| |||||
DB 89 QOQNSWPHT 97

RESULT 8
US-08-484-537-63
; Sequence 63, Application US/08484537
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US/07/590,274

; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-537-63

Query Match 90.7%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOOSTSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 9
US-08-484-537-87
; Sequence 87, Application US/08484537
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-537-87

Query Match 90.7%; Score 49; DB 8; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOOSTSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 10
US-09-325-000-21
; Sequence 21, Application US/09325000
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co. Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-00265005
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-325-000-21

Query Match 90.7%; Score 49; DB 17; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 89 QQSNWPHT 97

RESULT 11
US-09-325-000-22
; Sequence 22, Application US/09325000
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelling, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-0026500S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-325-000-22

Query Match 90.7%; Score 49; DB 17; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 89 QQSNWPHT 97

RESULT 12
PCT-US98-25828-45
; Sequence 45, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-45

Query Match 90.7%; Score 49; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 89 QQSNWPHT 97

RESULT 13
PCT-US98-25828-49
; Sequence 49, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-49

Query Match 90.7%; Score 49; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSTSWPHT 9
Db 89 QQSNWPHT 97

RESULT 14
PCT-US98-25828-55
; Sequence 55, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-55

Query Match 90.7%; Score 49; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQNSWPHT 97

RESULT 15
US-08-986-016-45
; Sequence 45, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsri 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-45

Query Match 90.7%; Score 49; DB 13; Length 109;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQNSWPHT 97

Search completed: March 28, 2001, 07:18:25
Job time: 1336 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:17 ; Search time 213.09 Seconds
(without alignments)
0.557 Million cell updates/sec

Title: US-09-016-061-88
Perfect score: 54
Sequence: 1 QOSTSWPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:**

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep:**
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep:**
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep:**
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:**
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep:**
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	68.5	794	5	US-09-489-039A-10909
2	36	66.7	10	5	US-09-445-602A-17
3	36	66.7	20	5	US-09-445-602A-25
4	36	66.7	109	5	US-09-445-602A-6
5	35	64.8	111	1	PCT-US01-03537-11
6	35	64.8	154	5	US-09-352-616A-383
7	35	64.8	154	5	US-09-759-143-383
8	35	64.8	154	5	US-09-679-426-383
9	35	64.8	154	5	US-09-685-166-383
10	35	64.8	154	5	US-09-679-272-383
11	35	64.8	154	5	US-09-780-669-383
12	35	64.8	161	5	US-09-759-143-846
13	35	64.8	161	5	US-09-679-426-846
14	35	64.8	161	5	US-09-685-166-846
15	35	64.8	161	5	US-09-780-669-846
16	35	64.8	216	5	US-09-489-039A-9538
17	34	63.0	41	5	US-09-009-843D-235
18	34	63.0	112	1	PCT-US01-03537-58
19	34	63.0	112	1	PCT-US01-03537-61
20	34	63.0	112	1	PCT-US01-03537-70
21	34	63.0	310	5	US-09-488-725A-2779
22	34	63.0	324	5	US-09-488-725A-6351
23	34	63.0	397	5	US-09-488-725A-2732
24	34	63.0	479	5	US-09-488-725A-6304
25	33	61.1	40	5	US-09-209-462B-173
26	33	61.1	109	1	PCT-US01-01432-78
27	33	61.1	109	1	PCT-US01-01432-106

RESULT 1
US-09-489-039A-10909
; Sequence 10909, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10909
; LENGTH: 794
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10909

ALIGNMENTS

28	33	61.1	308	5	US-09-510-332-117	Sequence 117, App
29	32	59.3	72	1	PCT-US01-01340-744	Sequence 744, App
30	32	59.3	96	1	PCT-US01-02723-219	Sequence 219, App
31	32	59.3	116	5	US-09-489-039A-12769	Sequence 12769, A
32	32	59.3	185	1	PCT-US01-01565-79	Sequence 79, Appl
33	32	59.3	265	5	US-09-489-039A-12065	Sequence 12065, A
34	32	59.3	272	5	US-09-782-980-30	Sequence 30, Appl
35	32	59.3	306	5	US-09-489-039A-8745	Sequence 8745, Ap
36	32	59.3	435	5	US-09-489-039A-7287	Sequence 7287, Ap
37	32	59.3	575	5	US-09-510-949-2	Sequence 2, Appl
38	32	59.3	774	5	US-09-782-980-16	Sequence 16, Appl
39	32	59.3	774	5	US-09-702-572-7	Sequence 7, Appl
40	32	59.3	836	5	US-09-573-872-10	Sequence 10, Appl
41	32	59.3	871	5	US-09-573-872-2	Sequence 2, Appl
42	32	59.3	1215	5	US-09-488-725A-7133	Sequence 7133, Ap
43	32	59.3	1250	5	US-09-488-725A-3563	Sequence 3563, Ap
44	32	59.3	1811	6	US-60-261-976-288	Sequence 288, App
45	31	57.4	111	1	PCT-US01-03537-59	Sequence 59, Appl

Query Match 68.5%; Score 37; DB 5; Length 794;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 185 QOSTSWP 191

RESULT 2
US-09-445-602A-17
; Sequence 17, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: Ruiz, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNIT
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445,602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-17

Query Match          66.7%; Score 36; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
   ||| |||
Db 1 QQSNWSP 7

RESULT 3
US-09-445-602A-25
; Sequence 25, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445, 602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-25

Query Match          66.7%; Score 36; DB 5; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
   ||| |||
Db 5 QQSNWSP 11

RESULT 4
US-09-445-602A-6
; Sequence 6, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445, 602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-6

Query Match          66.7%; Score 36; DB 5; Length 109;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
   ||| |||
Db 90 QQSNWSP 96

RESULT 5
PCT-US01-03537-11
; Sequence 11, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03537-11

Query Match          64.8%; Score 35; DB 1; Length 111;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QOSTSWPHT 9
   ||| |||
Db 95 QSTHWPF 102

RESULT 6
US-09-352-616A-383
; Sequence 383, Application US/09352616A
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
```

ORGANISM: Homo sapiens
US-09-352-616A-383

Query Match 64.8%; Score 35; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy 2 QSTSWPHT 9
| | | | |
Db 9 QGARWPHT 16

RESULT 7
US-09-759-143-383
; Sequence 383, Application US/09759143
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-383

Query Match 64.8%; Score 35; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy 2 QSTSWPHT 9
| | | | |
Db 9 QGARWPHT 16

RESULT 8
US-09-679-426-383
; Sequence 383, Application US/09679426
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 383
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
US-09-679-426-383

Query Match 64.8%; Score 35; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QSTSWPHT 9
| | | | |
Db 9 QGARWPHT 16

RESULT 9
US-09-685-166-383
; Sequence 383, Application US/09685166
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166-383

Query Match 64.8%; Score 35; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QSTSWPHT 9
| | | | |
Db 9 QGARWPHT 16

RESULT 10

US-09-679-272-383
 ; Sequence 383, Application US/09679272
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Cheever, Martin
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.534
 ; CURRENT APPLICATION NUMBER: US/09/679,272
 ; CURRENT FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 476
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 383
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-679-272-383

Query Match 64.8%; Score 35; DB 5; Length 154;
 Best Local Similarity 62.5%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QSTSWPHT 9
 | | | | |
 Db 9 QGARWPHT 16

RESULT 11
 US-09-780-669-383
 ; Sequence 383, Application US/09780669
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C24
 ; CURRENT APPLICATION NUMBER: US/09/780,669
 ; CURRENT FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 943
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 383
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-780-669-383

Query Match 64.8%; Score 35; DB 5; Length 154;
 Best Local Similarity 62.5%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QSTSWPHT 9

Db 9 QGARWPHT 16
 | | | | |

RESULT 12
 US-09-759-143-846
 ; Sequence 846, Application US/09759143
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 846
 ; LENGTH: 161
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-759-143-846

Query Match 64.8%; Score 35; DB 5; Length 161;
 Best Local Similarity 62.5%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QSTSWPHT 9
 | | | | |
 Db 16 QGARWPHT 23

RESULT 13
 US-09-679-426-846
 ; Sequence 846, Application US/09679426
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C20
 ; CURRENT APPLICATION NUMBER: US/09/679,426


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; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 846
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-846

```

```

Query Match          64.8%; Score 35; DB 5; Length 161;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 2 QSTSWPHT 9
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DB 16 QGARWPHT 23

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RESULT 14

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US-09-685-166-846
; Sequence 846, Application US/09685166
; GENERAL INFORMATION:
; APPLICANT: Xu, JiangChun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 846
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166-846

```

```

Query Match          64.8%; Score 35; DB 5; Length 161;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 2 QSTSWPHT 9
   | 1111
DB 16 QGARWPHT 23

```

RESULT 15

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US-09-780-669-846
; Sequence 846, Application US/09780669
; GENERAL INFORMATION:
; APPLICANT: Xu, JiangChun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.

```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 846
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-669-846

```

```

Query Match          64.8%; Score 35; DB 5; Length 161;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2 QSTSWPHT 9
   | 1111
DB 16 QGARWPHT 23

```

```

Search completed: March 28, 2001, 07:22:17
Job time: 1509 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:25 ; Search time 828.17 Seconds
(without alignments)
1.583 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgnl_7/ptodata/1/paa/pctus_COMB.pep.*
- 2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
- 13: /cgnl_7/ptodata/1/paa/US089_COMB.pep.*
- 14: /cgnl_7/ptodata/1/paa/US090_COMB.pep.*
- 15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
- 16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
- 17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
- 18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
- 19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
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- 21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	51	100.0	9	17	US-09-339-922A-90
3	45	88.2	9	6	US-08-232-081-6
4	45	88.2	9	6	US-08-232-081A-6
5	45	88.2	9	14	US-09-016-061-92
6	45	88.2	9	17	US-09-339-922A-92
7	45	88.2	107	6	US-08-232-081-9
8	45	88.2	107	6	US-08-232-081A-9
9	44	86.3	9	14	US-09-016-061-46
10	44	86.3	9	17	US-09-339-922A-46
11	44	86.3	107	11	US-08-790-540-4

12	44	86.3	107	11	US-08-790-540-8	Sequence 8, Appli
13	44	86.3	107	11	US-08-790-540A-4	Sequence 4, Appli
14	44	86.3	107	11	US-08-790-540A-8	Sequence 8, Appli
15	44	86.3	107	11	US-08-791-391-4	Sequence 4, Appli
16	44	86.3	107	11	US-08-791-391-8	Sequence 8, Appli
17	44	86.3	107	11	US-08-791-391-32	Sequence 32, Appli
18	44	86.3	107	11	US-08-791-391A-4	Sequence 4, Appli
19	44	86.3	107	11	US-08-791-391A-8	Sequence 8, Appli
20	44	86.3	107	11	US-08-791-391A-32	Sequence 32, Appli
21	44	86.3	107	14	US-09-016-061-4	Sequence 4, Appli
22	44	86.3	107	14	US-09-016-061-8	Sequence 8, Appli
23	44	86.3	107	14	US-09-016-061-32	Sequence 32, Appli
24	44	86.3	107	17	US-09-339-922A-4	Sequence 4, Appli
25	44	86.3	107	17	US-09-339-922A-8	Sequence 8, Appli
26	44	86.3	107	17	US-09-339-922A-32	Sequence 32, Appli
27	41	80.4	105	1	PCT-US98-04987-17	Sequence 17, Appli
28	41	80.4	105	1	PCT-US98-04987-21	Sequence 21, Appli
29	41	80.4	105	22	US-60-039-609-17	Sequence 17, Appli
30	41	80.4	105	22	US-60-039-609-21	Sequence 21, Appli
31	41	80.4	107	1	PCT-US98-04987-10	Sequence 10, Appli
32	41	80.4	107	22	US-60-039-609-10	Sequence 10, Appli
33	41	80.4	108	1	PCT-US98-04987-7	Sequence 7, Appli
34	41	80.4	108	22	US-60-039-609-7	Sequence 7, Appli
35	41	80.4	112	1	PCT-US98-04987-14	Sequence 14, Appli
36	41	80.4	112	22	US-60-039-609-14	Sequence 14, Appli
37	40	78.4	33	7	US-08-307-868-12	Sequence 12, Appli
38	40	78.4	33	9	US-08-525-539-12	Sequence 12, Appli
39	40	78.4	33	9	US-08-525-539A-12	Sequence 12, Appli
40	40	78.4	107	3	US-07-804-464A-1	Sequence 1, Appli
41	40	78.4	107	3	US-07-808-464-1	Sequence 1, Appli
42	40	78.4	107	3	US-07-881-109-7	Sequence 7, Appli
43	40	78.4	107	3	US-07-881-109A-7	Sequence 7, Appli
44	40	78.4	107	4	US-08-082-842-1	Sequence 1, Appli
45	40	78.4	107	5	US-08-107-669B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-016-061-90
; Sequence 90, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
;
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-90

Query Match 100.0%; Score 51; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 1 QOQSGSWPLT 9

RESULT 2
US-09-339-922A-90
; Sequence 90, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-90

Query Match 100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 1 QOQSGSWPLT 9

RESULT 3
US-08-232-081-6
; Sequence 6, Application US/08232081
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, Tomoyuki
; APPLICANT: GOMI, Hideyuki
; APPLICANT: WIJENES, John
; APPLICANT: NOGUCHI, Hiroshi
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
US-08-232-081-6
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 323319/1991
; FILING DATE: 06-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP92/01583
; FILING DATE: 03-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081-6

Query Match 88.2%; Score 45; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 1 QOQSGSWPLT 9

RESULT 4
US-08-232-081A-6
; Sequence 6, Application US/08232081A
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, Tomoyuki
; APPLICANT: GOMI, Hideyuki
; APPLICANT: WIJENES, John
; APPLICANT: NOGUCHI, Hiroshi
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081A
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 323319/1991
; FILING DATE: 06-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP92/01583
; FILING DATE: 03-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484P
US-08-232-081A-6
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081A-6

Query Match 88.2%; Score 45; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
||| |||||
Db 1 QOQSSWPLT 9

RESULT 5
US-09-016-061-92
; Sequence 92, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-92

Query Match 88.2%; Score 45; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
||| |||||

Db 1 QOQSGSWPQT 9

RESULT 6
US-09-339-922A-92
; Sequence 92, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-92

Query Match 88.2%; Score 45; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
||| |||||
Db 1 QOQSGSWPQT 9

RESULT 7
US-08-232-081-9
; Sequence 9, Application US/08232081
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, Tomoyuki
; APPLICANT: GOMI, Hideyuki
; APPLICANT: WIJDENES, John
; APPLICANT: NOGUCHI, Hiroshi
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081
FILING DATE: 10-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323319/1991
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP92/01583
FILING DATE: 03-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081-9

Query Match 88.2%; Score 45; DB 6; Length 107;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 89 QOQSSSWPLT 97

RESULT 8
US-08-232-081A-9
; Sequence 9, Application US/08232081A
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, Tomoyuki
; APPLICANT: GOMI, Hideyuki
; APPLICANT: WJDNES, John
; APPLICANT: NOGUCHI, Hiroshi
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081A
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 323319/1991
; FILING DATE: 06-DEC-1991
; PRIOR APPLICATION NUMBER: PCT/JP92/01583
; FILING DATE: 03-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-232-081A-9

Query Match 88.2%; Score 45; DB 6; Length 107;
Best Local Similarity 88.9%; Pred. No. 4;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QOQSGSWPLT 9
Db 89 QOQSSSWPLT 97

RESULT 9
US-09-016-061-46
; Sequence 46, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-46

Query Match 86.3%; Score 44; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 1 QOQSGSWPHT 9

RESULT 10
US-09-339-922A-46
; Sequence 46, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 46
LENGTH: 9
TYPE: PRT
ORGANISM: Mus musculus
US-09-339-922A-46

Query Match 86.3%; Score 44; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
| | | | | | | |
DB 1 QOQSGSWPHT 9

RESULT 11
US-08-790-540-4
Sequence 4, Application US/08790540
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540-4

Query Match 86.3%; Score 44; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
| | | | | | | |
DB 89 QOQSGSWPHT 97

RESULT 12
US-08-790-540-8
Sequence 8, Application US/08790540
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540-8

Query Match 86.3%; Score 44; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
| | | | | | | |
DB 89 QOQSGSWPHT 97

RESULT 13
US-08-790-540A-4
Sequence 4, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-4

Query Match 86.3%; Score 44; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 QQSGSWPHT 97

RESULT 14
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match 86.3%; Score 44; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 QQSGSWPHT 97

RESULT 15
US-08-791-391-4
; Sequence 4, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391-4

Query Match 86.3%; Score 44; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
| | | | | | | |
Db 89 QQSGSWPHT 97

Search completed: March 28, 2001, 07:18:26
Job time: 1337 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:17 ; Search time 213.09 Seconds
(without alignments)
0.557 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QQSGSWPLT 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgnl_7/ptodata/2/paa/US00_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	72.5	10	5	US-09-445-602A-17
2	37	72.5	20	5	US-09-445-602A-25
3	37	72.5	109	5	US-09-445-602A-6
4	35	68.6	943	5	US-09-201-228A-132
5	34	66.7	794	5	US-09-489-039A-10909
6	33	64.7	124	5	US-09-489-039A-11700
7	33	64.7	183	5	US-09-489-039A-14327
8	33	64.7	441	5	US-09-794-422-4
9	33	64.7	640	5	US-09-489-039A-14146
10	33	64.7	962	5	US-09-731-166-2
11	32	62.7	119	5	US-09-489-039A-11460
12	32	62.7	121	5	US-09-489-039A-12703
13	32	62.7	127	1	PCT-US01-01324-1850
14	32	62.7	216	5	US-09-489-039A-9538
15	32	62.7	305	5	US-09-489-039A-10184
16	32	62.7	502	5	US-09-489-039A-13376
17	32	62.7	785	5	US-09-488-725A-2538
18	32	62.7	794	5	US-09-488-725A-6110
19	32	62.7	1312	5	US-09-407-427-8
20	32	62.7	1313	5	US-09-407-427-9
21	32	62.7	1402	5	US-09-445-353A-2
22	31	60.8	56	1	PCT-US01-00911-134
23	31	60.8	62	1	PCT-US01-02723-12
24	31	60.8	72	1	PCT-US01-01340-744
25	31	60.8	112	1	PCT-US01-03537-62
26	31	60.8	176	5	US-09-522-433A-26
27	31	60.8	176	5	US-09-522-433B-26

28	31	60.8	265	1	PCT-US01-01434-113	Sequence 113, Appl
29	31	60.8	301	5	US-09-489-039A-9894	Sequence 9894, Ap
30	31	60.8	349	5	US-09-488-725A-2892	Sequence 2892, Ap
31	31	60.8	375	5	US-09-488-725A-1866	Sequence 1866, Ap
32	31	60.8	380	5	US-09-488-725A-6464	Sequence 6464, Ap
33	31	60.8	412	5	US-09-489-039A-13259	Sequence 13259, A
34	31	60.8	430	5	US-09-488-725A-5438	Sequence 5438, Ap
35	31	60.8	430	5	US-09-488-725A-5439	Sequence 5439, Ap
36	31	60.8	434	5	US-09-488-725A-12836	Sequence 12836, A
37	31	60.8	512	5	US-09-489-039A-12836	Sequence 12836, A
38	31	60.8	553	5	US-09-188-082-16	Sequence 16, Appl
39	31	60.8	612	5	US-09-488-725A-5724	Sequence 5724, Ap
40	31	60.8	716	5	US-09-489-039A-10841	Sequence 10841, A
41	31	60.8	835	6	US-60-259-128-4854	Sequence 4854, Ap
42	31	60.8	1072	5	US-09-201-228A-549	Sequence 549, App
43	30	58.8	69	5	US-09-489-039A-9111	Sequence 9111, Ap
44	30	58.8	106	5	US-09-488-725A-2580	Sequence 2580, Ap
45	30	58.8	180	5	US-09-489-039A-11734	Sequence 11734, A

ALIGNMENTS

RESULT 1
US-09-445-602A-17
; Sequence 17, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNIT
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445, 602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Mus musculus
US-09-445-602A-17

Query Match 72.5%; Score 37; DB 5; Length 10;
Best Local Similarity 75.0%; Pred.No. 0.69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPL 8
Db 1 QQSNWPV 8
III III

RESULT 2
US-09-445-602A-25
; Sequence 25, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNIT
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445, 602A
; CURRENT FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-25

Query Match 72.5%; Score 37; DB 5; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPL 8
Db 5 QQSNSWPV 12

RESULT 3
US-09-445-602A-6
; Sequence 6, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irvin
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445, 602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-6

Query Match 72.5%; Score 37; DB 5; Length 109;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPL 8
Db 90 QQSNSWPV 97

RESULT 4
US-09-201-228A-132
; Sequence 132, Application US/09201228A
; GENERAL INFORMATION:
; APPLICANT: Griffois, Remy
; APPLICANT: Hoiseth, Susan K.
; APPLICANT: Zagursky, Robert John
; APPLICANT: Metcalf, Benjamin J.
; APPLICANT: Peek, Joel A.
; APPLICANT: Sankaran, Banumathi
; APPLICANT: Fletcher, Leah Diane
; TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
; TITLE OF INVENTION: AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN
; TITLE OF INVENTION: PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF
; TITLE OF INVENTION: INFECTION

; FILE REFERENCE: 9710-0004-999
; CURRENT APPLICATION NUMBER: US/09/201,228A
; CURRENT FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/107,077
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: FR 97-16034
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: FR 97-15041
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 5981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-201-228A-132

Query Match 68.6%; Score 35; DB 5; Length 943;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SSGSWPLT 9
Db 461 SGLWPLT 467

RESULT 5
US-09-489-039A-10909
; Sequence 10909, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10909
; LENGTH: 794
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10909

Query Match 66.7%; Score 34; DB 5; Length 794;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPL 8
Db 185 QQOTSWPL 192

RESULT 6
US-09-489-039A-11700
; Sequence 11700, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11700
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11700

Query Match 64.7%; Score 33; DB 5; Length 124;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCGSWPLT 9
| | | | |
DB 9 KSGSWPLT 15

RESULT 7

US-09-489-039A-14327
; Sequence 14327, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14327
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14327

Query Match 64.7%; Score 33; DB 5; Length 183;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSGSWPL 8
:::|::|
DB 76 KKAGSWPI 83

RESULT 8

US-09-794-422-4
; Sequence 4, Application US/09794422
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-422-4

Query Match 64.7%; Score 33; DB 5; Length 441;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWP 7
| | | | |
DB 403 QRRGSWP 409

RESULT 9

US-09-489-039A-14146
; Sequence 14146, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14146
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (586)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-489-039A-14146

Query Match 64.7%; Score 33; DB 5; Length 640;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9
|:|::|::|
DB 391 QKSGSWIFT 399

RESULT 10

US-09-731-166-2
; Sequence 2, Application US/09731166
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccarides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,993
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 962
; TYPE: PRT
; ORGANISM: Zea mays
US-09-731-166-2

Query Match 64.7%; Score 33; DB 5; Length 962;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSGSWPL 8
|:|::|::|
DB 804 KNEGSWPL 811

RESULT 11

US-09-489-039A-11460
; Sequence 11460, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11460
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11460

Query Match 62.7%; Score 32; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SGSWP 7
Db 2 SGSWP 6

RESULT 12
US-09-489-039A-12703
; Sequence 12703, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12703
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12703

Query Match 62.7%; Score 32; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SGSWP 7
Db 72 SGSWP 76

RESULT 13
PCT-US01-01324-1850
; Sequence 1850, Application PC/TUS0101324
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC002PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01324
; CURRENT FILING DATE: 2001-01-14
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 5116
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1850
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (92)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

PCT-US01-01324-1850

Query Match 62.7%; Score 32; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSWPL 8
Db 44 GSWPL 48

RESULT 14
US-09-489-039A-9538
; Sequence 9538, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9538
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9538

Query Match 62.7%; Score 32; DB 5; Length 216;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
Db 67 QQSLSWP 73

RESULT 15
US-09-489-039A-10184
; Sequence 10184, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10184
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10184

Query Match 62.7%; Score 32; DB 5; Length 305;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GSWPLT 9
Db 253 GCWPLT 258

Search completed: March 28, 2001, 07:22:18
Job time: 1510 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:26 ; Search time 828.17 Seconds
(without alignments)
1.583 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QSGSGSWPQT 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
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22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	52	100.0	9	14	US-09-016-061-92
2	52	100.0	9	17	US-09-339-922A-92
3	47	90.4	9	14	US-09-016-061-46
4	47	90.4	9	17	US-09-339-922A-46
5	47	90.4	107	11	US-08-790-540-4
6	47	90.4	107	11	US-08-790-540-8
7	47	90.4	107	11	US-08-790-540A-4
8	47	90.4	107	11	US-08-790-540A-8
9	47	90.4	107	11	US-08-791-391-4
10	47	90.4	107	11	US-08-791-391-8
11	47	90.4	107	11	US-08-791-391-32

12	47	90.4	107	11	US-08-791-391A-4	Sequence 4, Appli
13	47	90.4	107	11	US-08-791-391A-8	Sequence 8, Appli
14	47	90.4	107	11	US-08-791-391A-32	Sequence 32, Appl
15	47	90.4	107	14	US-09-016-061-4	Sequence 4, Appli
16	47	90.4	107	14	US-09-016-061-8	Sequence 8, Appli
17	47	90.4	107	14	US-09-016-061-32	Sequence 32, Appl
18	47	90.4	107	14	US-09-339-922A-4	Sequence 4, Appli
19	47	90.4	107	17	US-09-339-922A-8	Sequence 8, Appli
20	47	90.4	107	17	US-09-339-922A-32	Sequence 32, Appl
21	45	86.5	9	14	US-09-016-061-90	Sequence 90, Appl
22	45	86.5	9	17	US-09-339-922A-90	Sequence 2, Appli
23	41	78.8	9	13	PCT-US98-25828-2	Sequence 2, Appli
24	41	78.8	9	13	US-08-986-016-2	Sequence 86, Appl
25	41	78.8	9	14	US-09-016-061-86	Sequence 86, Appl
26	41	78.8	9	17	US-09-339-922A-86	Sequence 62, Appl
27	41	78.8	107	8	US-08-484-537-62	Sequence 62, Appl
28	41	78.8	107	8	US-08-484-537-63	Sequence 63, Appl
29	41	78.8	107	8	US-08-484-537-87	Sequence 87, Appl
30	41	78.8	107	17	US-09-325-000-21	Sequence 21, Appl
31	41	78.8	107	17	US-09-325-000-22	Sequence 22, Appl
32	41	78.8	109	1	PCT-US98-25828-45	Sequence 45, Appl
33	41	78.8	109	1	PCT-US98-25828-49	Sequence 49, Appl
34	41	78.8	109	1	PCT-US98-25828-55	Sequence 55, Appl
35	41	78.8	109	13	US-08-986-016-45	Sequence 45, Appl
36	41	78.8	109	13	US-08-986-016-49	Sequence 49, Appl
37	41	78.8	109	13	US-08-986-016-55	Sequence 55, Appl
38	41	78.8	127	8	US-08-484-537-83	Sequence 83, Appl
39	40	76.9	33	7	US-08-307-868-12	Sequence 12, Appl
40	40	76.9	33	9	US-08-525-539-12	Sequence 12, Appl
41	40	76.9	33	9	US-08-525-539A-12	Sequence 12, Appl
42	40	76.9	107	3	US-07-804-464A-1	Sequence 1, Appli
43	40	76.9	107	3	US-07-808-464-1	Sequence 1, Appli
44	40	76.9	107	3	US-07-881-109-7	Sequence 7, Appli
45	40	76.9	107	3	US-07-881-109A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-016-061-92
; Sequence 92, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-92

Query Match 100.0%; Score 52; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOQSGSWPQT 9
Db 1 QOQSGSWPQT 9

RESULT 2
US-09-339-922A-92
; Sequence 92, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-92

Query Match 100.0%; Score 52; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOQSGSWPQT 9
Db 1 QOQSGSWPQT 9

RESULT 3
US-09-016-061-46
; Sequence 46, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-46

Query Match 90.4%; Score 47; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QOQSGSWPQT 9
Db 1 QOQSGSWPHT 9

RESULT 4

US-09-339-922A-46
; Sequence 46, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-46

Query Match 90.4%; Score 47; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QOQSGSWPQT 9
Db 1 QOQSGSWPHT 9

RESULT 5

US-08-790-540-4
; Sequence 4, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

COOUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540-4

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 89 QOQSGSWPHT 97

RESULT 6
US-08-790-540-8
Sequence 8, Application US/08790540
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-790-540-8

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 89 QOQSGSWPHT 97

RESULT 7
US-08-790-540A-4
Sequence 4, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540A-4

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPQT 9
Db 89 QOQSGSWPHT 97

RESULT 8
US-08-790-540A-8
Sequence 8, Application US/08790540A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

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; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match          90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 89 QOQSGSWPHT 97

RESULT 9
US-08-791-391-4
; Sequence 4, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391-4

Query Match          90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 89 QOQSGSWPHT 97

RESULT 10
US-08-791-391-8
; Sequence 8, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391-8

Query Match          90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPOT 9
Db 89 QOQSGSWPHT 97

RESULT 11
US-08-791-391-32
; Sequence 32, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-32

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPOT 9
Db 89 QQSGSWPHT 97

RESULT 12
US-08-791-391A-4
; Sequence 4, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-4

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPOT 9
Db 89 QQSGSWPHT 97

RESULT 13
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-8

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPOT 9
Db 89 QQSGSWPHT 97

RESULT 14
US-08-791-391A-32
; Sequence 32, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/791,391A
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-32

Query Match 90.4%; Score 47; DB 11; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPOT 9
| | | | | | |
Db 89 QOQSGSWPHT 97

RESULT 15
US-09-016-061-4
Sequence 4, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-4

Query Match 90.4%; Score 47; DB 14; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPOT 9
| | | | | | |
Db 89 QOQSGSWPHT 97

Search completed: March 28, 2001, 07:18:26
Job time: 1337 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:18 ; Search time 213.09 Seconds
(without alignments)
0.557 Million cell updates/sec

Title: US-09-016-061-92

Perfect score: 52

Sequence: 1 QQSGSWPQT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	69.2	10	US-09-445-602A-17	Sequence 17, Appl
2	36	69.2	20	US-09-445-602A-25	Sequence 25, Appl
3	36	69.2	109	US-09-445-602A-6	Sequence 6, Appl
4	35	67.3	256	US-09-489-039A-11264	Sequence 11264, A
5	35	67.3	409	US-60-258-272-111	Sequence 111, Appl
6	35	67.3	534	US-09-576-455-2	Sequence 2, Appl
7	34	65.4	1402	US-09-443-353A-2	Sequence 20, Appl
8	34	65.4	1496	US-60-262-351-20	Sequence 132, Appl
9	33	63.5	78	PCT-US01-01397-132	Sequence 4, Appl
10	33	63.5	441	US-09-794-422-4	Sequence 744, Appl
11	32	61.5	72	PCT-US01-01340-744	Sequence 11460, A
12	32	61.5	119	US-09-489-039A-11460	Sequence 12703, A
13	32	61.5	121	US-09-489-039A-12703	Sequence 6796, Ap
14	32	61.5	211	US-09-488-725A-6796	Sequence 9538, Ap
15	32	61.5	216	US-09-489-039A-9538	Sequence 13376, A
16	32	61.5	502	US-09-489-039A-13376	Sequence 5649, Ap
17	32	61.5	611	US-09-488-725A-5649	Sequence 5650, Ap
18	32	61.5	611	US-09-488-725A-5650	Sequence 2077, A
19	32	61.5	698	US-09-488-725A-2077	Sequence 10841, A
20	32	61.5	716	US-09-489-039A-10841	Sequence 796, Appl
21	31	59.6	132	PCT-US01-05614-796	Sequence 26, Appl
22	31	59.6	176	US-09-522-433A-796	Sequence 26, Appl
23	31	59.6	176	US-09-522-433B-26	Sequence 14327, A
24	31	59.6	183	US-09-489-039A-14327	Sequence 10944, A
25	31	59.6	302	US-09-489-039A-10944	Sequence 11712, A
26	31	59.6	336	US-09-489-039A-11712	Sequence 3230, Ap
27	31	59.6	353	US-09-488-725A-3230	

28 31 59.6 410 5 US-09-489-039A-12498 Sequence 12498, A
29 31 59.6 640 5 US-09-489-039A-14146 Sequence 14146, A
30 31 59.6 3623 5 US-09-341-461-2 Sequence 2, Appl
31 30 57.7 42 1 PCT-US01-05614-252 Sequence 252, App
32 30 57.7 103 5 US-09-489-039A-11339 Sequence 11339, A
33 30 57.7 180 5 US-09-489-039A-11734 Sequence 11734, A
34 30 57.7 182 5 US-09-489-039A-8631 Sequence 8631, Ap
35 30 57.7 186 5 US-09-673-763-12 Sequence 12, Appl
36 30 57.7 203 5 US-09-489-039A-13751 Sequence 13751, A
37 30 57.7 246 5 US-09-738-973-60 Sequence 60, Appl
38 30 57.7 284 5 US-09-636-499-19 Sequence 19, Appl
39 30 57.7 341 5 US-09-489-039A-9169 Sequence 9169, Ap
40 30 57.7 355 5 US-09-595-298A-1858 Sequence 1858, Ap
41 30 57.7 355 5 US-09-636-499-15 Sequence 15, Appl
42 30 57.7 370 5 US-09-595-298A-1857 Sequence 1857, Ap
43 30 57.7 372 5 US-09-489-039A-7338 Sequence 7338, Ap
44 30 57.7 418 5 US-09-738-973-62 Sequence 62, Appl
45 30 57.7 418 5 US-09-738-973-82 Sequence 82, Appl

ALIGNMENTS

RESULT 1
US-09-445-602A-17
; Sequence 17, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNIT
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445,602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRF
; ORGANISM: Mus musculus
US-09-445-602A-17

Query Match 69.2%; Score 36; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.94; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1;

QY 1 QQSGSWP 7

Db 1 QQSNWP 7

RESULT 2

US-09-445-602A-25
; Sequence 25, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNIT
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445,602A
; CURRENT FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-25

Query Match 69.2%; Score 36; DB 5; Length 20;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
Db 5 QQNSWP 11

RESULT 3
US-09-445-602A-6
; Sequence 6, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irvin
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445,602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-6

Query Match 69.2%; Score 36; DB 5; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWP 7
Db 90 QQNSWP 96

RESULT 4
US-09-489-039A-11264
; Sequence 11264, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11264
; LENGTH: 256

; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11264

Query Match 67.3%; Score 35; DB 5; Length 256;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQSGSWPQT 9
Db 97 QSSGQWDQT 105

RESULT 5
US-60-258-272-111
; Sequence 111, Application US/60258272
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL0001041
; CURRENT APPLICATION NUMBER: US/60/258,272
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 409
; TYPE: PRT
; ORGANISM: HUMAN
US-60-258-272-111

Query Match 67.3%; Score 35; DB 6; Length 409;
Best Local Similarity 62.5%; Pred. No. 6.3;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPQ 8
Db 102 QSNGRWPQ 109

RESULT 6
US-09-576-455-2
; Sequence 2, Application US/09576455
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 46745, A NOVEL HUMAN ACYLTRANSFERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-054001
; CURRENT APPLICATION NUMBER: US/09/576,455
; CURRENT FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-576-455-2

Query Match 67.3%; Score 35; DB 5; Length 534;
Best Local Similarity 62.5%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPQ 8
Db 195 QSNGRWPQ 202

RESULT 7

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US-09-445-353A-2
; Sequence 2, Application US/09445353A
; GENERAL INFORMATION:
; APPLICANT: Rosenfeld, et al., Michael
; TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
; FILE REFERENCE: 6627-PA1021
; CURRENT APPLICATION NUMBER: US/09/445.353A
; CURRENT FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1402
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-353A-2

Query Match 65.4%; Score 34; DB 5; Length 1402;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPQ 8
Db 1013 QPGSWPE 1019

RESULT 8
US-60-262-351-20
; Sequence 20, Application US/60262351
; GENERAL INFORMATION:
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Broadus, Julie
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: PB/5-50058PI
; CURRENT APPLICATION NUMBER: US/60/262.351
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-60-262-351-20

Query Match 65.4%; Score 34; DB 6; Length 1496;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPQT 9
Db 722 QSGSQPQT 729

RESULT 9
PCT-US01-01397-132
; Sequence 132, Application PC/TUS0101397
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 23 Human Secreted Proteins
; FILE REFERENCE: PS731PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01397
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/226,281
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 78
; TYPE: PRT
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; ORGANISM: Homo sapiens
PCT-US01-01397-132

Query Match 63.5%; Score 33; DB 1; Length 78;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGSWPQ 8
Db 43 SGQWPQ 48

RESULT 10
US-09-794-422-4
; Sequence 4, Application US/09794422
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794.422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-422-4

Query Match 63.5%; Score 33; DB 5; Length 441;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWP 7
Db 403 QRRGWP 409

RESULT 11
PCT-US01-01340-744
; Sequence 744, Application PC/TUS0101340
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01340
; CURRENT FILING DATE: 2001-01-14
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 744
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (64)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-01340-744

Query Match 61.5%; Score 32; DB 1; Length 72;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 QOQSGSWPQ 8
||: |||:
Db 30 QQAQSWPK 37

RESULT 12
US-09-489-039A-11460
; Sequence 11460, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11460
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11460

Query Match 61.5%; Score 32; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWP 7
|||||
Db 2 SGSWP 6

RESULT 13
US-09-489-039A-12703
; Sequence 12703, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12703
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12703

Query Match 61.5%; Score 32; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWP 7
|||||
Db 72 SGSWP 76

RESULT 14
US-09-488-725A-6796
; Sequence 6796, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pf_fl_genes_b Versions 1.0
; SEQ ID NO 6796
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(212)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-6796

Query Match 61.5%; Score 32; DB 5; Length 211;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QSGSWPQ 8
| | | | |
Db 111 QPGCWQP 117

RESULT 15
US-09-489-039A-9538
; Sequence 9538, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9538
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9538

Query Match 61.5%; Score 32; DB 5; Length 216;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7
||| |||
Db 67 QOQSLSWP 73

Search completed: March 28, 2001, 07:22:19
Job time: 1511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:26 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHCSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_Main.*
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2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	14	US-09-016-061-94
2	55	100.0	10	17	US-09-339-922A-96
3	51	92.7	10	17	US-09-016-061-60
4	51	92.7	10	14	US-09-339-922A-60
5	49	89.1	10	14	US-09-016-061-68
6	49	89.1	10	14	US-09-016-061-96
7	49	89.1	10	17	US-09-339-922A-68
8	49	89.1	10	17	US-09-339-922A-94
9	46	83.6	10	14	US-09-016-061-70
10	46	83.6	10	14	US-09-016-061-80
11	46	83.6	10	17	US-09-339-922A-70

12	46	83.6	10	17	US-09-339-922A-80	Sequence 80, Appl
13	45	81.8	10	14	US-09-016-061-40	Sequence 40, Appl
14	45	81.8	10	14	US-09-016-061-72	Sequence 72, Appl
15	45	81.8	10	14	US-09-016-061-74	Sequence 74, Appl
16	45	81.8	10	14	US-09-016-061-76	Sequence 76, Appl
17	45	81.8	10	14	US-09-016-061-78	Sequence 78, Appl
18	45	81.8	10	17	US-09-339-922A-40	Sequence 40, Appl
19	45	81.8	10	17	US-09-339-922A-72	Sequence 72, Appl
20	45	81.8	10	17	US-09-339-922A-74	Sequence 74, Appl
21	45	81.8	10	17	US-09-339-922A-76	Sequence 76, Appl
22	45	81.8	10	17	US-09-339-922A-78	Sequence 78, Appl
23	45	81.8	117	1	PCT-US98-25828-54	Sequence 54, Appl
24	45	81.8	117	1	PCT-US98-25828-56	Sequence 56, Appl
25	45	81.8	117	11	US-08-790-540-2	Sequence 2, Appl
26	45	81.8	117	11	US-08-790-540-6	Sequence 6, Appl
27	45	81.8	117	11	US-08-790-540A-2	Sequence 2, Appl
28	45	81.8	117	11	US-08-790-540A-6	Sequence 6, Appl
29	45	81.8	117	11	US-08-791-391-2	Sequence 2, Appl
30	45	81.8	117	11	US-08-791-391-6	Sequence 6, Appl
31	45	81.8	117	11	US-08-791-391A-2	Sequence 2, Appl
32	45	81.8	117	11	US-08-791-391A-6	Sequence 6, Appl
33	45	81.8	117	13	US-08-986-016-54	Sequence 54, Appl
34	45	81.8	117	13	US-08-986-016-56	Sequence 56, Appl
35	45	81.8	117	14	US-09-016-061-2	Sequence 2, Appl
36	45	81.8	117	14	US-09-016-061-6	Sequence 6, Appl
37	45	81.8	117	17	US-09-339-922A-2	Sequence 2, Appl
38	45	81.8	117	17	US-09-339-922A-6	Sequence 6, Appl
39	45	81.8	118	1	PCT-US98-25828-50	Sequence 50, Appl
40	45	81.8	118	1	PCT-US98-25828-51	Sequence 51, Appl
41	45	81.8	118	1	PCT-US98-25828-52	Sequence 52, Appl
42	45	81.8	118	1	PCT-US98-25828-53	Sequence 53, Appl
43	45	81.8	118	13	US-08-986-016-50	Sequence 50, Appl
44	45	81.8	118	13	US-08-986-016-51	Sequence 51, Appl
45	45	81.8	118	13	US-08-986-016-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-94
; Sequence 94, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-94

Query Match          100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSFAS 10
    |||||
Db 1 ARNHGSFAS 10

RESULT 2
US-09-339-922A-96
; Sequence 96, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-96

Query Match          100.0%; Score 55; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSFAS 10
    |||||
Db 1 ARNHGSFAS 10

RESULT 3
US-09-016-061-60
; Sequence 60, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-60
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Query Match          92.7%; Score 51; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ARNHGSFA 9
    |||||
Db 1 ARNHGSFA 9
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RESULT 4

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US-09-339-922A-60
; Sequence 60, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-60
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Query Match          92.7%; Score 51; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ARNHGSFA 9
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Db 1 ARNHGSFA 9
```

RESULT 5

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US-09-016-061-68
; Sequence 68, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-68

Query Match 89.1%; Score 49; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARNHGGSFAS 10
||||:|||||
DB 1 ARHNYGSFAS 10

RESULT 6

US-09-016-061-96
Sequence 96, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-96

Query Match 89.1%; Score 49; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARNHGGSFAS 10
||||:|||||
DB 1 ARHNYGSFAS 10

RESULT 7

US-09-339-922A-68
Sequence 68, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-68

Query Match 89.1%; Score 49; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARNHGGSFAS 10
||||:|||||
DB 1 ARHNYGSFAS 10

RESULT 8

US-09-339-922A-94
Sequence 94, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 94
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-94

Query Match 89.1%; Score 49; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEFAS 10
| | | | | | | | | |
Db 1 ARNHGSEFYS 10

RESULT 9
US-09-016-061-70
; Sequence 70, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

QY 1 ARNHGSEFAS 10
| | | | | | | | | |
Db 1 ARNHGSEFYS 10

RESULT 10
US-09-016-061-80
; Sequence 80, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 83.6%; Score 46; DB 14; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.048;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSEFAS 10
| | | | | | | | | |
Db 1 ARNHGSEFAT 10

RESULT 10
US-09-016-061-80
; Sequence 80, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 83.6%; Score 46; DB 17; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.048;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-80

Query Match 83.6%; Score 46; DB 14; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.048;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSEFAS 10
| | | | | | | | | |
Db 1 ARNHGSEFAA 10

RESULT 11
US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-70

Query Match 83.6%; Score 46; DB 17; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.048;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAS 10
||||:||||:
Db 1 ARHNHGSFAT 10

RESULT 12

US-09-339-922A-80

; Sequence 80, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-80

Query Match 83.6%; Score 46; DB 17; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.048;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFAS 10
||||:||||:
Db 1 ARHNHGSFAT 10

RESULT 13

US-09-016-061-40

; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-40

Query Match 81.8%; Score 45; DB 14; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.073;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
||||:||||:
Db 1 ARHNHGSFA 9

RESULT 14

US-09-016-061-72

; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match 81.8%; Score 45; DB 14; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.073;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
||||:||||:
Db 1 ARHNHGSFA 9

RESULT 15

US-09-016-061-74

; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-74

Query Match 81.8%; Score 45; DB 14; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.073;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARNHGSFA 9
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:26
Job time: 1337 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:19 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-94

Perfect score: 55

Sequence: 1 ARNHGSPAS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 1317366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	69.1	196	5	US-09-741-669-368
2	35	63.6	291	1	PCT-US00-30086-11
3	35	63.6	274	1	PCT-US00-30086-2
4	35	63.6	681	1	PCT-US00-30086-4
5	34	61.8	94	5	US-09-557-917-14
6	34	61.8	94	5	US-09-557-917-45
7	34	61.8	94	5	US-09-557-917-48
8	34	61.8	94	5	US-09-557-917-77
9	34	61.8	94	5	US-09-557-917-84
10	34	61.8	94	5	US-09-557-917-90
11	34	61.8	94	5	US-09-557-917-101
12	34	61.8	237	5	US-09-488-725A-3528
13	34	61.8	482	6	US-09-269-308-4703
14	33	60.0	216	5	US-09-489-039A-7908
15	33	60.0	426	5	US-09-489-039A-13845
16	32	58.2	136	5	US-09-489-039A-9897
17	32	58.2	231	5	US-09-172-952-32
18	32	58.2	231	5	US-09-172-952-33
19	32	58.2	231	5	US-09-557-735-32
20	32	58.2	231	5	US-09-557-735-33
21	32	58.2	238	5	US-09-172-952-18
22	32	58.2	238	5	US-09-557-735-18
23	32	58.2	285	5	US-09-489-039A-12402
24	32	58.2	465	6	US-09-257-931-3140
25	32	58.2	465	6	US-09-253-625-2533
26	32	58.2	465	6	US-09-269-308-4162
27	31	56.4	173	5	US-09-489-039A-9058

28 31 56.4 183 6 US-60-258-272-114 Sequence 114, Appl
29 31 56.4 254 6 US-60-257-931-3589 Sequence 3589, Ap
30 31 56.4 254 6 US-60-233-625-2761 Sequence 2761, Ap
31 31 56.4 254 6 US-60-269-308-4611 Sequence 4611, Ap
32 31 56.4 265 5 US-09-732-091-44 Sequence 44, Appl
33 31 56.4 703 5 US-09-595-298A-796 Sequence 796, Appl
34 31 56.4 787 5 US-09-107-433-4612 Sequence 4612, Ap
35 30 54.5 13 5 US-09-635-434-4 Sequence 4, Appli
36 30 54.5 73 1 PCT-US01-01322-605 Sequence 605, Appl
37 30 54.5 94 5 US-09-557-917-39 Sequence 39, Appl
38 30 54.5 94 5 US-09-557-917-59 Sequence 59, Appl
39 30 54.5 94 5 US-09-557-917-63 Sequence 63, Appl
40 30 54.5 127 5 US-09-488-725A-5806 Sequence 5806, Ap
41 30 54.5 196 1 PCT-US01-01435-63 Sequence 63, Appl
42 30 54.5 198 5 US-09-595-298A-784 Sequence 784, Appl
43 30 54.5 200 5 US-09-595-298A-783 Sequence 783, Appl
44 30 54.5 224 5 US-09-595-298A-782 Sequence 782, Appl
45 30 54.5 225 1 PCT-US01-01435-117 Sequence 117, Appl

ALIGNMENTS

RESULT 1
US-09-741-669-368
; Sequence 368, Application US/09741669
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlssen, Kari L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741.669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-368

Query Match 69.1%, Score 38; DB 5; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNHGSF 8
| | | | |
Db 105 HNHGSF 110

RESULT 2
PCT-US00-30086-11
; Sequence 11, Application PC/TUS0030086
; GENERAL INFORMATION:
; APPLICANT: Mello, Charlene M.
; APPLICANT: Arcidiacono, Steven
; TITLE OF INVENTION: Novel Purification and Fiber Spinning Techniques for
; FILE REFERENCE: ARMY-03665
; CURRENT APPLICATION NUMBER: PCT/US00/30086
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Nephila clavipes
PCT-US00-30086-11

Query Match 63.6%; Score 35; DB 1; Length 74;
 Best Local Similarity 75.0%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HHGGSFAS 10
 I:|||||
 Db 8 HHGSMAS 15

RESULT 3
 PCT-US00-30086-2
 ; Sequence 2, Application PC/TUS0030086
 ; GENERAL INFORMATION:
 ; APPLICANT: Mello, Charlene M.
 ; APPLICANT: Arcidiacono, Steven
 ; TITLE OF INVENTION: Novel Purification and Fiber Spinning Techniques for
 ; TITLE OF INVENTION: Protein Fibers
 ; FILE REFERENCE: ARMY-03665
 ; CURRENT APPLICATION NUMBER: PCT/US00/30086
 ; CURRENT FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 291
 ; TYPE: PRT
 ; ORGANISM: Nephila clavipes
 PCT-US00-30086-2

Query Match 63.6%; Score 35; DB 1; Length 291;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HHGGSFAS 10
 I:|||||
 Db 8 HHGSMAS 15

RESULT 4
 PCT-US00-30086-4
 ; Sequence 4, Application PC/TUS0030086
 ; GENERAL INFORMATION:
 ; APPLICANT: Mello, Charlene M.
 ; APPLICANT: Arcidiacono, Steven
 ; TITLE OF INVENTION: Novel Purification and Fiber Spinning Techniques for
 ; TITLE OF INVENTION: Protein Fibers
 ; FILE REFERENCE: ARMY-03665
 ; CURRENT APPLICATION NUMBER: PCT/US00/30086
 ; CURRENT FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 681
 ; TYPE: PRT
 ; ORGANISM: Nephila clavipes
 PCT-US00-30086-4

Query Match 63.6%; Score 35; DB 1; Length 681;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HHGGSFAS 10
 I:|||||
 Db 8 HHGSMAS 15

RESULT 5
 US-09-557-917-14
 ; Sequence 14, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko

; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-14

Query Match 61.8%; Score 34; DB 5; Length 94;
 Best Local Similarity 66.7%; Pred. No. 5.1;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFAS 10
 |||||
 Db 80 RHNYGVFES 88

RESULT 6
 US-09-557-917-45
 ; Sequence 45, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-45

Query Match 61.8%; Score 34; DB 5; Length 94;
 Best Local Similarity 66.7%; Pred. No. 5.1;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNGSFAS 10
 |||||
 Db 80 RHNYGVFES 88

RESULT 7
 US-09-557-917-48
 ; Sequence 48, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko

; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 61.8%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 8
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 61.8%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 9
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF

; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 61.8%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 10
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 61.8%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNGSFAS 10
Db 80 RHNYGVFES 88

RESULT 11
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77579
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-357-917-101

Query Match 61.8%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY '2 RHNHGSPAS 10
| | | | | | |
Db 80 RHNYGVFES 88

RESULT 12
US-09-488-725A-3528
; Sequence 3528, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Huseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3528
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3528

Query Match 61.8%; Score 34; DB 5; Length 237;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
: | | | | :
Db 177:KHNGHAY 183

RESULT 13

US-60-269-308-4703
; Sequence 4703, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in Staphylococcus aureus, ps
; TITLE OF INVENTION: aeruginosa, Klebsiella pneumoniae, Salmonella typhimurium, an
; TITLE OF INVENTION: faecalis
; FILE REFERENCE: ELITRA-017PRS
; CURRENT APPLICATION NUMBER: US/60/269,308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4703
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-60-269-308-4703

Query Match 61.8%; Score 34; DB 6; Length 482;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
| | | | | | |
Db 29 ARHNDGEF 36

RESULT 14
US-09-489-039A-7908
; Sequence 7908, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7908
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7908

Query Match 60.0%; Score 33; DB 5; Length 216;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSFAS 10
: | | | | | | |
Db 60 DHGSFAS 66

RESULT 15
US-09-489-039A-13845
; Sequence 13845, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29

;
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13845
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13845

Query Match 60.0%; Score 33; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RHNG 6
Db 18 RHNG 22

Search completed: March 28, 2001, 07:22:19
Job time: 1511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:26 ; Search time 828.17 Seconds
(Without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGSPYS 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
1: /cgnl_7/ptodata/1/paa/PCRVUS_COMB.pep.*
2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
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16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	58	100.0	10	14	US-09-016-061-96
2	58	100.0	10	17	US-09-339-922A-94
3	52	89.7	10	14	US-09-016-061-100
4	52	89.7	10	17	US-09-339-922A-100
5	49	84.5	10	14	US-09-016-061-94
6	49	84.5	10	17	US-09-339-922A-96
7	48	82.8	10	14	US-09-016-061-66
8	48	82.8	10	14	US-09-016-061-98
9	48	82.8	10	17	US-09-339-922A-66
10	48	82.8	10	17	US-09-339-922A-98
11	47	81.0	10	14	US-09-016-061-60

12	47	81.0	10	17	US-09-339-922A-60	Sequence 60, Appl
13	45	77.6	129	18	US-09-428-944-2741	Sequence 2741, Ap
14	43	74.1	10	14	US-09-016-061-68	Sequence 68, Appl
15	43	74.1	10	17	US-09-339-922A-68	Sequence 68, Appl
16	41	70.7	10	14	US-09-016-061-40	Sequence 40, Appl
17	41	70.7	10	14	US-09-016-061-64	Sequence 64, Appl
18	41	70.7	10	14	US-09-016-061-70	Sequence 70, Appl
19	41	70.7	10	14	US-09-016-061-72	Sequence 72, Appl
20	41	70.7	10	14	US-09-016-061-74	Sequence 74, Appl
21	41	70.7	10	14	US-09-016-061-76	Sequence 76, Appl
22	41	70.7	10	14	US-09-016-061-80	Sequence 80, Appl
23	41	70.7	10	14	US-09-016-061-88	Sequence 88, Appl
24	41	70.7	10	17	US-09-339-922A-40	Sequence 40, Appl
25	41	70.7	10	17	US-09-339-922A-64	Sequence 64, Appl
26	41	70.7	10	17	US-09-339-922A-70	Sequence 70, Appl
27	41	70.7	10	17	US-09-339-922A-72	Sequence 72, Appl
28	41	70.7	10	17	US-09-339-922A-74	Sequence 74, Appl
29	41	70.7	10	17	US-09-339-922A-76	Sequence 76, Appl
30	41	70.7	10	17	US-09-339-922A-78	Sequence 78, Appl
31	41	70.7	10	17	US-09-339-922A-80	Sequence 80, Appl
32	41	70.7	117	1	PCT-US98-25828-54	Sequence 54, Appl
33	41	70.7	117	11	US-08-790-540-2	Sequence 2, Appl
34	41	70.7	117	11	US-08-790-540-6	Sequence 6, Appl
35	41	70.7	117	11	US-08-790-540A-2	Sequence 2, Appl
36	41	70.7	117	11	US-08-791-391-2	Sequence 2, Appl
37	41	70.7	117	11	US-08-791-391A-2	Sequence 2, Appl
38	41	70.7	117	11	US-08-791-391A-6	Sequence 6, Appl
39	41	70.7	117	11	US-08-791-391A-2	Sequence 2, Appl
40	41	70.7	117	11	US-08-791-391A-6	Sequence 6, Appl
41	41	70.7	117	11	US-08-791-391A-2	Sequence 2, Appl
42	41	70.7	117	13	US-08-986-016-54	Sequence 54, Appl
43	41	70.7	117	13	US-08-986-016-56	Sequence 56, Appl
44	41	70.7	117	14	US-09-016-061-2	Sequence 2, Appl
45	41	70.7	117	14	US-09-016-061-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-96
; Sequence 96, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-96

Query Match 100.0%; Score 58; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSEFYS 10
Db 1 ARNHGSEFYS 10

RESULT 2

US-09-339-922A-94
; Sequence 94, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-94

Query Match 100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSEFYS 10
Db 1 ARNHGSEFYS 10

RESULT 3

US-09-016-061-100
; Sequence 100, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016, 061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-100

Query Match 89.7%; Score 52; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSEFYS 10
Db 1 ARNHGSEFYS 10

RESULT 4

US-09-339-922A-100
; Sequence 100, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-100

Query Match 89.7%; Score 52; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSEFYS 10
Db 1 ARNHGSEFYS 10

RESULT 5

US-09-016-061-94
; Sequence 94, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-94

Query Match: 84.5%; Score 49; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGFSY 10
| | | | | | | | | |
DB 1 ARNHGFSAS 10

RESULT 6
US-09-339-922A-96
; Sequence 96, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-96

Query Match: 84.5%; Score 49; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGFSY 10
| | | | | | | | | |
DB 1 ARNHGFSAS 10

RESULT 7
US-09-016-061-66
; Sequence 66, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-66

Query Match: 82.8%; Score 48; DB 14; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.029;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGFSY 9
| | | | | | | | | |
DB 1 ARNHGFSY 9

RESULT 8
US-09-016-061-98
; Sequence 98, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-98

Query Match 82.8%; Score 48; DB 14; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.029;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPY 9
||||:||||
Db 1 ARHNYGSFY 9

RESULT 9

US-09-339-922A-66
; Sequence 66, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-66

Query Match 82.8%; Score 48; DB 17; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.029;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPY 9
||||:||||
Db 1 ARHNYGSFY 9

RESULT 10

US-09-339-922A-98
; Sequence 98, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren

; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-98

Query Match 82.8%; Score 48; DB 17; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.029;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPY 9
||||:||||
Db 1 ARHNYGSFY 9

RESULT 11

US-09-016-061-60
; Sequence 60, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-60

Query Match 81.0%; Score 47; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-09-016-061-68
; Sequence 68, Application US/09016061

Query Match 74.1%; Score 43; DB 17; Length 10;
Best Local Similarity 80.0%; Pred. NO. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNHGSFYS 10
Db 1 ARHNHGSFAS 10

Search completed: March 28, 2001, 07:18:27
Job time: 1338 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:19 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: us-09-016-061-96
Perfect score: 58
Sequence: 1 ARHNGSPYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgnl_1/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_1/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgnl_1/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_1/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_1/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_1/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	65.5	196	5	US-09-741-669-368
2	37	63.8	334	5	US-09-488-725A-1864
3	37	63.8	382	5	US-09-488-725A-5436
4	36	62.1	552	5	US-09-489-039A-13735
5	36	62.1	557	5	US-09-489-039A-13795
6	34	58.6	145	1	PCT-US01-02570-29
7	34	58.6	145	5	US-09-751-518-29
8	34	58.6	237	5	US-09-488-725A-3528
9	34	58.6	482	6	US-60-269-308-4703
10	33	56.9	94	5	US-09-557-917-14
11	33	56.9	94	5	US-09-557-917-45
12	33	56.9	94	5	US-09-557-917-48
13	33	56.9	94	5	US-09-557-917-77
14	33	56.9	94	5	US-09-557-917-84
15	33	56.9	94	5	US-09-557-917-90
16	33	56.9	94	5	US-09-557-917-101
17	33	56.9	376	5	US-09-488-725A-2041
18	33	56.9	388	5	US-09-488-725A-5613
19	33	56.9	426	5	US-09-489-039A-13845
20	33	56.9	502	5	US-09-679-187-12
21	33	56.9	503	5	US-09-679-187-2
22	32	55.2	81	5	US-09-759-143-556
23	32	55.2	81	5	US-09-679-426-556
24	32	55.2	81	5	US-09-685-166-556
25	32	55.2	81	5	US-09-780-669-556
26	32	55.2	218	5	US-09-489-039A-10326
27	32	55.2	252	5	US-09-465-587-187

28 32 55.2 407 5 US-09-489-039A-7924 Sequence 7924, Ap
29 32 55.2 474 5 US-09-684-458-4 Sequence 4, Appli
30 32 55.2 483 5 US-09-489-039A-9906 Sequence 9906, Ap
31 32 55.2 739 5 US-09-489-039A-11874 Sequence 11874, A
32 32 55.2 758 5 US-09-499-468-39 Sequence 39, Appl
33 31 53.4 260 5 US-09-794-764-179 Sequence 179, App
34 31 53.4 685 5 US-09-489-039A-11090 Sequence 11090, A
35 31 53.4 787 5 US-09-107-433-4612 Sequence 4612, Ap
36 30 51.7 13 5 US-09-635-434-4 Sequence 4, Appli
37 30 51.7 73 1 PCT-US01-01322-605 Sequence 605, App
38 30 51.7 83 1 PCT-US01-01324-2372 Sequence 2372, Ap
39 30 51.7 116 5 US-09-214-095D-15 Sequence 15, Appl
40 30 51.7 116 5 US-09-214-095D-90 Sequence 90, Appl
41 30 51.7 116 5 US-09-214-095D-90 Sequence 90, Appl
42 30 51.7 198 5 US-09-595-298A-784 Sequence 784, App
43 30 51.7 200 5 US-09-595-298A-783 Sequence 783, App
44 30 51.7 224 5 US-09-595-298A-782 Sequence 782, App
45 30 51.7 226 5 US-09-171-741C-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-741-669-368
; Sequence 368, Application US/09741669
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; proliferation of E. coli
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-368

Query Match 65.5%; Score 38; DB 5; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 HNHGSF 8
DB 105 HNHGSF 110

RESULT 2
US-09-488-725A-1864
; Sequence 1864, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450

; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US09/662,191
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: US09/693,036
 ; PRIOR FILING DATE: 2000-10-19
 ; PRIOR APPLICATION NUMBER: US09/727,344
 ; PRIOR FILING DATE: 2000-11-29
 ; NUMBER OF SEQ ID NOS: 7144
 ; SOFTWARE: pt_FL_genes_b Versions 1.0
 ; SEQ ID NO 1864
 ; LENGTH: 355
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-488-725A-1864

Query Match 63.8%; Score 37; DB 5; Length 354;
 Best Local Similarity 60.0%; Pred. No. 8.2;
 Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 1 ARNHGSEFYS 10
 I: I I I I I
 Db 196 AKHGSFAFYS 205

RESULT 3
 US-09-488-725A-5436
 ; Sequence 5436, Application US/09488725A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq Inc
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
 ; FILE REFERENCE: 784FLPCT
 ; CURRENT APPLICATION NUMBER: US/09/488,725A
 ; PRIOR APPLICATION NUMBER: US/09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: US09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: US09/620,312
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: US09/653,450
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US09/662,191
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: US09/693,036
 ; PRIOR FILING DATE: 2000-10-19
 ; PRIOR APPLICATION NUMBER: US09/727,344
 ; NUMBER OF SEQ ID NOS: 7144
 ; SOFTWARE: pt_FL_genes_b Versions 1.0
 ; SEQ ID NO 5436
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-488-725A-5436

Query Match 63.8%; Score 37; DB 5; Length 382;
 Best Local Similarity 60.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 1 ARNHGSEFYS 10
 I: I I I I I
 Db 224 AKHGSFAFYS 233

RESULT 4
 US-09-489-039A-13735
 ; Sequence 13735, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13735
 ; LENGTH: 552
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13735

Query Match 62.1%; Score 36; DB 5; Length 552;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 ARNHGSGFY 9
 I I I I I
 Db 475 ACKHGGFY 483

RESULT 5
 US-09-489-039A-13795
 ; Sequence 13795, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 13795
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13795

Query Match 62.1%; Score 36; DB 5; Length 557;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 ARNHGSGFY 9
 I I I I I
 Db 482 ACKHGGFY 490

RESULT 6
 PCT-US01-02570-29
 ; Sequence 29, Application PC/TUS0102570
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; APPLICANT: Boyle, Bryan J
 ; APPLICANT: Kuo, Chiauyn
 ; APPLICANT: Mize, Nancy K
 ; APPLICANT: Haley, Dana A
 ; APPLICANT: Arterburn, Matthew C
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Liu, Chinghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Drmanac, Radoje T
 ; APPLICANT: Yeung, George
 ; APPLICANT: Palencia, Servando
 ; TITLE OF INVENTION: Methods and Materials Relating to Leukocyte
 ; TITLE OF INVENTION: Immunoglobulin Receptor-Like (LIR-Like) Polypeptides
 ; TITLE OF INVENTION: and Polynucleotides

```
; FILE REFERENCE: 21272-023(HVS-19CIP)
; CURRENT APPLICATION NUMBER: PCT/US01/02570
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: Not Yet Assigned
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 09/642,610
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/524,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-02570-29
```

```
Query Match 58.6%; Score 34; DB 1; Length 145;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 3 HNHGSFYS 10
   ||| |||
Db 102 HNHSEYS 109
```

```
RESULT 7
US-09-751-518-29
; Sequence 29, Application US/09751518
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Kuo, Chiauyn
; APPLICANT: Mize, Nancy K
; APPLICANT: Haley, Dana A
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; TITLE OF INVENTION: Methods and Materials Relating to Leukocyte
; TITLE OF INVENTION: Immunoglobulin Receptor-Like (LIR-Like) Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: HVS-19CIP
; CURRENT APPLICATION NUMBER: US/09/751,518
; CURRENT FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 09/642,610
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/524,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 145
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-518-29
```

```
Query Match 58.6%; Score 34; DB 5; Length 145;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 3 HNHGSFYS 10
   ||| |||
Db 102 HNHSEYS 109
```

```
RESULT 8
US-09-488-725A-3528
; Sequence 3528, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3528
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3528
```

```
Query Match 58.6%; Score 34; DB 5; Length 237;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 RHNHGSF 8
   |||||
Db 177 KHNHAY 183
```

```
RESULT 9
US-60-269-308-4703
; Sequence 4703, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in Staphylococcus aureus, Ps
; TITLE OF INVENTION: aeruginosa, Klebsiella pneumoniae, Salmonella typhimurium, an
; TITLE OF INVENTION: faecalis
; FILE REFERENCE: ELITRA.017PR5
; CURRENT APPLICATION NUMBER: US/60/269,308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4703
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-60-269-308-4703

Query Match 58.6%; Score 34; DB 6; Length 482;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
|||||
DB 29 ARNDGEF 36

RESULT 10
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFYS 10
|||||
DB 80 RHNHGVFES 88

RESULT 11
US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFYS 10
|||||
DB 80 RHNHGVFES 88

RESULT 12
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFYS 10
|||||
DB 80 RHNHGVFES 88

RESULT 13
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77

; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 | | | | |
Db 80 RHNGVFPES 88

RESULT 14
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 | | | | |
Db 80 RHNGVFPES 88

RESULT 15
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
 | | | | |
Db 80 RHNGVFPES 88

Search completed: March 28, 2001, 07:22:19
Job time: 1511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:27 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
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2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
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10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
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16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	58	100.0	10	14	US-09-016-061-98
2	58	100.0	10	17	US-09-339-922A-98
3	53	91.4	10	14	US-09-016-061-66
4	53	91.4	10	14	US-09-016-061-100
5	53	91.4	10	17	US-09-339-922A-66
6	53	91.4	10	17	US-09-339-922A-100
7	49	84.5	10	14	US-09-016-061-74
8	49	84.5	10	17	US-09-339-922A-74
9	48	82.8	10	14	US-09-016-061-96
10	48	82.8	10	17	US-09-339-922A-94
11	46	79.3	10	14	US-09-016-061-40
					Sequence 98, Appl
					Sequence 98, Appl
					Sequence 66, Appl
					Sequence 100, Appl
					Sequence 66, Appl
					Sequence 100, Appl
					Sequence 74, Appl
					Sequence 74, Appl
					Sequence 96, Appl
					Sequence 94, Appl
					Sequence 40, Appl

12	46	79.3	10	14	US-09-016-061-64	Sequence 64, Appl
13	46	79.3	10	14	US-09-016-061-68	Sequence 68, Appl
14	46	79.3	10	14	US-09-016-061-70	Sequence 70, Appl
15	46	79.3	10	14	US-09-016-061-72	Sequence 72, Appl
16	46	79.3	10	14	US-09-016-061-76	Sequence 76, Appl
17	46	79.3	10	14	US-09-016-061-78	Sequence 78, Appl
18	46	79.3	10	14	US-09-016-061-80	Sequence 80, Appl
19	46	79.3	10	17	US-09-339-922A-40	Sequence 40, Appl
20	46	79.3	10	17	US-09-339-922A-64	Sequence 64, Appl
21	46	79.3	10	17	US-09-339-922A-68	Sequence 68, Appl
22	46	79.3	10	17	US-09-339-922A-70	Sequence 70, Appl
23	46	79.3	10	17	US-09-339-922A-72	Sequence 72, Appl
24	46	79.3	10	17	US-09-339-922A-76	Sequence 76, Appl
25	46	79.3	10	17	US-09-339-922A-78	Sequence 78, Appl
26	46	79.3	10	17	US-09-339-922A-80	Sequence 80, Appl
27	46	79.3	117	1	PCT-US98-25828-54	Sequence 54, Appl
28	46	79.3	117	1	PCT-US98-25828-56	Sequence 56, Appl
29	46	79.3	117	11	US-08-790-540-2	Sequence 2, Appl
30	46	79.3	117	11	US-08-790-540-6	Sequence 6, Appl
31	46	79.3	117	11	US-08-790-540A-2	Sequence 2, Appl
32	46	79.3	117	11	US-08-790-540A-6	Sequence 6, Appl
33	46	79.3	117	11	US-08-791-391-2	Sequence 2, Appl
34	46	79.3	117	11	US-08-791-391-6	Sequence 6, Appl
35	46	79.3	117	11	US-08-791-391A-2	Sequence 2, Appl
36	46	79.3	117	11	US-08-791-391A-6	Sequence 6, Appl
37	46	79.3	117	13	US-08-986-016-54	Sequence 54, Appl
38	46	79.3	117	13	US-08-986-016-56	Sequence 56, Appl
39	46	79.3	117	14	US-09-016-061-2	Sequence 2, Appl
40	46	79.3	117	14	US-09-016-061-6	Sequence 6, Appl
41	46	79.3	117	17	US-09-339-922A-2	Sequence 2, Appl
42	46	79.3	117	17	US-09-339-922A-6	Sequence 6, Appl
43	46	79.3	118	1	PCT-US98-25828-50	Sequence 50, Appl
44	46	79.3	118	1	PCT-US98-25828-51	Sequence 51, Appl
45	46	79.3	118	1	PCT-US98-25828-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-98
; Sequence 98, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-98

Query Match 100.0%; Score 58; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
|||||
Db 1 ARHNYGSFYE 10

RESULT 2

US-09-339-922A-98
; Sequence 98, Application US/093399922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-98

Query Match 100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
|||||
Db 1 ARHNYGSFYE 10

RESULT 3

US-09-016-061-66
; Sequence 66, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-100

; APPLICATION NUMBER: US/09/016.061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-66

Query Match 91.4%; Score 53; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
|||||
Db 1 ARHNYGSFY 9

RESULT 4

US-09-016-061-100
; Sequence 100, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-100

Query Match 91.4%; Score 53; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
| | | | | | | | | |
Db 1 ARHNYGSFY 9

RESULT 5

US-09-339-922A-66
; Sequence 66, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-66

Query Match 91.4%; Score 53; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
| | | | | | | | | |
Db 1 ARHNYGSFY 9

RESULT 6

US-09-339-922A-100
; Sequence 100, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-100

Query Match 91.4%; Score 53; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
| | | | | | | | | |
Db 1 ARHNYGSFY 9

RESULT 7

US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-016-061-74

US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-016-061-74

Query Match 84.5%; Score 49; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 10
| | | | | | | | | |
Db 1 ARHNYGSFAE 10

RESULT 8

US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match 84.5%; Score 49; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
| | | | | | | | | |
DB 1 ARHNYGSFAE 10

RESULT 9

US-09-016-061-96
; Sequence 96, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-96

Query Match 82.8%; Score 48; DB 14; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
| | | | | | | | | |
DB 1 ARHNGHSFY 9

RESULT 10

US-09-339-922A-94
; Sequence 94, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren

; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-94

Query Match 82.8%; Score 48; DB 17; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
| | | | | | | | | |
DB 1 ARHNGHSFY 9

RESULT 11

US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-40

Query Match 79.3%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 12

US-09-016-061-64
 ; Sequence 64, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 64:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-016-061-64

Query Match 79.3%; Score 46; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 13

US-09-016-061-68
 ; Sequence 68, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California

; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-016-061-68

Query Match 79.3%; Score 46; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 14

US-09-016-061-70
 ; Sequence 70, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001

Search completed: March 28, 2001, 07:18:27
Job time: 1338 sec

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-70

Query Match 79.3%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
|||||||
Db 1 ARHNYGSF 8

RESULT 15
US-09-016-061-72
Sequence 72, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-72

Query Match 79.3%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
|||||||
Db 1 ARHNYGSF 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:19 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFYE 10

Scoring table:
BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pcp:*
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pcp:*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pcp:*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pcp:*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	62.1	94	5	US-09-557-917-14
2	36	62.1	94	5	US-09-557-917-45
3	36	62.1	94	5	US-09-557-917-48
4	36	62.1	94	5	US-09-557-917-77
5	36	62.1	94	5	US-09-557-917-84
6	36	62.1	94	5	US-09-557-917-90
7	36	62.1	94	5	US-09-557-917-101
8	35	60.3	690	5	US-09-489-039A-13988
9	34	58.6	150	5	US-09-316-633-351
10	34	58.6	197	5	US-09-595-329A-1075
11	34	58.6	288	6	US-60-259-128-4587
12	34	58.6	317	5	US-09-107-433-4862
13	34	58.6	610	5	US-09-489-039A-8216
14	33	56.9	246	5	US-09-595-329A-635
15	33	56.9	248	5	US-09-595-329A-634
16	33	56.9	275	5	US-09-595-329A-633
17	33	56.9	331	5	US-09-489-039A-9639
18	33	56.9	350	6	US-60-259-128-4660
19	33	56.9	512	5	US-09-107-433-5122
20	32	55.2	15	5	US-09-756-983-11
21	32	55.2	80	5	US-09-673-809-51
22	32	55.2	89	5	US-09-673-809-2
23	32	55.2	94	5	US-09-766-378-37
24	32	55.2	94	5	US-09-692-933-180
25	32	55.2	94	5	US-09-557-917-12
26	32	55.2	94	5	US-09-557-917-13
27	32	55.2	94	5	US-09-557-917-15

28	32	55.2	94	5	US-09-557-917-16	Sequence 16, Appl
29	32	55.2	94	5	US-09-557-917-17	Sequence 17, Appl
30	32	55.2	94	5	US-09-557-917-18	Sequence 18, Appl
31	32	55.2	94	5	US-09-557-917-19	Sequence 19, Appl
32	32	55.2	94	5	US-09-557-917-20	Sequence 20, Appl
33	32	55.2	94	5	US-09-557-917-21	Sequence 21, Appl
34	32	55.2	94	5	US-09-557-917-22	Sequence 22, Appl
35	32	55.2	94	5	US-09-557-917-24	Sequence 24, Appl
36	32	55.2	94	5	US-09-557-917-25	Sequence 25, Appl
37	32	55.2	94	5	US-09-557-917-26	Sequence 26, Appl
38	32	55.2	94	5	US-09-557-917-27	Sequence 27, Appl
39	32	55.2	94	5	US-09-557-917-28	Sequence 28, Appl
40	32	55.2	94	5	US-09-557-917-29	Sequence 28, Appl
41	32	55.2	94	5	US-09-557-917-30	Sequence 30, Appl
42	32	55.2	94	5	US-09-557-917-31	Sequence 31, Appl
43	32	55.2	94	5	US-09-557-917-32	Sequence 32, Appl
44	32	55.2	94	5	US-09-557-917-33	Sequence 33, Appl
45	32	55.2	94	5	US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 2
US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aiga, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 62.1%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
Db 80 RHNYGVF 86

RESULT 8
US-09-489-039A-13988
; Sequence 13988, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13988
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13988

Query Match 60.3%; Score 35; DB 5; Length 690;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFYE 10
 |||||
Db 447 NYGIFYE 453

RESULT 9
US-09-316-633-351
; Sequence 351, Application US/09316633
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Derived from a
; TITLE OF INVENTION: Human Mesangial Cell Library
; FILE REFERENCE: MLN98-16pA
; CURRENT APPLICATION NUMBER: US/09/316,633
; CURRENT FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/087,052
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 351
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
; NAME/KEY: VARIANT
; LOCATION: (1)...(150)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-316-633-351

Query Match 58.6%; Score 34; DB 5; Length 150;
Best Local Similarity 75.0%; Pred. No. 8.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 ||:||||
Db 117 HNWLSFYE 124

RESULT 10
US-09-595-329A-1075
; Sequence 1075, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948p
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)...(197)
; OTHER INFORMATION: Ceres Seq. ID no. 1013791
; NAME/KEY: misc.feature
; LOCATION: ()...()

; OTHER INFORMATION: xaa is any aa, unknown or other
US-09-595-329A-1075

Query Match 58.6%; Score 34; DB 5; Length 197;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFYE 10
|||||
Db 89 NYGSHYE 95

RESULT 11
US-60-259-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Target Discovery
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ. ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 58.6%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
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Db 93 HNYGAF 98

RESULT 12
US-09-107-433-4862
; Sequence 4862, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4862:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...317
; SEQUENCE DESCRIPTION: SEQ ID NO: 4862:
US-09-107-433-4862

Query Match 58.6%; Score 34; DB 5; Length 317;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
|||||
Db 307 HKYGDFY 313

RESULT 13
US-09-489-039A-8216
; Sequence 8216, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8216
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8216

Query Match 58.6%; Score 34; DB 5; Length 610;
Best Local Similarity 60.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10 ,
|||||
Db 556 AEHNVGHLYE 565

RESULT 14
US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635
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Query Match 56.9%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 RHNYGS 7
Db 131 KHNYGS 136
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RESULT 15
US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VVACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634
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Query Match 56.9%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 RHNYGS 7
Db 133 KHNYGS 138
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Search completed: March 28, 2001, 07:22:19
Job time: 1511 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:27 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNGSPYS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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- 11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
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- 19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
- 20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	14	US-09-016-061-100
2	57	100.0	10	17	US-09-339-922A-100
3	53	93.0	10	14	US-09-016-061-66
4	53	93.0	10	14	US-09-016-061-98
5	53	93.0	10	17	US-09-339-922A-66
6	53	93.0	10	17	US-09-339-922A-98
7	52	91.2	10	14	US-09-016-061-96
8	52	91.2	10	17	US-09-339-922A-94
9	48	84.2	10	14	US-09-016-061-68
10	48	84.2	10	17	US-09-339-922A-68
11	46	80.7	10	14	US-09-016-061-40

12	46	80.7	10	14	US-09-016-061-64	Sequence 54, Appl
13	46	80.7	10	14	US-09-016-061-70	Sequence 70, Appl
14	46	80.7	10	14	US-09-016-061-72	Sequence 72, Appl
15	46	80.7	10	14	US-09-016-061-74	Sequence 74, Appl
16	46	80.7	10	14	US-09-016-061-76	Sequence 76, Appl
17	46	80.7	10	14	US-09-016-061-78	Sequence 78, Appl
18	46	80.7	10	14	US-09-016-061-80	Sequence 80, Appl
19	46	80.7	10	17	US-09-339-922A-40	Sequence 40, Appl
20	46	80.7	10	17	US-09-339-922A-64	Sequence 64, Appl
21	46	80.7	10	17	US-09-339-922A-70	Sequence 70, Appl
22	46	80.7	10	17	US-09-339-922A-72	Sequence 72, Appl
23	46	80.7	10	17	US-09-339-922A-74	Sequence 74, Appl
24	46	80.7	10	17	US-09-339-922A-76	Sequence 76, Appl
25	46	80.7	10	17	US-09-339-922A-78	Sequence 78, Appl
26	46	80.7	10	17	US-09-339-922A-80	Sequence 80, Appl
27	46	80.7	117	1	PCT-US98-25828-54	Sequence 54, Appl
28	46	80.7	117	1	PCT-US98-25828-56	Sequence 56, Appl
29	46	80.7	117	11	US-08-790-540-2	Sequence 2, Appl
30	46	80.7	117	11	US-08-790-540-6	Sequence 6, Appl
31	46	80.7	117	11	US-08-790-540A-2	Sequence 2, Appl
32	46	80.7	117	11	US-08-790-540A-6	Sequence 6, Appl
33	46	80.7	117	11	US-08-791-391-2	Sequence 2, Appl
34	46	80.7	117	11	US-08-791-391-6	Sequence 6, Appl
35	46	80.7	117	11	US-08-791-391A-2	Sequence 2, Appl
36	46	80.7	117	11	US-08-791-391A-6	Sequence 6, Appl
37	46	80.7	117	13	US-08-986-016-54	Sequence 54, Appl
38	46	80.7	117	13	US-08-986-016-56	Sequence 56, Appl
39	46	80.7	117	14	US-09-016-061-2	Sequence 2, Appl
40	46	80.7	117	14	US-09-016-061-6	Sequence 6, Appl
41	46	80.7	117	17	US-09-339-922A-2	Sequence 2, Appl
42	46	80.7	117	17	US-09-339-922A-6	Sequence 6, Appl
43	46	80.7	118	1	PCT-US98-25828-50	Sequence 50, Appl
44	46	80.7	118	1	PCT-US98-25828-51	Sequence 51, Appl
45	46	80.7	118	1	PCT-US98-25828-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-100
; Sequence 100, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001


```

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-100

Query Match          100.0%; Score 57; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10
Db 1 ARHNYGSFYS 10

RESULT 2
US-09-339-922A-100
; Sequence 100, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 100
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-100

Query Match          100.0%; Score 57; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10
Db 1 ARHNYGSFYS 10

RESULT 3
US-09-016-061-66
; Sequence 66, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-66
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-66

Query Match          93.0%; Score 53; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
Db 1 ARHNYGSFY 9

RESULT 4
US-09-016-061-98
; Sequence 98, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-98
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Query Match 93.0%; Score 53; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
| | | | | | | | | |
Db 1 ARHNYGSFY 9

RESULT 5

US-09-339-922A-66
; Sequence 66, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-66

Query Match 93.0%; Score 53; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
| | | | | | | | | |
Db 1 ARHNYGSFY 9

RESULT 6

US-09-339-922A-98
; Sequence 98, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: Complementarity determining region (CDR)
US-09-339-922A-98

Query Match 93.0%; Score 53; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFY 9
| | | | | | | | | |
Db 1 ARHNYGSFY 9

RESULT 7

US-09-016-061-96
; Sequence 96, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-96

Query Match 91.2%; Score 52; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0033;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10
| | | | | | | | | |
Db 1 ARHNYGSFYS 10

RESULT 8

US-09-339-922A-94
; Sequence 94, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-94

Query Match 91.2%; Score 52; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0033;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10

|||||

Db 1 ARHNGSFYS 10

RESULT 9

US-09-016-061-68

; Sequence 68, Application US/09016061

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; APPLICANT: Glaser, Scott M.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061

; FILING DATE: 30-JAN-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/791,391

; FILING DATE: 30-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2965

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-016-061-68

Query Match 84.2%; Score 48; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10

|||||

Db 1 ARHNGSFAS 10

RESULT 10

US-09-339-922A-68

; Sequence 68, Application US/09339922A

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren

0

; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536

; CURRENT APPLICATION NUMBER: US/09/339,922A

; CURRENT FILING DATE: 1999-06-24

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Patent Ver. 2.1

; SEQ ID NO 68

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Mutated

; OTHER INFORMATION: complementarity determining region (CDR)

US-09-339-922A-68

Query Match 84.2%; Score 48; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10

|||||

Db 1 ARHNGSFAS 10

RESULT 11

US-09-016-061-40

; Sequence 40, Application US/09016061

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; APPLICANT: Glaser, Scott M.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

; NUCLEIC ACIDS ENCODING SAME AND METHODS OF USE

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061

; FILING DATE: 30-JAN-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/791,391

; FILING DATE: 30-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2965

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-016-061-40

Query Match 80.7%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 12

US-09-016-061-64
 ; Sequence 64, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 64:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-016-061-64

Query Match 80.7%; Score 46; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 13

US-09-016-061-70
 ; Sequence 70, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California

COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,061
 FILING DATE: 30-JAN-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/791,391
 FILING DATE: 30-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-IX 2965
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-016-061-70

Query Match 80.7%; Score 46; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 14

US-09-016-061-72
 ; Sequence 72, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-72

Query Match 80.7%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
|||||
DB 1 ARHNYGSF 8

RESULT 15
US-09-016-061-74
Sequence 74, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-74

Query Match 80.7%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
|||||
DB 1 ARHNYGSF 8

Search completed: March 28, 2001, 07:18.27
Job time: 1338 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:19 ; Search time 213.09 seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-100

Perfect score: 57

Sequence: 1 ARHNGSFYS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pcp.*

2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pcp.*

3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pcp.*

4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pcp.*

5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pcp.*

6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	66.7	94	5	US-09-557-917-14
2	38	66.7	94	5	US-09-557-917-45
3	38	66.7	94	5	US-09-557-917-48
4	38	66.7	94	5	US-09-557-917-77
5	38	66.7	94	5	US-09-557-917-84
6	38	66.7	94	5	US-09-557-917-90
7	38	66.7	94	5	US-09-557-917-101
8	36	63.2	354	5	US-09-488-725A-1864
9	36	63.2	382	5	US-09-488-725A-5436
10	35	61.4	317	5	US-09-107-433-4862
11	34	59.6	94	5	US-09-557-917-39
12	34	59.6	94	5	US-09-557-917-59
13	34	59.6	94	5	US-09-557-917-63
14	34	59.6	288	6	US-60-259-128-4587
15	33	57.9	94	5	US-09-557-917-55
16	33	57.9	94	5	US-09-557-917-62
17	33	57.9	94	5	US-09-557-917-87
18	33	57.9	94	5	US-09-557-917-108
19	33	57.9	246	5	US-09-595-329A-635
20	33	57.9	248	5	US-09-595-329A-634
21	33	57.9	275	5	US-09-595-329A-633
22	33	57.9	512	5	US-09-107-433-5122
23	32	56.1	15	5	US-09-756-983-11
24	32	56.1	80	5	US-09-673-809-51
25	32	56.1	89	5	US-09-673-809-2
26	32	56.1	94	5	US-09-766-378-37
27	32	56.1	94	5	US-09-692-933-180

28	32	56.1	94	5	US-09-557-917-12	Sequence 12, Appl
29	32	56.1	94	5	US-09-557-917-13	Sequence 13, Appl
30	32	56.1	94	5	US-09-557-917-15	Sequence 15, Appl
31	32	56.1	94	5	US-09-557-917-16	Sequence 16, Appl
32	32	56.1	94	5	US-09-557-917-17	Sequence 17, Appl
33	32	56.1	94	5	US-09-557-917-18	Sequence 18, Appl
34	32	56.1	94	5	US-09-557-917-19	Sequence 19, Appl
35	32	56.1	94	5	US-09-557-917-20	Sequence 20, Appl
36	32	56.1	94	5	US-09-557-917-21	Sequence 21, Appl
37	32	56.1	94	5	US-09-557-917-22	Sequence 22, Appl
38	32	56.1	94	5	US-09-557-917-24	Sequence 24, Appl
39	32	56.1	94	5	US-09-557-917-25	Sequence 25, Appl
40	32	56.1	94	5	US-09-557-917-26	Sequence 26, Appl
41	32	56.1	94	5	US-09-557-917-27	Sequence 27, Appl
42	32	56.1	94	5	US-09-557-917-28	Sequence 28, Appl
43	32	56.1	94	5	US-09-557-917-29	Sequence 29, Appl
44	32	56.1	94	5	US-09-557-917-30	Sequence 30, Appl
45	32	56.1	94	5	US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1

US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 66.7%; Score 38; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RHNGSFYS 10
Db 80 RHNGVFES 88

RESULT 2

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-45

Query Match 66.7%; Score 38; DB 5; Length 94;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
 ||||| |
 Db 80 RHNYGVFES 88

RESULT 3

US-09-557-917-48
 ; Sequence 48, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 48
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-48

Query Match 66.7%; Score 38; DB 5; Length 94;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
 ||||| |
 Db 80 RHNYGVFES 88

RESULT 4

US-09-557-917-77
 ; Sequence 77, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 77
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-77

Query Match 66.7%; Score 38; DB 5; Length 94;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
 ||||| |
 Db 80 RHNYGVFES 88

RESULT 5

US-09-557-917-84
 ; Sequence 84, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 84
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-84

Query Match 66.7%; Score 38; DB 5; Length 94;
 Best Local Similarity 77.8%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 RHNYGSFYS 10
 ||||| |
 Db 80 RHNYGVFES 88

RESULT 6

US-09-557-917-90
 ; Sequence 90, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 66.7%; Score 38; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
| | | | | | | |
Db 80 RHNYGVFES 88

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 66.7%; Score 38; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
| | | | | | | |
Db 80 RHNYGVFES 88

RESULT 8
US-09-488-725A-1864
; Sequence 1864, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 1864
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-1864

Query Match 63.2%; Score 36; DB 5; Length 354;
Best Local Similarity 60.0%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10
| | | | | | | |
Db 196 AKHSGAFYS 205

RESULT 9
US-09-488-725A-5436
; Sequence 5436, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 5436
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5436

Query Match 63.2%; Score 36; DB 5; Length 382;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYS 10
| | | | | | | |
Db 224 AKHSGAFYS 233

RESULT 10
US-09-107-433-4862
; Sequence 4862, Application US/09107433
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinietello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4862:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...317
SEQUENCE DESCRIPTION: SEQ ID NO: 4862:
US-09-107-433-4862

Query Match 61.4%; Score 35; DB 5; Length 317;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
DB 307 HKYGFYFA 314

RESULT 11
US-09-557-917-39
Sequence 39, Application US/09557917
GENERAL INFORMATION:
APPLICANT: Aida, Yoko
TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/557,917
CURRENT FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 09/147,550
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: PCT/JP97/02485
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: JP 8-190933
PRIOR FILING DATE: 1996-07-19

PRIOR APPLICATION NUMBER: JP 9-77979
PRIOR FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 94
TYPE: PRT
ORGANISM: BOVINE
US-09-557-917-39

Query Match 59.6%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
DB 80 RHNYGGMES 88

RESULT 12
US-09-557-917-59
Sequence 59, Application US/09557917
GENERAL INFORMATION:
APPLICANT: Aida, Yoko
TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/557,917
CURRENT FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 09/147,550
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: PCT/JP97/02485
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: JP 8-190933
PRIOR FILING DATE: 1996-07-19
PRIOR APPLICATION NUMBER: JP 9-77979
PRIOR FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 94
TYPE: PRT
ORGANISM: BOVINE
US-09-557-917-59

Query Match 59.6%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
DB 80 RHNYGGMES 88

RESULT 13
US-09-557-917-63
Sequence 63, Application US/09557917
GENERAL INFORMATION:
APPLICANT: Aida, Yoko
TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/557,917
CURRENT FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 09/147,550
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: PCT/JP97/02485
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: JP 8-190933
PRIOR FILING DATE: 1996-07-19
PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-63

Query Match 59.6%; Score 34; DB 5; Length 94;
Best Local Similarity 86.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
| | | | |
Db 80 RHNYGGWES 88

RESULT 14

US-60-259-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Target Discovery
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 59.6%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
| | | | |
Db 93 HNYGAF 98

RESULT 15

US-09-557-917-55
; Sequence 55, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 94
; TYPE: PRT

; ORGANISM: BOVINE
US-09-557-917-55

Query Match 57.9%; Score 33; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFYS 10
| | | | |
Db 80 RHNYGGVES 88

Search completed: March 28, 2001, 07:22:19
Job time: 1511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:13 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNYGSFAD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	69.6	479	5	US-09-489-039A-13978
2	36	64.3	94	5	US-09-557-917-14
3	36	64.3	94	5	US-09-557-917-45
4	36	64.3	94	5	US-09-557-917-48
5	36	64.3	94	5	US-09-557-917-77
6	36	64.3	94	5	US-09-557-917-84
7	36	64.3	94	5	US-09-557-917-90
8	36	64.3	94	5	US-09-557-917-101
9	34	60.7	239	5	US-09-107-433-3471
10	34	60.7	288	6	US-60-259-128-4587
11	33	58.9	246	5	US-09-595-329A-635
12	33	58.9	246	5	US-09-595-329A-634
13	33	58.9	275	5	US-09-595-329A-633
14	32	57.1	15	5	US-09-756-983-11
15	32	57.1	80	5	US-09-673-809-51
16	32	57.1	89	5	US-09-673-809-2
17	32	57.1	94	5	US-09-766-378-37
18	32	57.1	94	5	US-09-692-933-180
19	32	57.1	94	5	US-09-557-917-12
20	32	57.1	94	5	US-09-557-917-13
21	32	57.1	94	5	US-09-557-917-15
22	32	57.1	94	5	US-09-557-917-16
23	32	57.1	94	5	US-09-557-917-17
24	32	57.1	94	5	US-09-557-917-18
25	32	57.1	94	5	US-09-557-917-19
26	32	57.1	94	5	US-09-557-917-20
27	32	57.1	94	5	US-09-557-917-21

28	32	57.1	94	5	US-09-557-917-22	Sequence 22, Appl
29	32	57.1	94	5	US-09-557-917-24	Sequence 24, Appl
30	32	57.1	94	5	US-09-557-917-25	Sequence 25, Appl
31	32	57.1	94	5	US-09-557-917-26	Sequence 26, Appl
32	32	57.1	94	5	US-09-557-917-27	Sequence 27, Appl
33	32	57.1	94	5	US-09-557-917-28	Sequence 28, Appl
34	32	57.1	94	5	US-09-557-917-29	Sequence 29, Appl
35	32	57.1	94	5	US-09-557-917-30	Sequence 30, Appl
36	32	57.1	94	5	US-09-557-917-31	Sequence 31, Appl
37	32	57.1	94	5	US-09-557-917-32	Sequence 32, Appl
38	32	57.1	94	5	US-09-557-917-33	Sequence 33, Appl
39	32	57.1	94	5	US-09-557-917-34	Sequence 34, Appl
40	32	57.1	94	5	US-09-557-917-35	Sequence 35, Appl
41	32	57.1	94	5	US-09-557-917-36	Sequence 36, Appl
42	32	57.1	94	5	US-09-557-917-37	Sequence 37, Appl
43	32	57.1	94	5	US-09-557-917-38	Sequence 38, Appl
44	32	57.1	94	5	US-09-557-917-39	Sequence 39, Appl
45	32	57.1	94	5	US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-489-039A-13978
; Sequence 13978, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13978
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13978

Query Match 69.6%; Score 39; DB 5; Length 479;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAD 10
Db 85 RHDYRSFAD 93
||:| ||||
||:| ||||

RESULT 2

US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14

; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4

US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT

; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5

US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6

US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT

;
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE

US-09-557-917-101

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 9
US-09-107-433-3471
; Sequence 3471, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...239
; SEQUENCE DESCRIPTION: SEQ ID NO: 3471:
US-09-107-433-3471

Query Match 60.7%; Score 34; DB 5; Length 239;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAD 10
| | | | |
Db 75 RHIDYGREAD 83

RESULT 10

US-60-259-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 60.7%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
:|||||
Db 93 HNYGAF 98

RESULT 11

US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 58.9%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
:|||||
Db 131 KNYGS 136

RESULT 12

US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634

Query Match 58.9%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
:|||||
Db 133 KNYGS 138

RESULT 13

US-09-595-329A-633
; Sequence 633, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(275)
; OTHER INFORMATION: Ceres Seq. ID no. 1013209
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-633

Query Match 58.9%; Score 33; DB 5; Length 275;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
:|||||
Db 160 KNYGS 165

RESULT 14

US-09-756-983-11
; Sequence 11, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF

; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-983-11

Query Match 57.1%; Score 32; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
|
|
|
|
|
Db 11 RHNYG 15

RESULT 15
US-09-673-809-51
; Sequence 51, Application US/09673809
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-51

Query Match 57.1%; Score 32; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
|
|
|
|
|
Db 74 RHNYG 78

Search completed: March 28, 2001, 07:22:13
Job time: 1505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:20 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNGSPAE 10

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
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6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
13: /cgnl_7/ptodata/1/paa/US089_COMB.pep.*
14: /cgnl_7/ptodata/1/paa/US090_COMB.pep.*
15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
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22: /cgnl_7/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	55	100.0	10	14	US-09-016-061-74
2	55	100.0	10	17	US-09-339-922A-74
3	52	94.5	10	14	US-09-016-061-72
4	52	94.5	10	17	US-09-339-922A-72
5	50	90.9	10	14	US-09-016-061-40
6	50	90.9	10	14	US-09-016-061-68
7	50	90.9	10	14	US-09-016-061-70
8	50	90.9	10	14	US-09-016-061-76
9	50	90.9	10	14	US-09-016-061-78
10	50	90.9	10	14	US-09-016-061-80
11	50	90.9	10	17	US-09-339-922A-40
					Sequence 74, Appl
					Sequence 74, Appl
					Sequence 72, Appl
					Sequence 72, Appl
					Sequence 40, Appl
					Sequence 68, Appl
					Sequence 70, Appl
					Sequence 76, Appl
					Sequence 78, Appl
					Sequence 80, Appl
					Sequence 40, Appl

12	50	90.9	10	17	US-09-339-922A-68	Sequence 68, Appl
13	50	90.9	10	17	US-09-339-922A-70	Sequence 70, Appl
14	50	90.9	10	17	US-09-339-922A-76	Sequence 76, Appl
15	50	90.9	10	17	US-09-339-922A-78	Sequence 78, Appl
16	50	90.9	10	17	US-09-339-922A-80	Sequence 80, Appl
17	50	90.9	117	1	PCT-US98-25828-54	Sequence 54, Appl
18	50	90.9	117	1	PCT-US98-25828-56	Sequence 56, Appl
19	50	90.9	117	11	US-08-790-540-2	Sequence 2, Appl
20	50	90.9	117	11	US-08-790-540-6	Sequence 6, Appl
21	50	90.9	117	11	US-08-790-540A-2	Sequence 2, Appl
22	50	90.9	117	11	US-08-790-540A-6	Sequence 6, Appl
23	50	90.9	117	11	US-08-791-391-2	Sequence 2, Appl
24	50	90.9	117	11	US-08-791-391-6	Sequence 6, Appl
25	50	90.9	117	11	US-08-791-391A-2	Sequence 2, Appl
26	50	90.9	117	11	US-08-791-391A-6	Sequence 6, Appl
27	50	90.9	117	13	US-08-986-016-54	Sequence 54, Appl
28	50	90.9	117	13	US-08-986-016-56	Sequence 56, Appl
29	50	90.9	117	14	US-09-016-061-2	Sequence 2, Appl
30	50	90.9	117	14	US-09-016-061-6	Sequence 6, Appl
31	50	90.9	117	17	US-09-339-922A-2	Sequence 2, Appl
32	50	90.9	117	17	US-09-339-922A-6	Sequence 6, Appl
33	50	90.9	118	1	PCT-US98-25828-50	Sequence 50, Appl
34	50	90.9	118	1	PCT-US98-25828-51	Sequence 51, Appl
35	50	90.9	118	1	PCT-US98-25828-52	Sequence 52, Appl
36	50	90.9	118	1	PCT-US98-25828-53	Sequence 53, Appl
37	50	90.9	118	13	US-08-986-016-50	Sequence 50, Appl
38	50	90.9	118	13	US-08-986-016-51	Sequence 51, Appl
39	50	90.9	118	13	US-08-986-016-52	Sequence 52, Appl
40	50	90.9	119	13	US-08-986-016-53	Sequence 53, Appl
41	50	90.9	130	1	PCT-US98-25828-44	Sequence 44, Appl
42	50	90.9	130	13	US-08-986-016-44	Sequence 44, Appl
43	49	89.1	10	14	US-09-016-061-98	Sequence 98, Appl
44	49	89.1	10	17	US-09-339-922A-98	Sequence 98, Appl
45	47	85.5	10	14	US-09-016-061-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Camobelli, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001


```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-74

Query Match          100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
   |1111111111|
Db 1 ARHNYGSFAE 10

RESULT 2
US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match          100.0%; Score 55; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
   |1111111111|
Db 1 ARHNYGSFAE 10

RESULT 3
US-09-016-061-72
; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match          94.5%; Score 52; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
   |1111111111|
Db 1 ARHNYGSFAD 10

RESULT 4
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match          94.5%; Score 52; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
   |1111111111|
Db 1 ARHNYGSFAD 10

RESULT 5
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-40

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||

Db 1 ARHNYGSFA 9

RESULT 6
US-09-016-061-68
Sequence 68, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-68

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||

Db 1 ARHNYGSFA 9

RESULT 7
US-09-016-061-70
Sequence 70, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||

Db 1 ARHNYGSFA 9

RESULT 8

US-09-016-061-76

Sequence 76, Application US/09016061

GENERAL INFORMATION:

APPLICANT: Huse, William D.

APPLICANT: Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,061

FILING DATE: 30-JAN-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/791,391

FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2965

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-016-061-76

Query Match 90.9%; Score 50; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 10

US-09-016-061-80

Sequence 80, Application US/09016061

GENERAL INFORMATION:

APPLICANT: Huse, William D.

APPLICANT: Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,061

FILING DATE: 30-JAN-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/791,391

FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2965

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-016-061-76

Query Match 90.9%; Score 50; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 9

US-09-016-061-78

Sequence 78, Application US/09016061

GENERAL INFORMATION:

APPLICANT: Huse, William D.

APPLICANT: Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-016-061-80

Query Match 90.9%; Score 50; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 11

US-09-339-922A-40
 ; Sequence 40, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-339-922A-40

Query Match 90.9%; Score 50; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 12

US-09-339-922A-68
 ; Sequence 68, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 68
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Mutated
 ; OTHER INFORMATION: complementarity determining region (CDR)
 US-09-339-922A-68

Query Match 90.9%; Score 50; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9
 |||||

RESULT 13

US-09-339-922A-70
 ; Sequence 70, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 70
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Mutated
 ; OTHER INFORMATION: complementarity determining region (CDR)
 US-09-339-922A-70

Query Match 90.9%; Score 50; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 14

US-09-339-922A-76
 ; Sequence 76, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 76
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Mutated
 ; OTHER INFORMATION: complementarity determining region (CDR)
 US-09-339-922A-76

Query Match 90.9%; Score 50; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 15

US-09-339-922A-78
 ; Sequence 78, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 78
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-78

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSEA 9
Db 1 ARHNYGSEA 9

Search completed: March 28, 2001, 07:18:21
Job time: 1332 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:13 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSPAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	36	65.5	94	5	US-09-557-917-14
2	36	65.5	94	5	US-09-557-917-45
3	36	65.5	94	5	US-09-557-917-48
4	36	65.5	94	5	US-09-557-917-77
5	36	65.5	94	5	US-09-557-917-84
6	36	65.5	94	5	US-09-557-917-90
7	36	65.5	94	5	US-09-557-917-101
8	35	63.6	288	6	US-60-259-128-4587
9	35	63.6	479	5	US-09-489-039A-13978
10	33	60.0	246	5	US-09-595-329A-635
11	33	60.0	248	5	US-09-595-329A-634
12	33	60.0	275	5	US-09-595-329A-633
13	33	60.0	468	5	US-09-107-433-3743
14	32	58.2	15	5	US-09-756-983-11
15	32	58.2	80	5	US-09-673-809-51
16	32	58.2	89	5	US-09-673-809-2
17	32	58.2	94	5	US-09-766-378-37
18	32	58.2	94	5	US-09-692-933-180
19	32	58.2	94	5	US-09-557-917-12
20	32	58.2	94	5	US-09-557-917-13
21	32	58.2	94	5	US-09-557-917-15
22	32	58.2	94	5	US-09-557-917-16
23	32	58.2	94	5	US-09-557-917-17
24	32	58.2	94	5	US-09-557-917-18
25	32	58.2	94	5	US-09-557-917-19
26	32	58.2	94	5	US-09-557-917-20
27	32	58.2	94	5	US-09-557-917-21

28	32	58.2	94	5	US-09-557-917-22	Sequence 22, Appl
29	32	58.2	94	5	US-09-557-917-24	Sequence 24, Appl
30	32	58.2	94	5	US-09-557-917-25	Sequence 25, Appl
31	32	58.2	94	5	US-09-557-917-26	Sequence 26, Appl
32	32	58.2	94	5	US-09-557-917-27	Sequence 27, Appl
33	32	58.2	94	5	US-09-557-917-28	Sequence 28, Appl
34	32	58.2	94	5	US-09-557-917-29	Sequence 29, Appl
35	32	58.2	94	5	US-09-557-917-30	Sequence 30, Appl
36	32	58.2	94	5	US-09-557-917-31	Sequence 31, Appl
37	32	58.2	94	5	US-09-557-917-32	Sequence 32, Appl
38	32	58.2	94	5	US-09-557-917-33	Sequence 33, Appl
39	32	58.2	94	5	US-09-557-917-34	Sequence 34, Appl
40	32	58.2	94	5	US-09-557-917-35	Sequence 35, Appl
41	32	58.2	94	5	US-09-557-917-36	Sequence 36, Appl
42	32	58.2	94	5	US-09-557-917-37	Sequence 37, Appl
43	32	58.2	94	5	US-09-557-917-38	Sequence 38, Appl
44	32	58.2	94	5	US-09-557-917-39	Sequence 39, Appl
45	32	58.2	94	5	US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1

US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 2

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8
US-09-557-917-101
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288

; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 63.6%; Score 35; DB 6; Length 288;
Best Local Similarity 62.5%; Pred. No. 7.6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAE 10
| | | | |
Db 93 HNYGAPQ 100

RESULT 9
US-09-489-039A-13978
; Sequence 13978, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13978
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13978

Query Match 63.6%; Score 35; DB 5; Length 479;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFAE 10
| | | | |
Db 85 RHNYGSFAE 93

RESULT 10
US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; FILE REFERENCE: Thereby
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)...(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: (1)...()
; OTHER INFORMATION: xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 60.0%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
:|||||
Db 131 KHNYS 136

RESULT 11
US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634

Query Match 60.0%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
:|||||
Db 133 KHNYS 138

RESULT 12
US-09-595-329A-633
; Sequence 633, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(275)
; OTHER INFORMATION: Ceres Seq. ID no. 1013209
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-633

Query Match 60.0%; Score 33; DB 5; Length 275;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
:|||||
Db 160 KHNYS 165

RESULT 13
US-09-107-433-3743
; Sequence 3743, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3743:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...468
SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

Query Match 60.0%; Score 33; DB 5; Length 468;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
||| ||
Db 423 ARHPYKGIGE 432

RESULT 14
US-09-756-983-11
; Sequence 11, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; CHARACTERIZATION AND MODULATION OF

; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 03/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-983-11

Query Match 58.2%; Score 32; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHYNG 6
|||||
Db 11 RHYNG 15

RESULT 15
US-09-809-51
; Sequence 51, Application US/09673809
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-51

Query Match 58.2%; Score 32; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHYNG 6
|||||
Db 74 RHYNG 78

Search completed: March 28, 2001, 07:22:13
Job time: 1505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:21 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
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3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US08_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	55	100.0	10	14	US-09-016-061-76
2	55	100.0	10	17	US-09-339-922A-76
3	50	90.9	10	14	US-09-016-061-40
4	50	90.9	10	14	US-09-016-061-68
5	50	90.9	10	14	US-09-016-061-70
6	50	90.9	10	14	US-09-016-061-72
7	50	90.9	10	14	US-09-016-061-74
8	50	90.9	10	14	US-09-016-061-78
9	50	90.9	10	14	US-09-016-061-80
10	50	90.9	10	17	US-09-339-922A-40
11	50	90.9	10	17	US-09-339-922A-68

12	50	90.9	10	17	US-09-339-922A-70
13	50	90.9	10	17	US-09-339-922A-72
14	50	90.9	10	17	US-09-339-922A-74
15	50	90.9	10	17	US-09-339-922A-78
16	50	90.9	10	17	US-09-339-922A-80
17	50	90.9	117	1	PCT-US98-25828-54
18	50	90.9	117	1	PCT-US98-25828-56
19	50	90.9	117	11	US-08-790-540-2
20	50	90.9	117	11	US-08-790-540-6
21	50	90.9	117	11	US-08-790-540A-2
22	50	90.9	117	11	US-08-790-540A-6
23	50	90.9	117	11	US-08-791-391-2
24	50	90.9	117	11	US-08-791-391-6
25	50	90.9	117	11	US-08-791-391A-2
26	50	90.9	117	11	US-08-791-391A-6
27	50	90.9	117	13	US-08-986-016-54
28	50	90.9	117	13	US-08-986-016-56
29	50	90.9	117	14	US-09-016-061-2
30	50	90.9	117	14	US-09-016-061-6
31	50	90.9	117	17	US-09-339-922A-2
32	50	90.9	117	17	US-09-339-922A-6
33	50	90.9	118	1	PCT-US98-25828-50
34	50	90.9	118	1	PCT-US98-25828-51
35	50	90.9	118	1	PCT-US98-25828-52
36	50	90.9	118	1	PCT-US98-25828-53
37	50	90.9	118	13	US-08-986-016-50
38	50	90.9	118	13	US-08-986-016-51
39	50	90.9	118	13	US-08-986-016-52
40	50	90.9	119	13	US-08-986-016-53
41	50	90.9	130	1	PCT-US98-25828-44
42	50	90.9	130	13	US-08-986-016-44
43	47	85.5	10	14	US-09-016-061-62
44	47	85.5	10	17	US-09-339-922A-62
45	46	83.6	10	17	US-09-339-922A-100

ALIGNMENTS

RESULT 1
US-09-016-061-76
Sequence 76, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-76

Query Match          100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
Db 1 ARHNYGSFAM 10

RESULT 2
US-09-339-922A-76
; Sequence 76, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-76

Query Match          100.0%; Score 55; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
Db 1 ARHNYGSFAM 10

RESULT 3
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-40
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-40

Query Match          90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 4
US-09-016-061-68
; Sequence 68, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-68
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Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 5

US-09-016-061-70
; Sequence 70, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 6

US-09-016-061-72
; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 7

US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 8

US-09-016-061-72
; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 9

US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 10

US-09-016-061-72
; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-74

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 8
US-09-016-061-78
; Sequence 78, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-78

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 9
US-09-016-061-80
; Sequence 80, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-80

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 10
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT

ORGANISM: Mus musculus
US-09-339-922A-40

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||
Db 1 ARHNYGSFA 9

RESULT 11
US-09-339-922A-68
; Sequence 68, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-68

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||
Db 1 ARHNYGSFA 9

RESULT 12
US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-70

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9
|||||

RESULT 13
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||
Db 1 ARHNYGSFA 9

RESULT 14
US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
|||||
Db 1 ARHNYGSFA 9

RESULT 15
US-09-339-922A-78
; Sequence 78, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 78
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
US-09-339-922A-78

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:21
Job time: 1332 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:13 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSPAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	65.5	94	5	US-09-557-917-14
2	36	65.5	94	5	US-09-557-917-45
3	36	65.5	94	5	US-09-557-917-48
4	36	65.5	94	5	US-09-557-917-77
5	36	65.5	94	5	US-09-557-917-84
6	36	65.5	94	5	US-09-557-917-90
7	36	65.5	94	5	US-09-557-917-101
8	34	61.8	288	6	US-60-259-128-4587
9	33	60.0	246	5	US-09-595-329A-635
10	33	60.0	248	5	US-09-595-329A-634
11	33	60.0	275	5	US-09-595-329A-633
12	33	60.0	475	5	US-09-489-039A-13978
13	32	58.2	15	5	US-09-756-983-11
14	32	58.2	80	5	US-09-673-809-51
15	32	58.2	89	5	US-09-673-809-2
16	32	58.2	94	5	US-09-766-378-37
17	32	58.2	94	5	US-09-692-933-180
18	32	58.2	94	5	US-09-557-917-12
19	32	58.2	94	5	US-09-557-917-13
20	32	58.2	94	5	US-09-557-917-15
21	32	58.2	94	5	US-09-557-917-16
22	32	58.2	94	5	US-09-557-917-17
23	32	58.2	94	5	US-09-557-917-18
24	32	58.2	94	5	US-09-557-917-19
25	32	58.2	94	5	US-09-557-917-20
26	32	58.2	94	5	US-09-557-917-21
27	32	58.2	94	5	US-09-557-917-22

28	32	58.2	94	5	US-09-557-917-24	Sequence 24, Appl
29	32	58.2	94	5	US-09-557-917-25	Sequence 25, Appl
30	32	58.2	94	5	US-09-557-917-26	Sequence 26, Appl
31	32	58.2	94	5	US-09-557-917-27	Sequence 27, Appl
32	32	58.2	94	5	US-09-557-917-28	Sequence 28, Appl
33	32	58.2	94	5	US-09-557-917-29	Sequence 29, Appl
34	32	58.2	94	5	US-09-557-917-30	Sequence 30, Appl
35	32	58.2	94	5	US-09-557-917-31	Sequence 31, Appl
36	32	58.2	94	5	US-09-557-917-32	Sequence 32, Appl
37	32	58.2	94	5	US-09-557-917-33	Sequence 33, Appl
38	32	58.2	94	5	US-09-557-917-34	Sequence 34, Appl
39	32	58.2	94	5	US-09-557-917-35	Sequence 35, Appl
40	32	58.2	94	5	US-09-557-917-36	Sequence 36, Appl
41	32	58.2	94	5	US-09-557-917-37	Sequence 37, Appl
42	32	58.2	94	5	US-09-557-917-38	Sequence 38, Appl
43	32	58.2	94	5	US-09-557-917-39	Sequence 39, Appl
44	32	58.2	94	5	US-09-557-917-40	Sequence 40, Appl
45	32	58.2	94	5	US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 65.5% Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 3
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 4
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 5
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 80 RHNYGVF 86

RESULT 6
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/Jp97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 0.97;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 8
US-09-557-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Target Discovery
; FILE REFERENCE: GRACEL
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288

; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 61.8%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 8.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
| | | | |
Db 93 HNYGAF 98

RESULT 9
US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc.feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 60.0%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
| | | | |
Db 131 RHNYGS 136

RESULT 10
US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
; NAME/KEY: misc.feature
; LOCATION: ()..()

; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634

Query Match 60.0%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
Db 133 KHYGS 138

RESULT 11
US-09-595-329A-633
; Sequence 633, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE OF INVENTION: VYACHESLAV, Brover
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(275)
; OTHER INFORMATION: Ceres Seq. ID no. 1013209
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-633

Query Match 60.0%; Score 33; DB 5; Length 275;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
Db 160 KHYGS 165

RESULT 12
US-09-489-039A-13978
; Sequence 13978, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13978
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13978

Query Match 60.0%; Score 33; DB 5; Length 479;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
Db 85 RHDYRSFA 92

RESULT 13
US-09-756-983-11
; Sequence 11, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; FILE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-983-11

Query Match 58.2%; Score 32; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 11 RHNYG 15

RESULT 14
US-09-673-809-51
; Sequence 51, Application US/09673809
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-51

Query Match 58.2%; Score 32; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 74 RHNYG 78

RESULT 15
US-09-673-809-2
; Sequence 2, Application US/09673809
; GENERAL INFORMATION:

; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-2

Query Match 58.2%; Score 32; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RHNYG 6
Db 75 RHNYG 79

Search completed: March 28, 2001, 07:22:14
Job time: 1506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:21 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNGSPAG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_Main.*
1: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	14	US-09-016-061-78
2	56	100.0	10	17	US-09-339-922A-78
3	50	89.3	10	14	US-09-016-061-40
4	50	89.3	10	14	US-09-016-061-68
5	50	89.3	10	14	US-09-016-061-70
6	50	89.3	10	14	US-09-016-061-72
7	50	89.3	10	14	US-09-016-061-74
8	50	89.3	10	14	US-09-016-061-76
9	50	89.3	10	14	US-09-016-061-80
10	50	89.3	10	17	US-09-339-922A-40
11	50	89.3	10	17	US-09-339-922A-68

12	50	89.3	10	17	US-09-339-922A-70	Sequence 70, Appl
13	50	89.3	10	17	US-09-339-922A-72	Sequence 72, Appl
14	50	89.3	10	17	US-09-339-922A-74	Sequence 74, Appl
15	50	89.3	10	17	US-09-339-922A-76	Sequence 76, Appl
16	50	89.3	10	17	US-09-339-922A-80	Sequence 80, Appl
17	50	89.3	117	1	PCT-US98-25828-54	Sequence 54, Appl
18	50	89.3	117	1	PCT-US98-25828-56	Sequence 56, Appl
19	50	89.3	117	11	US-08-790-540-2	Sequence 2, Appl
20	50	89.3	117	11	US-08-790-540-6	Sequence 6, Appl
21	50	89.3	117	11	US-08-790-540A-2	Sequence 2, Appl
22	50	89.3	117	11	US-08-790-540A-6	Sequence 6, Appl
23	50	89.3	117	11	US-08-791-391-2	Sequence 2, Appl
24	50	89.3	117	11	US-08-791-391-6	Sequence 6, Appl
25	50	89.3	117	11	US-08-791-391A-2	Sequence 2, Appl
26	50	89.3	117	11	US-08-791-391A-6	Sequence 6, Appl
27	50	89.3	117	13	US-08-986-016-54	Sequence 54, Appl
28	50	89.3	117	13	US-08-986-016-56	Sequence 56, Appl
29	50	89.3	117	14	US-09-016-061-2	Sequence 2, Appl
30	50	89.3	117	14	US-09-016-061-6	Sequence 6, Appl
31	50	89.3	117	17	US-09-339-922A-2	Sequence 2, Appl
32	50	89.3	117	17	US-09-339-922A-6	Sequence 6, Appl
33	50	89.3	118	1	PCT-US98-25828-50	Sequence 50, Appl
34	50	89.3	118	1	PCT-US98-25828-51	Sequence 51, Appl
35	50	89.3	118	1	PCT-US98-25828-52	Sequence 52, Appl
36	50	89.3	118	1	PCT-US98-25828-53	Sequence 53, Appl
37	50	89.3	118	13	US-08-986-016-50	Sequence 50, Appl
38	50	89.3	118	13	US-08-986-016-51	Sequence 51, Appl
39	50	89.3	118	13	US-08-986-016-52	Sequence 52, Appl
40	50	89.3	119	13	US-08-986-016-53	Sequence 53, Appl
41	50	89.3	130	1	PCT-US98-25828-44	Sequence 44, Appl
42	50	89.3	130	13	US-08-986-016-44	Sequence 44, Appl
43	47	83.9	10	14	US-09-016-061-62	Sequence 62, Appl
44	47	83.9	10	17	US-09-339-922A-62	Sequence 62, Appl
45	46	82.1	10	17	US-09-339-922A-100	Sequence 100, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-78
; Sequence 78, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-016-061-78

Query Match 100.0%; Score 56; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10
 |||||
 Db 1 ARHNYGSFAG 10

RESULT 2

US-09-339-922A-78

; Sequence 78, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 78
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Mutated
 ; OTHER INFORMATION: Complementarity determining region (CDR)
 US-09-339-922A-78

Query Match 100.0%; Score 56; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10
 |||||
 Db 1 ARHNYGSFAG 10

RESULT 3

US-09-016-061-40

; Sequence 40, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016.061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-016-061-40

Query Match 89.3%; Score 50; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 4

US-09-016-061-68

; Sequence 68, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016.061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2965
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-016-061-68

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Query Match      89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 5
US-09-016-061-70
; Sequence 70, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 31,815
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match      89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 6
US-09-016-061-72
; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 31,815
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match      89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 7
US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 31,815
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70
```


NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-74

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 8
US-09-016-061-76
; Sequence 76, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-76

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 9
US-09-016-061-80
; Sequence 80, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-80

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 10
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
LENGTH: 10
TYPE: PRT

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 11
US-09-339-922A-68
; Sequence 68, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-68

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 12
US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-70

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 14
US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339, 922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 15
US-09-339-922A-76
; Sequence 76, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 76
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
US-09-339-922A-76

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:21
Job time: 1332 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:14 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNYGSPAG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution...

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	64.3	94	5	US-09-557-917-14
2	36	64.3	94	5	US-09-557-917-45
3	36	64.3	94	5	US-09-557-917-48
4	36	64.3	94	5	US-09-557-917-77
5	36	64.3	94	5	US-09-557-917-84
6	36	64.3	94	5	US-09-557-917-90
7	36	64.3	94	5	US-09-557-917-101
8	34	60.7	288	6	US-60-259-128-4587
9	34	60.7	385	5	US-09-489-039A-11917
10	34	60.7	386	6	US-60-269-308-4695
11	34	60.7	866	5	US-09-488-725A-3407
12	34	60.7	923	5	US-09-488-725A-6979
13	33	58.9	246	5	US-09-595-329A-635
14	33	58.9	275	5	US-09-595-329A-634
15	33	58.9	275	5	US-09-595-329A-633
16	33	58.9	385	5	US-09-489-039A-13700
17	33	58.9	407	4	US-08-861-774D-28
18	33	58.9	479	5	US-09-489-039A-13978
19	32	57.1	15	5	US-09-756-983-11
20	32	57.1	80	5	US-09-673-809-51
21	32	57.1	89	5	US-09-673-809-2
22	32	57.1	94	5	US-09-766-378-37
23	32	57.1	94	5	US-09-692-933-180
24	32	57.1	94	5	US-09-557-917-12
25	32	57.1	94	5	US-09-557-917-13
26	32	57.1	94	5	US-09-557-917-15
27	32	57.1	94	5	US-09-557-917-16

28 32 57.1 94 5 US-09-557-917-17 Sequence 17, Appl
29 32 57.1 94 5 US-09-557-917-18 Sequence 18, Appl
30 32 57.1 94 5 US-09-557-917-19 Sequence 19, Appl
31 32 57.1 94 5 US-09-557-917-20 Sequence 20, Appl
32 32 57.1 94 5 US-09-557-917-21 Sequence 21, Appl
33 32 57.1 94 5 US-09-557-917-22 Sequence 22, Appl
34 32 57.1 94 5 US-09-557-917-24 Sequence 24, Appl
35 32 57.1 94 5 US-09-557-917-25 Sequence 25, Appl
36 32 57.1 94 5 US-09-557-917-26 Sequence 26, Appl
37 32 57.1 94 5 US-09-557-917-27 Sequence 27, Appl
38 32 57.1 94 5 US-09-557-917-28 Sequence 28, Appl
39 32 57.1 94 5 US-09-557-917-29 Sequence 29, Appl
40 32 57.1 94 5 US-09-557-917-30 Sequence 30, Appl
41 32 57.1 94 5 US-09-557-917-31 Sequence 31, Appl
42 32 57.1 94 5 US-09-557-917-32 Sequence 32, Appl
43 32 57.1 94 5 US-09-557-917-33 Sequence 33, Appl
44 32 57.1 94 5 US-09-557-917-34 Sequence 34, Appl
45 32 57.1 94 5 US-09-557-917-111 Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 64.3% Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 80 RHNYGVF 86

RESULT 2
US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 64.3%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8
US-09-259-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288

; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 60.7%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 93 HNYGAF 98

RESULT 9
US-09-489-039A-11917
; Sequence 11917, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11917
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11917

Query Match 60.7%; Score 34; DB 5; Length 385;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAG 10
Db 257 ARHGGGAFSG 266

RESULT 10
US-60-269-308-4695
; Sequence 4695, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in Staphylococcus aureus, Ps
; FILE REFERENCE: aeruginosa, Klebsiella pneumoniae, Salmonella typhimurium, an
; FILE REFERENCE: faecalis
; CURRENT APPLICATION NUMBER: US/60/269,308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4695
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-60-269-308-4695

Query Match 60.7%; Score 34; DB 6; Length 386;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAG 10
Db 257 ARHGGGAFSG 266

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Db 262 ARHGGAFSG 271

RESULT 11
; Sequence 3407, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3407
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3407

Query Match 60.7%; Score 34; DB 5; Length 866;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
:||||:|
Db 794 YNYGSYGG 801

RESULT 12
US-09-488-725A-6979
; Sequence 6979, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0

; SEQ ID NO 6979
; LENGTH: 923
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6979

Query Match 60.7%; Score 34; DB 5; Length 923;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
:||||:|
Db 851 YNYGSYGG 858

RESULT 13
US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 58.9%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
:||||
Db 131 KHNYGS 136

RESULT 14
US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
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; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634

Query Match 58.9%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
:|||||
Db 133 KHYGS 138

RESULT 15
US-09-595-329A-633
; Sequence 633, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(275)
; OTHER INFORMATION: Ceres Seq. ID no. 1013209
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-633

Query Match 58.9%; Score 33; DB 5; Length 275;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
:|||||
Db 160 KHYGS 165

Search completed: March 28, 2001, 07:22:14
Job time: 1506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:21 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFPA 10

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	14	US-09-016-061-80
2	54	100.0	10	17	US-09-339-922A-80
3	51	94.4	10	17	US-09-016-061-68
4	51	94.4	10	17	US-09-339-922A-68
5	50	92.6	10	14	US-09-016-061-40
6	50	92.6	10	14	US-09-016-061-70
7	50	92.6	10	14	US-09-016-061-72
8	50	92.6	10	14	US-09-016-061-74
9	50	92.6	10	14	US-09-016-061-76
10	50	92.6	10	14	US-09-016-061-78
11	50	92.6	10	17	US-09-339-922A-40

12	50	92.6	10	17	US-09-339-922A-70
13	50	92.6	10	17	US-09-339-922A-72
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15	50	92.6	10	17	US-09-339-922A-76
16	50	92.6	10	17	US-09-339-922A-78
17	50	92.6	117	1	PCT-US98-25828-54
18	50	92.6	117	1	PCT-US98-25828-56
19	50	92.6	117	11	US-08-790-540-2
20	50	92.6	117	11	US-08-790-540-6
21	50	92.6	117	11	US-08-790-540A-2
22	50	92.6	117	11	US-08-790-540A-6
23	50	92.6	117	11	US-08-791-391-2
24	50	92.6	117	11	US-08-791-391-6
25	50	92.6	117	11	US-08-791-391A-2
26	50	92.6	117	11	US-08-791-391A-6
27	50	92.6	117	13	US-08-986-016-54
28	50	92.6	117	13	US-08-986-016-56
29	50	92.6	117	14	US-09-016-061-2
30	50	92.6	117	14	US-09-016-061-6
31	50	92.6	117	17	US-09-339-922A-2
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33	50	92.6	118	1	PCT-US98-25828-50
34	50	92.6	118	1	PCT-US98-25828-51
35	50	92.6	118	1	PCT-US98-25828-52
36	50	92.6	118	1	PCT-US98-25828-53
37	50	92.6	118	13	US-08-986-016-50
38	50	92.6	118	13	US-08-986-016-51
39	50	92.6	118	13	US-08-986-016-52
40	50	92.6	119	13	US-08-986-016-53
41	50	92.6	130	1	PCT-US98-25828-44
42	50	92.6	130	13	US-08-986-016-44
43	47	87.0	10	14	US-09-016-061-62
44	47	87.0	10	17	US-09-339-922A-62
45	46	85.2	10	17	US-09-339-922A-100

ALIGNMENTS

RESULT 1
US-09-016-061-80
; Sequence 80, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-016-061-80

Query Match          100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAA 10

RESULT 2
US-09-339-922A-80
; Sequence 80, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-80

Query Match          100.0%; Score 54; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAA 10

RESULT 3
US-09-016-061-68
; Sequence 68, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-016-061-80

Query Match          100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAA 10

RESULT 2
US-09-339-922A-80
; Sequence 80, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-80

Query Match          100.0%; Score 54; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAA 10

RESULT 3
US-09-016-061-68
; Sequence 68, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-68

Query Match          94.4%; Score 51; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0019;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAS 10

RESULT 4
US-09-339-922A-68
; Sequence 68, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-68

Query Match          94.4%; Score 51; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0019;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
Db 1 ARHNYGSFAS 10

RESULT 5
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-40

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

DB 1 ARHNYGSFA 9
|||||

RESULT 6
US-09-016-061-70
SEQUENCE 70, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-70
Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
|||||

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-70

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

DB 1 ARHNYGSFA 9
|||||

RESULT 7
US-09-016-061-72
SEQUENCE 72, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-72
Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
|||||

DB 1 ARHNYGSFA 9
|||||

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

```

Db      1 ARHNYGSFA 9
RESULT 8
US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-74

Query Match          92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSFA 9
       1|1111111111
Db      1 ARHNYGSFA 9

RESULT 10
US-09-016-061-78
; Sequence 78, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-74

Query Match          92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSFA 9
       1|1111111111
Db      1 ARHNYGSFA 9

RESULT 9
US-09-016-061-76
; Sequence 76, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-76

Query Match          92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSFA 9
       1|1111111111
Db      1 ARHNYGSFA 9

RESULT 10
US-09-016-061-78
; Sequence 78, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-78

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 11
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 12
US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-70

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 14
US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 15
US-09-339-922A-76
; Sequence 76, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-76

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:21
Job time: 1332 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:14 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSPAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
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6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	66.7	94	5	US-09-557-917-14
2	36	66.7	94	5	US-09-557-917-45
3	36	66.7	94	5	US-09-557-917-48
4	36	66.7	94	5	US-09-557-917-77
5	36	66.7	94	5	US-09-557-917-84
6	36	66.7	94	5	US-09-557-917-90
7	36	66.7	94	5	US-09-557-917-101
8	34	63.0	288	6	US-60-259-128-4587
9	33	61.1	246	5	US-09-595-329A-635
10	33	61.1	248	5	US-09-595-329A-634
11	33	61.1	275	5	US-09-595-329A-633
12	33	61.1	479	5	US-09-489-039A-13978
13	32	59.3	15	5	US-09-756-983-11
14	32	59.3	80	5	US-09-673-809-51
15	32	59.3	89	5	US-09-673-809-2
16	32	59.3	94	5	US-09-766-378-37
17	32	59.3	94	5	US-09-692-933-180
18	32	59.3	94	5	US-09-557-917-12
19	32	59.3	94	5	US-09-557-917-13
20	32	59.3	94	5	US-09-557-917-15
21	32	59.3	94	5	US-09-557-917-16
22	32	59.3	94	5	US-09-557-917-17
23	32	59.3	94	5	US-09-557-917-18
24	32	59.3	94	5	US-09-557-917-19
25	32	59.3	94	5	US-09-557-917-20
26	32	59.3	94	5	US-09-557-917-21
27	32	59.3	94	5	US-09-557-917-22

28	32	59.3	94	5	US-09-557-917-24	Sequence 24, Appl
29	32	59.3	94	5	US-09-557-917-25	Sequence 25, Appl
30	32	59.3	94	5	US-09-557-917-26	Sequence 26, Appl
31	32	59.3	94	5	US-09-557-917-27	Sequence 27, Appl
32	32	59.3	94	5	US-09-557-917-28	Sequence 28, Appl
33	32	59.3	94	5	US-09-557-917-29	Sequence 29, Appl
34	32	59.3	94	5	US-09-557-917-30	Sequence 30, Appl
35	32	59.3	94	5	US-09-557-917-31	Sequence 31, Appl
36	32	59.3	94	5	US-09-557-917-32	Sequence 32, Appl
37	32	59.3	94	5	US-09-557-917-33	Sequence 33, Appl
38	32	59.3	94	5	US-09-557-917-35	Sequence 34, Appl
39	32	59.3	94	5	US-09-557-917-36	Sequence 35, Appl
40	32	59.3	94	5	US-09-557-917-37	Sequence 36, Appl
41	32	59.3	94	5	US-09-557-917-38	Sequence 37, Appl
42	32	59.3	94	5	US-09-557-917-39	Sequence 38, Appl
43	32	59.3	94	5	US-09-557-917-40	Sequence 39, Appl
44	32	59.3	94	5	US-09-557-917-40	Sequence 40, Appl
45	32	59.3	94	5	US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 2
US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 3
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 4
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 5
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 80 RHNYGVF 86

RESULT 6
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 66.7%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8
US-09-557-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; TITLE OF INVENTION: Target Discovery
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288

; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 63.0%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 93 HNYGAF 98

RESULT 9
US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: ()..
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 61.1%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
Db 131 KHNYGS 136

RESULT 10
US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
; NAME/KEY: misc_feature
; LOCATION: ()..
;

; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634

Query Match 61.1%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
Db 133 KHNYGS 138

RESULT 11
US-09-595-329A-633
; Sequence 633, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(275)
; OTHER INFORMATION: Ceres Seq. ID no. 1013209
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-633

Query Match 61.1%; Score 33; DB 5; Length 275;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
Db 160 KHNYGS 165

RESULT 12
US-09-489-039A-13978
; Sequence 13978, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13978
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13978

Query Match 61.1%; Score 33; DB 5; Length 479;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
Db 85 RHDYRSEA 92

RESULT 13
US-09-756-983-11
; Sequence 11, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-983-11

Query Match 59.3%; Score 32; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 11 RHNYG 15

RESULT 14
US-09-673-809-51
; Sequence 51, Application US/09673809
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-51

Query Match 59.3%; Score 32; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYG 6
Db 74 RHNYG 78

RESULT 15
US-09-673-809-2
; Sequence 2, Application US/09673809
; GENERAL INFORMATION:

; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-2

Query Match 59.3%; Score 32; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RHNYG 6
| | | | |
Db 75 RHNYG 79

Search completed: March 28, 2001, 07:22:14
Job time: 1506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:21 ; Search time 828.17 Seconds
(without alignments)
2.286 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQSISNLFHWY 13

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Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	72	100.0	13	17	US-09-339-922A-82
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4	65	90.3	13	14	US-09-016-061-42
5	65	90.3	13	17	US-09-339-922A-42
6	65	90.3	107	11	US-08-790-540-4
7	65	90.3	107	11	US-08-790-540-8
8	65	90.3	107	11	US-08-790-540A-4
9	65	90.3	107	11	US-08-790-540A-8
10	65	90.3	107	11	US-08-791-391-4
11	65	90.3	107	11	US-08-791-391-8

12	65	90.3	107	11	US-08-791-391-32	Sequence 32, Appl
13	65	90.3	107	11	US-08-791-391A-4	Sequence 4, Appli
14	65	90.3	107	11	US-08-791-391A-8	Sequence 8, Appli
15	65	90.3	107	11	US-08-791-391A-32	Sequence 32, Appli
16	65	90.3	107	14	US-09-016-061-4	Sequence 4, Appli
17	65	90.3	107	14	US-09-016-061-8	Sequence 8, Appli
18	65	90.3	107	14	US-09-016-061-32	Sequence 32, Appli
19	65	90.3	107	17	US-09-339-922A-4	Sequence 4, Appli
20	65	90.3	107	17	US-09-339-922A-8	Sequence 8, Appli
21	65	90.3	107	17	US-09-339-922A-32	Sequence 32, Appli
22	61	84.7	105	1	PCT-US98-04987-17	Sequence 17, Appl
23	61	84.7	105	1	PCT-US98-04987-21	Sequence 21, Appl
24	61	84.7	105	22	US-60-039-609-17	Sequence 17, Appl
25	61	84.7	105	22	US-60-039-609-21	Sequence 21, Appl
26	61	84.7	107	1	PCT-US98-04987-10	Sequence 10, Appl
27	61	84.7	107	22	US-60-039-609-10	Sequence 10, Appl
28	61	84.7	108	1	PCT-US98-04987-7	Sequence 7, Appli
29	61	84.7	108	22	US-60-039-609-7	Sequence 7, Appli
30	61	84.7	109	1	PCT-US98-25828-45	Sequence 45, Appl
31	61	84.7	109	13	US-08-986-016-45	Sequence 45, Appl
32	61	84.7	112	1	PCT-US98-04987-14	Sequence 14, Appl
33	61	84.7	112	22	US-60-039-609-14	Sequence 14, Appl
34	60	83.3	88	1	PCT-US99-09131-31	Sequence 31, Appl
35	60	83.3	88	17	US-09-300-970A-31	Sequence 31, Appl
36	60	83.3	107	1	PCT-US99-02949-8	Sequence 8, Appli
37	60	83.3	107	1	PCT-US99-02949-12	Sequence 12, Appl
38	60	83.3	107	14	US-09-026-291-8	Sequence 8, Appli
39	60	83.3	107	14	US-09-026-291-12	Sequence 12, Appl
40	60	83.3	107	16	US-09-247-352-8	Sequence 8, Appli
41	60	83.3	107	16	US-09-247-352-12	Sequence 12, Appl
42	60	83.3	107	18	US-09-438-954-3	Sequence 3, Appli
43	60	83.3	108	1	PCT-US99-02949-1	Sequence 1, Appli
44	60	83.3	108	10	US-08-617-835-5	Sequence 5, Appli
45	60	83.3	108	14	US-09-026-291-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-016-061-82
; Sequence 82, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-82

Query Match 100.0%; Score 72; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNFWLHWY 13
Db 1 QASQISNFWLHWY 13

RESULT 2

US-09-339-922A-82
; Sequence 82, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 13
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-82

Query Match 100.0%; Score 72; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNFWLHWY 13
Db 1 QASQISNFWLHWY 13

RESULT 3

US-09-419-788-29

; Sequence 29, Application US/09419788

; GENERAL INFORMATION:

; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil

; TITLE OF INVENTION: Molecular Pathogenicity Mediated Plant Disease
; FILE REFERENCE: 0147-0189P

; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18

; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16

; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16

; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-29

Query Match 94.4%; Score 68; DB 18; Length 259;
Best Local Similarity 92.3%; Pred. No. 0.00077;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNFWLHWY 13
Db 155 RASQISNFWLHWY 167

RESULT 4

US-09-016-061-42

; Sequence 42, Application US/09016061

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-42

Query Match 90.3%; Score 65; DB 14; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00014;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNFWLHWY 13
Db 1 QASQISNFWLHWY 13

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RESULT 5
US-09-922A-42
; Sequence 42, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-42

Query Match 90.3%; Score 65; DB 17; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00014;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLHWY 13
   ||||| ||||
Db 1 QASQISNHLHWY 13

RESULT 6
US-08-790-540-4
; Sequence 4, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-4

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLHWY 13
   ||||| ||||
Db 1 QASQISNHLHWY 36

RESULT 7
US-08-790-540-8
; Sequence 8, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-8

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLHWY 13
   ||||| ||||
Db 1 QASQISNHLHWY 36

RESULT 8
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: PatentIn Ver. 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-4

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 QASQISNHLHWY 13
   ||||| ||||
Db 1 QASQISNHLHWY 36

RESULT 7
US-08-790-540-8
; Sequence 8, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-8

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLHWY 13
   ||||| ||||
Db 1 QASQISNHLHWY 36

RESULT 8
US-08-790-540A-4
; Sequence 4, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: PatentIn Ver. 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-4

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/790,540A
 FILING DATE: 30-JAN-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-IX 2405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-790-540A-4

Query Match 90.3%; Score 65; DB 11; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQISNHLHWY 13
 Db 24 QASQISNHLHWY 36

RESULT 9
 US-08-790-540A-8
 ; Sequence 8, Application US/08790540A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/790,540A
 ; FILING DATE: 30-JAN-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2405
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-790-540A-8

Query Match 90.3%; Score 65; DB 11; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0011;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQISNHLHWY 13
 Db 24 QASQISNHLHWY 36

RESULT 10
 US-08-791-391-4
 ; Sequence 4, Application US/08791391
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/791,391
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 1482
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-791-391-4

Query Match 90.3%; Score 65; DB 11; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQISNHLHWY 13
 Db 24 QASQISNHLHWY 36

RESULT 11
 US-08-791-391-8
 ; Sequence 8, Application US/08791391
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.391
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391-8

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
DB 24 QASQISNHLHWY 36

RESULT 12
US-08-791-391-32
Sequence 32, Application US/08791391
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.391
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391-32

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
DB 24 QASQISNHLHWY 36

RESULT 13
US-08-791-391A-4
Sequence 4, Application US/08791391A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-4

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLHWY 13
DB 24 QASQISNHLHWY 36

RESULT 14
US-08-791-391A-8
Sequence 8, Application US/08791391A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700


```
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-8

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSSISNHLHWY 13
Db 24 QASQSSISNHLHWY 36

Search completed: March 28, 2001, 07:18:22
Job time: 1333 sec

; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-32

Query Match 90.3%; Score 65; DB 11; Length 107;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSSISNHLHWY 13
Db 24 QASQSSISNHLHWY 36

Search completed: March 28, 2001, 07:18:22
Job time: 1333 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:14 ; Search time 213.09 Seconds
(without alignments)
0.804 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQISNLFHWY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pap:*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pap:*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pap:*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pap:*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pap:*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	81.9	109	5	US-09-445-602A-6
2	57	79.2	124	5	US-09-297-344-10
3	53	73.6	88	5	US-09-297-344-9
4	53	73.6	105	5	US-09-147-443C-52
5	53	73.6	107	5	US-09-403-107-148
6	53	73.6	107	5	US-09-403-107-152
7	51	70.8	107	5	US-09-610-551A-66
8	51	70.8	107	5	US-09-607-756-2
9	50	69.4	108	5	US-09-530-237-2
10	49	68.1	107	5	US-09-403-107-142
11	49	68.1	107	5	US-09-403-107-149
12	46	63.9	105	5	US-09-147-443C-12
13	46	63.9	105	5	US-09-147-443C-40
14	46	63.9	105	5	US-09-147-443C-44
15	46	63.9	105	5	US-09-147-443C-48
16	46	63.9	105	5	US-09-147-443C-60
17	46	63.9	105	5	US-09-147-443C-64
18	46	63.9	105	5	US-09-610-551A-67
19	46	63.9	107	5	US-09-610-551A-67
20	46	63.9	107	5	US-09-610-551A-67
21	46	63.9	108	4	US-08-454-899C-100
22	45	62.5	107	5	US-09-711-485-149
23	45	62.5	111	5	US-09-385-673-14
24	44	61.1	106	5	US-09-147-443C-4
25	44	61.1	106	5	US-09-147-443C-20
26	44	61.1	107	5	US-09-711-485-162
27	43.5	60.4	214	5	US-09-653-755A-5

28	43	59.7	105	5	US-09-147-443C-16	Sequence 16, Appl
29	43	59.7	106	5	US-09-147-443C-8	Sequence 8, Appl
30	43	59.7	106	5	US-09-147-443C-32	Sequence 32, Appl
31	43	59.7	109	5	US-09-610-551A-69	Sequence 69, Appl
32	43	59.7	109	5	US-09-610-551A-69	Sequence 69, Appl
33	43	59.7	110	5	US-09-610-551A-70	Sequence 70, Appl
34	43	59.7	110	5	US-09-610-551A-70	Sequence 70, Appl
35	42.5	59.0	106	5	US-09-097-055A-89	Sequence 89, Appl
36	42.5	59.0	106	5	US-09-097-055A-89	Sequence 89, Appl
37	42	58.3	106	4	US-08-454-899C-10	Sequence 10, Appl
38	42	58.3	109	5	US-09-726-258-47	Sequence 47, Appl
39	42	58.3	124	4	US-08-454-899C-71	Sequence 71, Appl
40	42	58.3	128	4	US-08-454-899C-31	Sequence 31, Appl
41	42	58.3	128	4	US-08-454-899C-63	Sequence 63, Appl
42	42	58.3	128	4	US-08-454-899C-67	Sequence 67, Appl
43	41	56.9	110	5	US-09-672-609-13	Sequence 13, Appl
44	41	56.9	110	5	US-09-672-609-15	Sequence 15, Appl
45	41	56.9	110	5	US-09-672-609-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-445-602A-6

; Sequence 6, Application US/09445602A

; GENERAL INFORMATION:

; APPLICANT: Cohen, Irun

; APPLICANT: ROTTER, Varda

; APPLICANT: Wolkowicz, Roland

; APPLICANT: RUIZ, Pedro

; APPLICANT: EREZ-ALON, Neta

; APPLICANT: HERKEL, Johannes

; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY

; FILE REFERENCE: COHEN42

; CURRENT APPLICATION NUMBER: US/09/445,602A

; CURRENT FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: PCT/IL98/00266

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: IL 121041

; PRIOR FILING DATE: 1997-06-09

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-445-602A-6

Query Match 81.9%; Score 59; DB 5; Length 109;

Best Local Similarity 84.6%; Pred. No. 0.0034; 1; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13

:|||||||

Db 25 RASQISNLFHWY 37

RESULT 2

US-09-297-344-10

; Sequence 10, Application US/09297344

; GENERAL INFORMATION:

; APPLICANT: Deen, Keith C.

; APPLICANT: Dillon, Susan B.

; APPLICANT: Porter, Terence C.

; APPLICANT: Sweet, Raymond A.

; TITLE OF INVENTION: Human Monoclonal Antibodies

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

STATE: PA
COUNTRY: U.S.A.
ZIP: 19046
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/297,344
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,149
FILING DATE: 01-Nov-1997
ATTORNEY/AGENT INFORMATION:
NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5968
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-297-344-10

Query Match 79.2%; Score 57; DB 5; Length 124;
Best Local Similarity 69.2%; Pred. No. 0.008;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNFWY 13
Db 41 RATQSVSNFWY 53

RESULT 3
US-09-297-344-9
; Sequence 9, Application US/09297344
; GENERAL INFORMATION:
; APPLICANT: Deen, Keith C.
; Dillon, Susan B.
; Porter, Terence C.
; Sweet, Raymond A.
; TITLE OF INVENTION: Human Monoclonal Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19046
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/297,344
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,149
FILING DATE: 01-Nov-1997
ATTORNEY/AGENT INFORMATION:

NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5968
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-297-344-9

Query Match 73.6%; Score 53; DB 5; Length 88;
Best Local Similarity 69.2%; Pred. No. 0.026;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNFWY 13
Db 24 RASQSISSFWY 36

RESULT 4
US-09-147-443C-52
; Sequence 52, Application US/09147443C
; GENERAL INFORMATION:
; APPLICANT: Morell, Andreas
; Imboden, Martin
; APPLICANT: Stadler, Bodo
; APPLICANT: Miescher, Sylvia
; APPLICANT: Vogel, Monique
; APPLICANT: Amstutz, Hanspeter
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
; TITLE OF INVENTION: STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
; TITLE OF INVENTION: THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
; FILE REFERENCE: 6816/P63221USO
; CURRENT APPLICATION NUMBER: US/09/147,443C
; CURRENT FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: PCT/EP97/03253
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: EP 96810421.6
; PRIOR FILING DATE: 1996-06-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-147-443C-52

Query Match 73.6%; Score 53; DB 5; Length 105;
Best Local Similarity 69.2%; Pred. No. 0.031;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNFWY 13
Db 22 RASQSISSFWY 34

RESULT 5
US-09-403-107-148
; Sequence 148, Application US/09403107
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN

; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/09/403,107
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 148
; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN
US-09-403-107-148

Query Match 73.6%; Score 53; DB 5; Length 107;
Best Local Similarity 69.2%; Pred. No. 0.032;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNFWLHWY 13
Db 24 RASQSISSYLNWY 36

RESULT 6
US-09-403-107-152
; Sequence 152, Application US/09403107
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/09/403,107
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 152
; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN
US-09-403-107-152

Query Match 73.6%; Score 53; DB 5; Length 107;
Best Local Similarity 69.2%; Pred. No. 0.032;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNFWLHWY 13
Db 24 RASQSISSYLNWY 36

RESULT 7
US-09-610-551-66
; Sequence 66, Application US/09610551
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F, III
; APPLICANT: Burton, Dennis R
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,551
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 409.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-551-66

Query Match 70.8%; Score 51; DB 5; Length 107;
Best Local Similarity 61.5%; Pred. No. 0.067;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNFWLHWY 13
Db 22 RASQSISSYLNWY 34

RESULT 8
US-09-610-551A-66
; Sequence 66, Application US/09610551A
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F, III
; APPLICANT: Burton, Dennis R
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,551A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 409.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-551A-66

Query Match      70.8%; Score 51; DB 5; Length 107;
Best Local Similarity 61.5%; Pred. No. 0.067;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
Db 22 RASQSISSYNLWY 34

RESULT 9
US-09-607-756-2
; Sequence 2, Application US/09607756
; GENERAL INFORMATION:
; APPLICANT: Leung, Woon-Lam Susan
; APPLICANT: Swartz, James R.
; TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1711R1
; CURRENT APPLICATION NUMBER: US/09/607,756
; CURRENT FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/422,712
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Human
US-09-607-756-2

Query Match      70.8%; Score 51; DB 5; Length 237;
Best Local Similarity 61.5%; Pred. No. 0.14;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
Db 47 RASQDINNLWY 59

RESULT 10
US-09-530-237-2
; Sequence 2, Application US/09530237
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD
; TITLE OF INVENTION: Inducer for production of antigen-specific antibody, expression
; TITLE OF INVENTION: containing gene therefor, and method for inducing production of
; TITLE OF INVENTION: antibody
; FILE REFERENCE: SEI 98-30 PCT
; CURRENT APPLICATION NUMBER: US/09/530,237
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: JP 9/294393
; PRIOR FILING DATE: 1997-10-27
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; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Rattus
US-09-530-237-2

Query Match      69.4%; Score 50; DB 5; Length 108;
Best Local Similarity 53.8%; Pred. No. 0.099;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
Db 24 RASESVSTLMHWY 36

RESULT 11
US-09-403-107-142
; Sequence 142, Application US/09403107
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/09/403,107
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN
US-09-403-107-142

Query Match      68.1%; Score 49; DB 5; Length 107;
Best Local Similarity 61.5%; Pred. No. 0.14;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
Db 24 RTSQSISSYNLWY 36

RESULT 12
US-09-403-107-149
; Sequence 149, Application US/09403107
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/09/403,107
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 107
; TYPE: PRT
; ORGANISM: HUMAN
US-09-403-107-149

Query Match      68.1%; Score 49; DB 5; Length 107;
Best Local Similarity 61.5%; Pred. No. 0.14;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
Db 24 RTSQSISSYNLWY 36
```

Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSIISNLFHWY 13
:||||| :|:|
Db 22 RASQNIISYLNWY 34

RESULT 15

US-09-147-443C-44
; Sequence 44, Application US/09147443C
; GENERAL INFORMATION:
; APPLICANT: Morell, Andreas
; APPLICANT: Imboden, Martin
; APPLICANT: Stadler, Boda
; APPLICANT: Miescher, Sylvia
; APPLICANT: Vogel, Monique
; APPLICANT: Amstutz, Hanspeter
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
; TITLE OF INVENTION: STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
; TITLE OF INVENTION: THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
; FILE REFERENCE: 6816/P63221US0
; CURRENT APPLICATION NUMBER: US/09/147,443C
; CURRENT FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: PCT/EP97/03253
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: EP 96810421.6
; PRIOR FILING DATE: 1996-06-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-147-443C-44

Query Match 63.9%; Score 46; DB 5; Length 105;
Best Local Similarity 69.2%; Pred. No. 0.44;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSIISNLFHWY 13
:||||| :|:|
Db 22 RASQSIISNLFHWY 34

Search completed: March 28, 2001, 07:22:15
Job time: 1507 sec

RESULT 13
US-09-147-443C-12
; Sequence 12, Application US/09147443C
; GENERAL INFORMATION:
; APPLICANT: Morell, Andreas
; APPLICANT: Imboden, Martin
; APPLICANT: Stadler, Boda
; APPLICANT: Miescher, Sylvia
; APPLICANT: Vogel, Monique
; APPLICANT: Amstutz, Hanspeter
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
; TITLE OF INVENTION: STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
; TITLE OF INVENTION: THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
; FILE REFERENCE: 6816/P63221US0
; CURRENT APPLICATION NUMBER: US/09/147,443C
; CURRENT FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: PCT/EP97/03253
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: EP 96810421.6
; PRIOR FILING DATE: 1996-06-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-147-443C-12

Query Match 63.9%; Score 46; DB 5; Length 105;
Best Local Similarity 61.5%; Pred. No. 0.44;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSIISNLFHWY 13
:||||| :|:|
Db 22 RASQSIISYLNWY 34

RESULT 14

US-09-147-443C-40
; Sequence 40, Application US/09147443C
; GENERAL INFORMATION:
; APPLICANT: Morell, Andreas
; APPLICANT: Imboden, Martin
; APPLICANT: Stadler, Boda
; APPLICANT: Miescher, Sylvia
; APPLICANT: Vogel, Monique
; APPLICANT: Amstutz, Hanspeter
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
; TITLE OF INVENTION: STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
; TITLE OF INVENTION: THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
; FILE REFERENCE: 6816/P63221US0
; CURRENT APPLICATION NUMBER: US/09/147,443C
; CURRENT FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: PCT/EP97/03253
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: EP 96810421.6
; PRIOR FILING DATE: 1996-06-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-147-443C-40

Query Match 63.9%; Score 46; DB 5; Length 105;
Best Local Similarity 53.8%; Pred. No. 0.44;

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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:22 ; Search time 828.17 seconds

(without alignments)
1.934 Million cell updates/sec

Title: US-09-016-061-84

Perfect score: 49

Sequence: 1 LLIRYSSQIS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main: *

- 1: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgnl_7/ptodata/1/paa/US08_COMB.pep.*
- 5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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- 9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
- 13: /cgnl_7/ptodata/1/paa/US089_COMB.pep.*
- 14: /cgnl_7/ptodata/1/paa/US090_COMB.pep.*
- 15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
- 16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
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- 19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
- 20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	11	14	US-09-016-061-84
2	49	100.0	11	17	US-09-339-922A-84
3	44	89.8	11	14	US-09-016-061-44
4	44	89.8	11	17	US-09-339-922A-44
5	43	87.8	43	22	US-60-164-760-758
6	43	87.8	46	22	US-60-164-760-963
7	43	87.8	46	22	US-60-164-762-1122
8	43	87.8	66	22	US-60-160-203-4288
9	43	87.8	69	22	US-60-169-840-6293
10	43	87.8	74	22	US-60-164-762-875
11	43	87.8	88	1	PCT-US99-09131-30
					Sequence 84, Appl
					Sequence 84, Appl
					Sequence 44, Appl
					Sequence 758, Appl
					Sequence 963, Appl
					Sequence 1122, Appl
					Sequence 4288, Appl
					Sequence 6293, Appl
					Sequence 875, Appl
					Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-84
; Sequence 84, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

12	43	87.8	88	17	US-09-300-970A-30	Sequence 30, Appl
13	43	87.8	89	22	US-60-192-739-2860	Sequence 2860, Ap
14	43	87.8	89	22	US-60-194-243-2054	Sequence 2054, Ap
15	43	87.8	91	22	US-60-170-373-2286	Sequence 2286, Ap
16	43	87.8	91	22	US-60-170-374-1993	Sequence 1993, Ap
17	43	87.8	91	22	US-60-192-739-2861	Sequence 2861, Ap
18	43	87.8	98	22	US-60-194-243-2056	Sequence 2056, Ap
19	43	87.8	103	22	US-60-192-739-2862	Sequence 2862, Ap
20	43	87.8	103	22	US-60-194-243-2055	Sequence 2055, Ap
21	43	87.8	105	1	PCT-US98-04987-17	Sequence 17, Appl
22	43	87.8	105	1	PCT-US98-04987-21	Sequence 21, Appl
23	43	87.8	105	22	US-60-039-609-17	Sequence 17, Appl
24	43	87.8	105	22	US-60-039-609-21	Sequence 21, Appl
25	43	87.8	107	1	PCT-US98-04987-10	Sequence 10, Appl
26	43	87.8	107	3	US-07-804-464A-1	Sequence 1, Appl
27	43	87.8	107	3	US-07-808-464-1	Sequence 1, Appl
28	43	87.8	107	3	US-07-881-109-7	Sequence 7, Appl
29	43	87.8	107	3	US-07-881-109A-7	Sequence 7, Appl
30	43	87.8	107	4	US-08-082-842-1	Sequence 1, Appl
31	43	87.8	107	5	US-08-107-669B-1	Sequence 1, Appl
32	43	87.8	107	5	US-08-107-669C-1	Sequence 1, Appl
33	43	87.8	107	7	US-08-313-198-7	Sequence 7, Appl
34	43	87.8	107	8	US-08-472-788-1	Sequence 1, Appl
35	43	87.8	107	8	US-08-477-531-1	Sequence 1, Appl
36	43	87.8	107	8	US-08-477-531A-1	Sequence 1, Appl
37	43	87.8	107	8	US-08-484-537-62	Sequence 62, Appl
38	43	87.8	107	8	US-08-484-537-63	Sequence 63, Appl
39	43	87.8	107	8	US-08-484-537-87	Sequence 87, Appl
40	43	87.8	107	11	US-08-720-323-7	Sequence 7, Appl
41	43	87.8	107	14	US-09-037-980A-1	Sequence 1, Appl
42	43	87.8	107	14	US-09-037-980B-1	Sequence 1, Appl
43	43	87.8	107	15	US-09-160-911-9	Sequence 9, Appl
44	43	87.8	107	16	US-09-245-202A-1	Sequence 1, Appl
45	43	87.8	107	17	US-09-325-000-21	Sequence 21, Appl

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; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-016-061-84

Query Match      100.0%; Score 49; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 1 LLIRYSQSIS 11

RESULT 2
US-09-339-922A-84
; Sequence 84, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-84

Query Match      100.0%; Score 49; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 1 LLIRYSQSIS 11

RESULT 3
US-09-016-061-44
; Sequence 44, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-016-061-44

Query Match      89.8%; Score 44; DB 14; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 1 LLIRYSQSIS 11

RESULT 4
US-09-339-922A-44
; Sequence 44, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-44

Query Match      89.8%; Score 44; DB 17; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 1 LLIRYSQSIS 11

RESULT 5
US-60-164-760-758
; Sequence 758, Application US/60164760
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1000139
; CURRENT APPLICATION NUMBER: US/60/164,760
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 1060
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 758
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Human
; US-60-164-760-758

Query Match 87.8%; Score 43; DB 22; Length 43;
Best Local Similarity 81.8%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 31 LLIKYASQIS 41
|||:|:||||

RESULT 6
US-60-164-760-963
; Sequence 963, Application US/60164760
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000139
; CURRENT APPLICATION NUMBER: US/60/164,760
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 1060
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 963
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(46)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-164-760-963

Query Match 87.8%; Score 43; DB 22; Length 46;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 31 LLIKYASQIS 41
|||:|:||||

RESULT 7
US-60-164-762-1122
; Sequence 1122, Application US/60164762
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; FILE REFERENCE: CL000142
; CURRENT APPLICATION NUMBER: US/60/164,762
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 1244
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1122
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(46)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-164-762-1122

Query Match 87.8%; Score 43; DB 22; Length 46;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 31 LLIKYASQIS 41
|||:|:||||

RESULT 8
US-60-160-203-4288
; Sequence 4288, Application US/60160203
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS;
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; FILE REFERENCE: CL000116
; CURRENT APPLICATION NUMBER: US/60/160,203
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 6374
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4288
; LENGTH: 66
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(66)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-160-203-4288

Query Match 87.8%; Score 43; DB 22; Length 66;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 24 LLIKYASQIS 34
|||:|:||||

RESULT 9
US-60-169-840-6293
; Sequence 6293, Application US/60169840
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; FILE REFERENCE: CL000164
; CURRENT APPLICATION NUMBER: US/60/169,840
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 9628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6293
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(69)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-169-840-6293

Query Match 87.8%; Score 43; DB 22; Length 69;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQIS 11
Db 25 LLIKYASQIS 35
|||:|:||||

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; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/300,970A
; CURRENT FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/083,367
; PRIOR FILING DATE: 1998-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-300-970A-30

Query Match      87.8%; Score 43; DB 22; Length 74;
Best Local Similarity 81.8%; Pred. No. 0.41;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 48 LLIKYASQSSIS 56

RESULT 10
PCT-US99-09131-30
; Sequence 30, Application PCT/US9909131
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: PCT/US99/09131
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 60/083,367
; EARLIER FILING DATE: 1998-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
PCT-US99-09131-30

Query Match      87.8%; Score 43; DB 1; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 12
US-09-300-970A-30
; Sequence 30, Application US/09300970A
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000142
; CURRENT APPLICATION NUMBER: US/60/164,762
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 1244
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 875
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Human
US-60-164-762-875

Query Match      87.8%; Score 43; DB 17; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 13
US-60-192-739-2860
; Sequence 2860, Application US/60192739
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000406
; CURRENT APPLICATION NUMBER: US/60/192,739
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 4532
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2860
; LENGTH: 89
; TYPE: PRT
; ORGANISM: HUMAN
US-60-192-739-2860

Query Match      87.8%; Score 43; DB 22; Length 89;
Best Local Similarity 81.8%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 42 LLIKYASQSSIS 52

RESULT 14
US-60-194-243-2054
; Sequence 2054, Application US/60194243
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000417
; CURRENT APPLICATION NUMBER: US/60/194,243
; CURRENT FILING DATE: 2000-04-03
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000417
; CURRENT APPLICATION NUMBER: US/60/194,243
; CURRENT FILING DATE: 2000-04-03
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; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/300,970A
; CURRENT FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/083,367
; PRIOR FILING DATE: 1998-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-300-970A-30

Query Match      87.8%; Score 43; DB 17; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 46 LLIKYASQSSIS 56

RESULT 13
US-60-192-739-2860
; Sequence 2860, Application US/60192739
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000406
; CURRENT APPLICATION NUMBER: US/60/192,739
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 4532
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2860
; LENGTH: 89
; TYPE: PRT
; ORGANISM: HUMAN
US-60-192-739-2860

Query Match      87.8%; Score 43; DB 22; Length 89;
Best Local Similarity 81.8%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 42 LLIKYASQSSIS 52

RESULT 14
US-60-194-243-2054
; Sequence 2054, Application US/60194243
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000417
; CURRENT APPLICATION NUMBER: US/60/194,243
; CURRENT FILING DATE: 2000-04-03
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000417
; CURRENT APPLICATION NUMBER: US/60/194,243
; CURRENT FILING DATE: 2000-04-03
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;
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2054
; LENGTH: 89
; TYPE: PRT
; ORGANISM: HUMAN
US-60-194-243-2054

Query Match 87.8%; Score 43; DB 22; Length 89;
Best Local Similarity 81.8%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 42 LLIRYASQSSIS 52

RESULT 15
US-60-170-373-2286
; Sequence 2286, Application US/60170373
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000149
; CURRENT APPLICATION NUMBER: US/60/170,373
; CURRENT FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 4282
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2286
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Human
US-60-170-373-2286

Query Match 87.8%; Score 43; DB 22; Length 91;
Best Local Similarity 81.8%; Pred. No. 0.5;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSSQSSIS 11
Db 65 LLIRYASQSSIS 75

Search completed: March 28, 2001, 07:18:24
Job time: 1335 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:15 ; Search time 213.09 Seconds
(Without alignments)
0.680 Million cell updates/sec

Title: US-09-016-061-84

Perfect score: 49

Sequence: 1 LLIRYSQSIS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	79.6	109	5	US-09-445-602A-6
2	35	71.4	403	5	US-09-489-039A-13550
3	31	63.3	54	1	PCT-US01-02723-119
4	31	63.3	561	6	US-60-259-128-4577
5	31	63.3	812	5	US-09-488-725A-2446
6	31	63.3	832	5	US-09-488-725A-6018
7	30	61.2	297	6	US-60-257-931-3538
8	30	61.2	297	6	US-60-253-625-2710
9	30	61.2	297	6	US-60-269-308-4560
10	30	61.2	438	5	US-09-489-039A-13834
11	30	61.2	459	5	US-09-488-725A-2856
12	29	59.2	110	5	US-09-316-633-302
13	29	59.2	238	6	US-60-257-931-3007
14	29	59.2	238	6	US-60-269-308-4028
15	29	59.2	247	5	US-09-107-433-2806
16	29	59.2	624	6	US-60-257-931-2925
17	29	59.2	624	6	US-60-253-625-2130
18	29	59.2	624	6	US-60-269-308-3946
19	28	57.1	54	1	PCT-US00-32227-138
20	28	57.1	206	5	US-09-107-433-2696
21	28	57.1	234	5	US-09-107-433-3990
22	28	57.1	257	5	US-09-488-725A-7116
23	28	57.1	322	5	US-09-767-041-35
24	28	57.1	329	5	US-09-489-039A-9812
25	28	57.1	333	5	US-09-791-932-91
26	28	57.1	333	5	US-09-791-932-114
27	28	57.1	368	1	PCT-US00-32227-45

28	28	57.1	371	5	US-09-165-922A-10	Sequence 10, Appl
29	28	57.1	395	5	US-09-489-039A-7739	Sequence 7739, Ap
30	28	57.1	539	6	US-60-257-931-3555	Sequence 3555, Ap
31	28	57.1	539	6	US-60-253-625-2727	Sequence 2727, Ap
32	28	57.1	539	6	US-60-269-308-4577	Sequence 4577, Ap
33	28	57.1	582	5	US-09-489-039A-12055	Sequence 12055, A
34	28	57.1	687	5	US-09-529-063-73	Sequence 73, Appl
35	28	57.1	817	5	US-09-489-039A-8184	Sequence 8184, Ap
36	28	57.1	1150	5	US-09-488-725A-3544	Sequence 3544, Ap
37	28	57.1	4342	6	US-60-257-931-3424	Sequence 2596, Ap
38	28	57.1	4342	6	US-60-253-625-2596	Sequence 2596, Ap
39	28	57.1	4342	6	US-60-269-308-4446	Sequence 4446, Ap
40	27	55.1	65	5	US-09-465-587-316	Sequence 316, App
41	27	55.1	143	4	US-08-765-588A-8	Sequence 8, Appl
42	27	55.1	143	5	US-09-349-954A-8	Sequence 5, Appl
43	27	55.1	188	1	PCT-US00-01895A-5	Sequence 11, Appl
44	27	55.1	188	4	US-08-851-896-11	Sequence 6, Appl
45	27	55.1	188	4	US-08-765-588A-6	

ALIGNMENTS

RESULT 1
US-09-445-602A-6
; Sequence 6, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNIT
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445, 602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-6

Query Match 79.6%; Score 39; DB 5; Length 109;
Best Local Similarity 72.7%; Pred. No. 0.23;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIRYSQSIS 11
Db 47 LLIKFASQSIS 57
||||:|||||

RESULT 2
US-09-489-039A-13550
; Sequence 13550, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13550

; LENGTH: 403
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13550

Query Match 71.4%; Score 35; DB 5; Length 403;
Best Local Similarity 54.5%; Pred. No. 6.2;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSI 11
||:|||||:
Db 332 LLLKSSDSVT 342

RESULT 3
PCT-US01-02723-119
; Sequence 119, Application PC/TUS0102723
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Yeung, George
; APPLICANT: Ford, John E.
; APPLICANT: Boyle, Bryan J.
; APPLICANT: Arterburn, Matthew C.
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhou, Ping
; APPLICANT: Wehrman, Thomas
; TITLE OF INVENTION: NOVEL FETAL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-020
; CURRENT APPLICATION NUMBER: PCT/US01/02723
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/707,351
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/663,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 1262
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119
; LENGTH: 54
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US01-02723-119

Query Match 63.3%; Score 31; DB 1; Length 54;
Best Local Similarity 75.0%; Pred. No. 5.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLIRYSSQ 8
||:||||:
Db 40 LLLRFSSQ 47

RESULT 4
US-60-259-128-4577
; Sequence 4577, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4577
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4577

Query Match 63.3%; Score 31; DB 6; Length 561;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSI 10
||:|||||:
Db 43 LLIRYLSPSI 52

RESULT 5
US-09-488-725A-2446
; Sequence 2446, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2446
; LENGTH: 813
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2446

Query Match 63.3%; Score 31; DB 5; Length 812;
Best Local Similarity 63.6%; Pred. No. 86;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLIRYSSQSI 11
||:|||||:
Db 560 LLQRESSQFVS 570

RESULT 6
US-09-488-725A-6018
; Sequence 6018, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042

; FILE REFERENCE: ELITRA.017PR3
; CURRENT APPLICATION NUMBER: US09/620,312
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 6018
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6018

Query Match 63.3%; Score 31; DB 5; Length 832;
Best Local Similarity 63.6%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSSQSI 11
|||:||||:
DB 580 LLQRESSQFVS 590

RESULT 7
US-60-257-931-3538
; Sequence 3538, Application US/60257931
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, R
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Genes identified as essential in *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*
; FILE REFERENCE: ELITRA.017PR4
; CURRENT APPLICATION NUMBER: US/60/257,931
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 3592
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3538
; LENGTH: 297
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-60-257-931-3538

Query Match 61.2%; Score 30; DB 6; Length 297;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQSI 10
| |||:||||
DB 91 LARYSAESI 99

RESULT 8
US-60-253-625-2710
; Sequence 2710, Application US/60253625
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RH
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of essential genes in *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Salmonella typhimurium*
; FILE REFERENCE: ELITRA.017PR3
; CURRENT APPLICATION NUMBER: US/60/253,625
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 2768
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2710
; LENGTH: 297
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-60-253-625-2710

Query Match 61.2%; Score 30; DB 6; Length 297;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQSI 10
| |||:||||
DB 91 LARYSAESI 99

RESULT 9
US-60-269-308-4560
; Sequence 4560, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in *Staphylococcus aureus*, *Ps*
; FILE REFERENCE: ELITRA.017PR5
; CURRENT APPLICATION NUMBER: US/60/269,308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4560
; LENGTH: 297
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-60-269-308-4560

Query Match 61.2%; Score 30; DB 6; Length 297;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIRYSSQSI 10
| |||:||||
DB 91 LARYSAESI 99

RESULT 10
US-09-489-039A-13834
; Sequence 13834, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *KLEBSIELLA*
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13834
; LENGTH: 438
; TYPE: PRT
; ORGANISM: *Klebsiella pneumoniae*
US-09-489-039A-13834

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Query Match      61.2%; Score 30; DB 5; Length 438;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 IRYSSQSI 11
Db 337 LRYSSQSRVA 345

RESULT 11
US-09-488-725A-2856
; Sequence 2856, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2856
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2856

Query Match      61.2%; Score 30; DB 5; Length 459;
Best Local Similarity 62.5%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLIRYSQ 8
Db 38 IFVRYSSQ 45

RESULT 12
US-09-316-633-302
; Sequence 302, Application US/09316633
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Derived from a
; TITLE OF INVENTION: Human Mesangial Cell Library
; FILE REFERENCE: MLN98-10PA
; CURRENT APPLICATION NUMBER: US/09/316,633
; CURRENT FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/087,052
; PRIOR FILING DATE: 1998-05-27
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 110
; TYPE: PRT...
; ORGANISM: Homo sapiens
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FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(79)
; NAME/KEY: VARIANT
; LOCATION: (1)...(110)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-316-633-302

Query Match      59.2%; Score 29; DB 5; Length 110;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSQSI 10
Db 100 LLSGYSSSESI 109

RESULT 13
US-60-257-931-3007
; Sequence 3007, Application US/60257931
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, R
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Genes identified as essential in Staphylococcus aureus, Salmo
; TITLE OF INVENTION: typhimurium, Klebsiella pneumoniae and Pseudomonas aeruginos
; FILE REFERENCE: ELITRA.017PR4
; CURRENT APPLICATION NUMBER: US/60/257,931
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 3592
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3007
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-60-257-931-3007

Query Match      59.2%; Score 29; DB 6; Length 238;
Best Local Similarity 63.6%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLIRYSQSI 11
Db 173 LNIYSYSSKSI 183

RESULT 14
US-60-269-308-4028
; Sequence 4028, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in Staphylococcus aureus, Ps
; TITLE OF INVENTION: faecalis
; FILE REFERENCE: ELITRA.017PRS
; CURRENT APPLICATION NUMBER: US/60/269,308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4028
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-60-269-308-4028
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Job time: 1508 sec

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Query Match      59.2%; Score 29; DB 6; Length 238;
Best Local Similarity 63.6%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 LLIRYSSQSSIS 11
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Db      173 LNISYSSKSIT 183
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RESULT 15
US-09-107-433-2806
; Sequence 2806, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
;
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 2806:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...247
; SEQUENCE DESCRIPTION: SEQ ID NO: 2806:
US-09-107-433-2806

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Query Match 59.2%; Score 29; DB 5; Length 247;
Best Local Similarity 40.0%; Pred. No. 66;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 LIRYSSQSIG 11
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Db     144 LVRYKSEEA 153
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Search completed: March 28, 2001, 07:22:16

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:24 ; Search time 828.17 Seconds
(without alignments)
1.583 Million cell updates/sec

Title: US-09-016-061-86
Perfect score: 55
Sequence: 1 QOSNSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main.*

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2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
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10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	1 PCT-US98-25828-2	Sequence 2, Appli
2	55	100.0	9	13 US-08-986-016-2	Sequence 2, Appli
3	55	100.0	9	14 US-09-016-061-86	Sequence 86, Appl
4	55	100.0	9	17 US-09-339-922A-86	Sequence 86, Appl
5	55	100.0	107	8 US-08-484-537-62	Sequence 62, Appl
6	55	100.0	107	8 US-08-484-537-63	Sequence 63, Appl
7	55	100.0	107	8 US-08-484-537-87	Sequence 87, Appl
8	55	100.0	107	17 US-09-325-000-21	Sequence 21, Appl
9	55	100.0	107	17 US-09-325-000-22	Sequence 22, Appl
10	55	100.0	109	1 PCT-US98-25828-45	Sequence 45, Appl
11	55	100.0	109	1 PCT-US98-25828-49	Sequence 49, Appl

12	55	100.0	109	1 PCT-US98-25828-55	Sequence 55, Appl
13	55	100.0	109	13 US-08-986-016-45	Sequence 45, Appl
14	55	100.0	109	13 US-08-986-016-49	Sequence 49, Appl
15	55	100.0	109	13 US-08-986-016-55	Sequence 55, Appl
16	55	100.0	127	8 US-08-484-537-83	Sequence 83, Appl
17	50	90.9	259	18 US-09-419-788-29	Sequence 29, Appl
18	49	89.1	9	14 US-09-016-061-46	Sequence 46, Appl
19	49	89.1	9	14 US-09-016-061-88	Sequence 88, Appl
20	49	89.1	9	17 US-09-339-922A-46	Sequence 46, Appl
21	49	89.1	9	17 US-09-339-922A-88	Sequence 88, Appl
22	49	89.1	33	7 US-08-307-868-12	Sequence 12, Appl
23	49	89.1	33	9 US-08-525-539-12	Sequence 12, Appl
24	49	89.1	33	9 US-08-525-539A-12	Sequence 12, Appl
25	49	89.1	107	3 US-07-804-464A-1	Sequence 1, Appl
26	49	89.1	107	3 US-07-808-464-1	Sequence 1, Appl
27	49	89.1	107	3 US-07-881-109-7	Sequence 7, Appl
28	49	89.1	107	3 US-07-881-109A-7	Sequence 7, Appl
29	49	89.1	107	4 US-08-082-842-1	Sequence 1, Appl
30	49	89.1	107	5 US-08-107-669B-1	Sequence 1, Appl
31	49	89.1	107	5 US-08-107-669C-1	Sequence 1, Appl
32	49	89.1	107	7 US-08-313-198-7	Sequence 7, Appl
33	49	89.1	107	8 US-08-472-788-1	Sequence 1, Appl
34	49	89.1	107	8 US-08-477-531-1	Sequence 1, Appl
35	49	89.1	107	8 US-08-477-531A-1	Sequence 1, Appl
36	49	89.1	107	11 US-08-720-323-7	Sequence 7, Appl
37	49	89.1	107	11 US-08-790-540-4	Sequence 4, Appl
38	49	89.1	107	11 US-08-790-540-8	Sequence 8, Appl
39	49	89.1	107	11 US-08-790-540A-4	Sequence 4, Appl
40	49	89.1	107	11 US-08-790-540A-8	Sequence 8, Appl
41	49	89.1	107	11 US-08-791-391-4	Sequence 4, Appl
42	49	89.1	107	11 US-08-791-391-8	Sequence 8, Appl
43	49	89.1	107	11 US-08-791-391-32	Sequence 32, Appl
44	49	89.1	107	11 US-08-791-391A-4	Sequence 4, Appl
45	49	89.1	107	11 US-08-791-391A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
PCT-US98-25828-2
; Sequence 2, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-2

Query Match 100.0%; Score 55; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 1 QOSNSWPHT 9
RESULT 2
US-08-986-016-2
; Sequence 2, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.

APPLICANT: Rader, Christoph
TITLE OF INVENTION: Humanization of Murine Antibody
FILE REFERENCE: Tsri 598.0
CURRENT APPLICATION NUMBER: US/08/986.016A
CURRENT FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-2

Query Match 100.0%; Score 55; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
Db 1 QOSNSWPHT 9

RESULT 3
US-09-016-061-86
Sequence 86, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-86

Query Match 100.0%; Score 55; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
Db 1 QOSNSWPHT 9

RESULT 4
US-09-339-922A-86
Sequence 86, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-86

Query Match 100.0%; Score 55; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWPHT 9
Db 1 QOSNSWPHT 9

RESULT 5
US-08-484-537-62
Sequence 62, Application US/08484537
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

;; PRIOR APPLICATION DATA: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 62:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-484-537-62

Query Match 100.0%; Score 55; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 6
US-08-484-537-63
;; Sequence 63, Application US/08484537
;; GENERAL INFORMATION:
;; APPLICANT: QUEEN, Cary L.
;; APPLICANT: CO, Man Sung
;; APPLICANT: SCHNEIDER, William P.
;; APPLICANT: LANDOLFI, Nicholas F.
;; APPLICANT: COELINGH, Kathleen L.
;; APPLICANT: SELICK, Harold E.
;; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
;; NUMBER OF SEQUENCES: 113
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,537
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-484-537-63

Query Match 100.0%; Score 55; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 7
US-08-484-537-87
;; Sequence 87, Application US/08484537
;; GENERAL INFORMATION:
;; APPLICANT: QUEEN, Cary L.
;; APPLICANT: CO, Man Sung
;; APPLICANT: SCHNEIDER, William P.
;; APPLICANT: LANDOLFI, Nicholas F.
;; APPLICANT: COELINGH, Kathleen L.
;; APPLICANT: SELICK, Harold E.
;; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
;; NUMBER OF SEQUENCES: 113
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,537
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 87:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-484-537-87

Query Match 100.0%; Score 55; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 8

US-09-325-000-21
; Sequence 21, Application US/09325000
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-325-000-21

Query Match 100.0%; Score 55; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 9

US-09-325-000-22
; Sequence 22, Application US/09325000
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-325-000-22

Query Match 100.0%; Score 55; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 10
PCT-US98-25828-45
; SEQUENCE 45, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-45

Query Match 100.0%; Score 55; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 11
PCT-US98-25828-49
; SEQUENCE 49, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-49

Query Match 100.0%; Score 55; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 12
PCT-US98-25828-55
; SEQUENCE 55, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-55

Query Match 100.0%; Score 55; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 13
US-08-986-016-45
; SEQUENCE 45, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-45

Query Match 100.0%; Score 55; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNSWPHT 9
Db 89 QOSNSWPHT 97

RESULT 14
US-08-986-016-49
; SEQUENCE 49, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-49

Query Match 100.0%; Score 55; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QQSNSWPHT 9
| | | | |
Db 89 QQSNSWPHT 97

RESULT 15

US-08-986-016-55
; Sequence 55, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsr1 598.0
; CURRENT APPLICATION NUMBER: US/08/986, 016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-55

Query Match 100.0%; Score 55; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNSWPHT 9
| | | | |
Db 89 QQSNSWPHT 97

Search completed: March 28, 2001, 07:18:25
Job time: 1336 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:16 ; Search time 213.09 Seconds
(without alignments)
0.557 Million cell updates/sec

Title: US-09-016-061-86
Perfect score: 55
Sequence: 1 QQNSWPHPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	76.4	10	5	US-09-445-602A-17
2	42	76.4	20	5	US-09-445-602A-25
3	42	76.4	109	5	US-09-445-602A-6
4	38	69.1	265	5	US-09-489-039A-12065
5	35	63.6	41	5	US-09-005-843D-1235
6	35	63.6	310	5	US-09-488-725A-2779
7	35	63.6	324	5	US-09-488-725A-6351
8	34	61.8	774	5	US-09-782-980-16
9	34	61.8	774	5	US-09-702-572-7
10	33	60.0	40	5	US-09-205-462B-173
11	33	60.0	72	1	PCT-US01-01340-744
12	33	60.0	154	5	US-09-352-616A-383
13	33	60.0	154	5	US-09-759-143-383
14	33	60.0	154	5	US-09-679-426-383
15	33	60.0	154	5	US-09-685-166-383
16	33	60.0	154	5	US-09-679-272-383
17	33	60.0	154	5	US-09-780-669-383
18	33	60.0	161	5	US-09-759-143-846
19	33	60.0	161	5	US-09-679-426-846
20	33	60.0	161	5	US-09-685-166-846
21	33	60.0	161	5	US-09-780-669-846
22	33	60.0	189	6	US-60-266-855-12
23	33	60.0	216	5	US-09-489-039A-9538
24	33	60.0	254	5	US-09-489-039A-13102
25	32	58.2	37	1	PCT-US01-01324-2525
26	32	58.2	66	1	PCT-US01-01340-719
27	32	58.2	145	5	US-09-489-039A-13527

28	32	58.2	306	5	US-09-489-039A-8745	Sequence 8745, Ap
29	32	58.2	319	5	US-09-489-039A-13662	Sequence 13662, A
30	32	58.2	322	5	US-09-536-483A-5	Sequence 5, Appli
31	32	58.2	353	5	US-09-488-725A-3230	Sequence 3230, Ap
32	32	58.2	428	5	US-09-489-039A-7294	Sequence 7294, Ap
33	32	58.2	435	5	US-09-489-039A-7287	Sequence 7287, Ap
34	32	58.2	437	5	US-09-536-483A-4	Sequence 4, Appli
35	32	58.2	509	5	US-09-536-483A-3	Sequence 3, Appli
36	32	58.2	514	5	US-09-536-483A-2	Sequence 2, Appli
37	32	58.2	794	5	US-09-489-039A-10909	Sequence 10909, A
38	32	58.2	1228	5	US-09-463-402-2	Sequence 2, Appli
39	31	56.4	41	5	US-09-770-219-3	Sequence 3, Appli
40	31	56.4	72	5	US-09-381-150A-4	Sequence 4, Appli
41	31	56.4	87	5	US-09-381-150A-3	Sequence 3, Appli
42	31	56.4	133	5	US-09-455-486-13	Sequence 13, Appli
43	31	56.4	294	5	US-09-489-039A-12644	Sequence 12644, A
44	31	56.4	357	5	US-09-488-725A-2732	Sequence 2732, Ap
45	31	56.4	407	5	US-09-595-298A-1354	Sequence 1354, Ap

ALIGNMENTS

RESULT 1
US-09-445-602A-17
; Sequence 17, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445,602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-17

Query Match 76.4%; Score 42; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQNSWNP 7

Db 1 QQNSWNP 7

RESULT 2

US-09-445-602A-25
; Sequence 25, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445,602A
; CURRENT FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-25

Query Match 76.4%; Score 42; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWP 7
Db 5 QOSNSWP 11

RESULT 3
US-09-445-602A-6
; Sequence 6, Application US/09445602A
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irwin
; APPLICANT: ROTTER, Varda
; APPLICANT: Wolkowicz, Roland
; APPLICANT: RUIZ, Pedro
; APPLICANT: EREZ-ALON, Neta
; APPLICANT: HERKEL, Johannes
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR IMMUNITY
; FILE REFERENCE: COHEN42
; CURRENT APPLICATION NUMBER: US/09/445.602A
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: PCT/IL98/00266
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: IL 121041
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-602A-6

Query Match 76.4%; Score 42; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSNSWP 7
Db 90 QOSNSWP 96

RESULT 4
US-09-489-039A-12065
; Sequence 12065, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12065
; LENGTH: 265

; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12065

Query Match 69.1%; Score 38; DB 5; Length 265;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 8
Db 112 QOYNLWPH 119

RESULT 5
US-09-009-843D-235
; Sequence 235, Application US/09009843D
; GENERAL INFORMATION:
; APPLICANT: Arai, Naoko
; Masuda, Esteban S.
; Tokumitsu, Hiroshi
; TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
; NUMBER OF SEQUENCES: 266
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30; #2.0; and
word processor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,843D
; FILING DATE: 20-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/222,626
; FILING DATE: 04-APR-1994
; APPLICATION NUMBER: US 08/148,061
; FILING DATE: 05-NOV-1993
; APPLICATION NUMBER: US 08/113,971
; FILING DATE: 30-AUG-1993
; APPLICATION NUMBER: US 08/099,998
; FILING DATE: 30-JUL-1993
; APPLICATION NUMBER: US 08/088,483
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0392K3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 235:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 235:
US-09-009-843D-235

Query Match 63.6%; Score 35; DB 5; Length 41;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNSWPH 8
; : : : :
Db 12 EQTKAWPH 19

RESULT 6

US-09-488-725A-2779
; Sequence 2779, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2779
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-488-725A-2779

Query Match 63.6%; Score 35; DB 5; Length 310;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QOSNSWPH 8
; : : : :
Db 205 QSKDWP 211

RESULT 7

US-09-488-725A-6351
; Sequence 6351, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344

; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 6351
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6351

Query Match 63.6%; Score 35; DB 5; Length 324;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QOSNSWPH 8
; : : : :
Db 219 QSKDWP 225

RESULT 8

US-09-782-980-16
; Sequence 16, Application US/09782980
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STMTS PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: WNI-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-782-980-16

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Query Match          61.8%; Score 34; DB 5; Length 774;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSNWPH 8
   | :||||
Db 26 QYDSWPH 32

RESULT 9
US-09-702-572-7
; Sequence 7, Application US/09702572
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
; FILE REFERENCE: MNI-073
; CURRENT APPLICATION NUMBER: US/09/702,572
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-572-7

Query Match          61.8%; Score 34; DB 5; Length 774;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSNWPH 8
   | :||||
Db 26 QYDSWPH 32

RESULT 10
US-09-209-462B-173
; Sequence 173, Application US/09209462B
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 86 Human Secreted Proteins
; FILE REFERENCE: PZ008PI
; CURRENT APPLICATION NUMBER: US/09/209,462B
; CURRENT FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/12125
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/049,547
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,548
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,549
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,550
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,566
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,606
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,607
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,608
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,609
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,610
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,611
; PRIOR FILING DATE: 1997-06-13

Query Match          60.0%; Score 33; DB 5; Length 40;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QOSNSWPH 9
   | :||||
Db 20 EHGSPWPH 28

RESULT 11
PCT-US01-01340-744
; Sequence 744, Application PC/TUS0101340
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01340
; CURRENT FILING DATE: 2001-01-14
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 744
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```

```
; NAME/KEY: SITE
; LOCATION: (64)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-01340-744

Query Match          60.0%; Score 33; DB 1; Length 72;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQNSWP 7
Db 30 QQQSWP 36

RESULT 12
US-09-352-616A-383
; Sequence 383, Application US/09352616A
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352.616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-352-616A-383

Query Match          60.0%; Score 33; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QQNSWPHT 9
Db 9 QGARWPHT 16

RESULT 13
US-09-759-143-383
; Sequence 383, Application US/09759143
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759.143
; CURRENT FILING DATE: 2001-01-12
```

```
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-383

Query Match          60.0%; Score 33; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QQNSWPHT 9
Db 9 QGARWPHT 16

RESULT 14
US-09-679-426-383
; Sequence 383, Application US/09679426
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679.426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-383

Query Match          60.0%; Score 33; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QQNSWPHT 9
Db 9 QGARWPHT 16

RESULT 15
US-09-685-166-383
; Sequence 383, Application US/09685166
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
```

; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 383
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166-383

Query Match 60.0%; Score 33; DB 5; Length 154;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QSNWPHT 9
| | | | |
Db 9 QGARWPHT 16

Search completed: March 28, 2001, 07:22:17
Job time: 1509 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:27:17 ; Search time 141.45 Seconds
(without alignments)
56.164 Million cell updates/sec

Title: US-09-016-061-6
Perfect score: 612
Sequence: 1 EVLVESGGLVPGKSLRL.....RHNYGSFAYWGQGLTVTSA 117
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494.5	80.8	254	B31790	Ig heavy chain V r
2	486.5	79.5	121	H27888	Ig heavy chain V r
3	486	79.4	138	S09258	Ig heavy chain V r
4	483.5	79.0	112	A27889	Ig heavy chain V r
5	480.5	78.5	548	S38864	Ig epsilon chain C
6	479.5	78.3	113	S26468	Ig heavy chain V r
7	477.5	78.0	121	D27888	Ig heavy chain V r
8	476.5	77.9	123	G27888	Ig heavy chain V r
9	476	77.8	122	E27888	Ig heavy chain V r
10	472.5	77.2	119	F27888	Ig heavy chain V r
11	471	77.0	120	S55536	Ig heavy chain V r
12	467	76.3	111	PH1007	Ig heavy chain V r
13	466	76.1	117	HVMS34	Ig heavy chain V r
14	466	76.1	118	S20641	Ig heavy chain pre
15	466	76.1	119	S31108	Ig heavy chain V r
16	464.5	75.9	119	D27889	Ig heavy chain - h
17	463.5	75.7	123	S63597	Ig heavy chain V r
18	462	75.5	117	S78486	Ig heavy chain V r
19	462	75.5	119	C36005	Ig heavy chain V r
20	462	75.5	119	S31107	Ig heavy chain - h
21	462	75.5	120	S55537	Ig heavy chain V r
22	462	75.5	140	S31588	Ig heavy chain V r
23	461.5	75.4	128	PH0095	Ig kappa chain V r
24	461	75.3	117	PL0249	Ig heavy chain V r
25	461	75.3	120	S55539	Ig heavy chain V r
26	461	75.3	140	S31686	Ig heavy chain V r
27	461	75.3	152	B26471	Ig heavy chain pre
28	460	75.2	124	C27888	Ig heavy chain V r
29	459.5	75.1	118	PH0096	Ig heavy chain V r

ALIGNMENTS

RESULT 1

B31790

Ig heavy chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997

C:Accession: B31790

R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an

A:Reference number: A92686; MUID:89034213

A:Accession: B31790

A:Molecule type: mRNA

A:Residues: 1-254 <SCH>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 494.5; DB 2; Length 254;

Best Local Similarity 80.0%; Pred. No. 5.5e-39;

Matches 96; Conservative 10; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EVLVESGGLVPGKSLRLSCAAGFAPSSYDMSWVRQIPEKLEWAKVSSGGSTYY 60

Db 1 EVLVESGGLVPGKSLRLSCAAGFAPSSYDMSWVRQIPEKLEWAKVSSGGSTYY 60

Qy 61 LDTVQGRFTISRDNKNTLYLQWSSLNSEDYAMYCA---RHNYGSFAYWGQGLTVTSA 117

Db 61 PDSVKGRTISRDNKNTLYLQWSSLNSEDYAMYCA---RHNYGSFAYWGQGLTVTSA 120

RESULT 2

H27888

Ig heavy chain V region (H37-40) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: H27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: H27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

```
Best Local Similarity 83.2%; Pred. No. 2.4e-38;
Matches 94; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
```

QY 4 LVESGGGLVPGSLRLSCAASGFAFSSYDMSWVRQIPEKRLKEHWAKVSSGGGSTYYLDLT 63
|:||||||| |:||||||| | :||||||| |:||||||| |:||||||| |:|||||||
Db 1 LVESGGGLVPGSGLSKLSCAASGFSTSIYAMSVMRQSPERKLEWVAEISGGGSTYYPDTPDT 60
|:||||||| |:||||||| | :||||||| |:||||||| |:||||||| |:|||||||

QY 64 VOGREFTISRDNKNNTLYLQMSSLNSEDATMYCCARHNYGSFYAWGQGTLTVTS 116
|:||||||| |:||||||| | :||||||| |:||||||| |:||||||| |:|||||||
Db 61 VTGRFTISRDNKNNTLYLENSSLRSDEATMYCCARH-WEEEFAYWGQGTLTVTS 112
|:||||||| |:||||||| | :||||||| |:||||||| |:||||||| |:|||||||

RESULT 5
S38864
Ig epsilon chain C region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S38864
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of
A:Reference number: S38864
A:Accession: S38864
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <RIP>
A:Cross-references: EMBL:Z7397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C:Superfamily: Immunoglobulin homology
F:J55-421/Domain: Immunoglobulin homology <IMM>

Query Match 78.5%; Score 480.5; DB 2; Length 548;
Best Local Similarity 78.3%; Pred. No. 2.5e-37;
Matches 94; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVKPGRSLRLSCAASGFAFSYDMSWVRQIPEKRLKEHWAKVSSGGGSTYY 60
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||
Db 1 QVKLLSEGGDLVPKGSGSKLSCAASGLTFSYGSMWRQPDKRLEWVATISSCGTYTY 60
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||

QY 61 LDTVVGREFITSRDNKNNTLYQLMSSLNSEDATMYCCARHNYGS---PAYWGQGTLTVSA 117
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||
Db 61 PDSVKGREFTISRDNKNNTLYQLMSSLKSSEDATMYCCARGVSTMIRPAYWGQGTLTVSA 120
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||

RESULT 6
S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:I1-94/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 479.5; DB 2; Length 113;
Best Local Similarity 84.4%; Pred. No. 5.8e-38;
Matches 92; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 9 GLGVKPGSLRLSCAASGFAFSSYDMSWVRQIPEKRLKEHWAKVSSGGGSTYYLDTVQGRF 68
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||
Db 5 GLSVKPGSGLSKLSCAASGFAFSYDMSWVRQTPEKRLWEVATISSGGGSTYYPDTVKGRF 64
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||

QY 69 TISRDNKNNTLYLMQSSLNSEDATMYCCARHNYGSF---AYWGQGTLVT 114
|:||||| |:||||| | :||||| |:||||| |:||||| |:|||||

Db 65 TISRDNAKNTLYLQMSLSKSEDTAMYYCARHPYGNYYANDYWGQGTSTV 113

RESULT 7

D27888
Ig heavy chain V region (H37-60) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: D27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658
A:Accession: D27888
A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 477.5; DB 2; Length 121;
Best Local Similarity 77.7%; Pred. No. 9.5e-38;
Matches 94; Conservative 8; Mismatches 14; Indels 5; Gaps 1;

QY 1 EVQLVESGGGLVKGPRSLRLSCAASGFAFSSYDMSVWVRQIPEKRLWVAKVSSGGSTYY 60
Db 1 EVNLVESGGDLVKGPGSLKLSCAASGFAFSSYDMSVWVRQSPKRLWVATISSGGSTYDY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGS-----FAYWGQGTLTIV 115
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSNSEDALYICARQDIYINDDWFTYWGQGTLTIV 120

QY 116 S 116
Db 121 S 121

RESULT 8

G27888
Ig heavy chain V region (H28-A2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: G27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658
A:Accession: G27888
A:Molecule type: DNA
A:Residues: 1-123 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 476.5; DB 2; Length 123;
Best Local Similarity 78.9%; Pred. No. 1.2e-37;
Matches 97; Conservative 4; Mismatches 15; Indels 7; Gaps 2;

QY 1 EVQLVESGGGLVKGPRSLRLSCAASGFAFSSYDMSVWVRQIPEKRLWVAKVSSGGSTYY 60
Db 1 EVQLVESGGDLVKGPGSLKLSCAASGFTFSYAMSVWVRQSPKRLWVATISSGGSTYTY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYYCAR----HNYS----FAYWGQGTLY 113
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSNSEDALYICARQDIYINDDWFTYWGQGTLSV 120

QY 114 TVS 116
Db 121 TVS 123

RESULT 9

E27888
Ig heavy chain V region (H35-C6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: E27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: E27888
A:Molecule type: DNA
A:Residues: 1-122 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 476; DB 2; Length 122;
Best Local Similarity 77.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 8; Mismatches 14; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVKGPRSLRLSCAASGFAFSSYDMSVWVRQIPEKRLWVAKVSSGGSTYY 60
Db 1 DVKLVESGGDLVKGPGSLKLSCAASGFTFSYTMVWVRQTPKRLWVATISSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYYCAR----HNYSFA--YWGQGTLY 114
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSNSEDAMYYCTROGEGYRDDYANDYWGQGTSTV 120

QY 115 VS 116
Db 121 VS 122

RESULT 10

F27888
Ig heavy chain V region (H158-89H4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: F27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: F27888
A:Molecule type: DNA
A:Residues: 1-119 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 472.5; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 2.7e-37;
Matches 94; Conservative 7; Mismatches 15; Indels 3; Gaps 2;

QY 1 EVQLVESGGGLVKGPRSLRLSCAASGFAFSSYDMSVWVRQIPEKRLWVAKVSSGGSTYY 60
Db 1 DVKLVESGGDLVKGPGSLKLSCAASGFTFSYTMVWVRQTPKRLWVATISSGGSTYY 60

HVMS34

Ig heavy chain precursor V region (345) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J0502

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: J0501; MUID:89279149
A:Accession: J0502

A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ
A:Note: This sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 76.1%; Score 466; DB 1; Length 117;
Best Local Similarity 91.8%; Pred. No. 1.1e-36;
Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFAFSSYDMSVWROIPEKRLIEWAKVSSGGSTYY 60
Db 20 EVLVESGGGLVKPGSLRLSCAASGFAFSSYDMSVWROIPEKRLIEWAKVSSGGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYTCAR 98
Db 80 PDIVKGRFTISRDNKNTLYLQMSLSKSEDATMYTCAR 117

RESULT 14
S20641

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20641

R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
A:Reference number: S20639
A:Accession: S20641
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <LOS>

A:Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 466; DB 2; Length 118;
Best Local Similarity 76.3%; Pred. No. 1.1e-36;
Matches 90; Conservative 10; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFAFSSYDMSVWROIPEKRLIEWAKVSSGGSTYY 60
Db 1 EVLVESGGGLVKPGSLRLSCAASGFTFSNYIMFWVROTPAKRLEWVANISSGGNTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDATMYTCARHNYGSFA--YWGQGTLTIVS 116
Db 61 PDSVKGRTISRDNVNNILYLQMSLSRSEDATMYTCARRAYSNYALDFWQGQTSVTVS 118

RESULT 15
S31108

Ig heavy chain - human
C:Species: Homo sapiens (man)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:02:13 ; Search time 124.69 Seconds
(without alignments)
29.978 Million cell updates/sec

Title: US-09-016-061-6

Perfect score: 612

Sequence: 1 EVQLVESGGGLVKPGSRLR.....RHNYGFAYWGQGLTVTVA 117

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466	76.1	117	1 HV55_MOUSE	P18526 mus musculus
2	439	71.7	117	1 HV54_MOUSE	P18525 mus musculus
3	438.5	71.7	136	1 HV16_MOUSE	P01783 mus musculus
4	433.5	70.8	122	1 HV36_HUMAN	P01768 homo sapien
5	422.5	69.0	97	1 HV56_MOUSE	P18527 mus musculus
6	419	68.5	98	1 HV57_MOUSE	P18528 mus musculus
7	417.5	68.2	116	1 HV3T_HUMAN	P01781 homo sapien
8	412	67.3	117	1 HV53_MOUSE	P18524 mus musculus
9	408.5	66.7	119	1 HV37_MOUSE	P01807 mus musculus
10	408.5	66.7	119	1 HV40_MOUSE	P01810 mus musculus
11	408	66.7	117	1 HV58_MOUSE	P18529 mus musculus
12	407	66.5	121	1 HV3J_HUMAN	P01771 homo sapien
13	406.5	66.4	114	1 HV3B_HUMAN	P01763 homo sapien
14	403	65.8	117	1 HV3C_HUMAN	P01764 homo sapien
15	403	65.8	119	1 HV3L_HUMAN	P01770 homo sapien
16	401.5	65.6	126	1 HV3K_HUMAN	P01772 homo sapien
17	397.5	65.0	122	1 HV3H_HUMAN	P01769 homo sapien
18	393	64.2	117	1 HV59_MOUSE	P18530 mus musculus
19	389.5	63.6	122	1 HV3U_HUMAN	P01762 homo sapien
20	387	63.2	115	1 HV32_MOUSE	P01801 mus musculus
21	387	63.2	117	1 HV02_CANFA	P01785 canis famil
22	385	62.9	119	1 HV3L_HUMAN	P01773 homo sapien
23	384	62.7	120	1 HV3E_HUMAN	P01766 homo sapien
24	383.5	62.7	120	1 HV3U_HUMAN	P01762 homo sapien
25	382	62.4	113	1 HV3Q_MOUSE	P01799 mus musculus
26	381	62.3	115	1 HV3F_HUMAN	P01767 homo sapien
27	380.5	62.2	119	1 HV3M_HUMAN	P01774 homo sapien
28	379.5	62.0	119	1 HV38_MOUSE	P01808 mus musculus
29	379	61.9	115	1 HV33_MOUSE	P01802 mus musculus
30	378.5	61.8	114	1 HV01_CANFA	P01784 canis famil
31	378.5	61.8	116	1 HV05_CARAU	P19181 carassius a
32	377	61.6	113	1 HV27_MOUSE	P01796 mus musculus
33	375	61.3	118	1 HV39_MOUSE	P01809 mus musculus

ALIGNMENTS

RESULT 1

HV55_MOUSE

ID HV55_MOUSE STANDARD; PRT; 117 AA.

AC P18526;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

IG HEAVY CHAIN V REGION 345 PRECURSOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;

RX MEDLINE: 89279149;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during

the primary immune response.";

J. Exp. Med. 169:2007-2019(1989).

CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.

DR PIR: J0502: HVMS34;

DR INTERPRO: IPR003006;

DR PFWA: PF00047; Ig; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.

FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 55 68 FRAMEWORK 2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 86 117 FRAMEWORK 3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match

Best Local Similarity 76.1%; Score 466; DB 1; Length 117;

Matches 90; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVKPGSRLRSLCAASGFAFSSYDMSVNRQIPKRLRWAKVSSGGGTTY 60

Db 20 EVQLVESGGGLVKPGSLKSLCAASGFAFSSYDMSVNRQIPKRLRWAKVSSGGGTTY 79

Qy 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDATAMYYCAR 98

Db 80 PDTVGRTTISRDNKNTLYLQMSLSNSEDATAMYYCAR 117

RESULT 2

HV54_MOUSE

ID HV54_MOUSE STANDARD; PRT; 117 AA.

AC P18525;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE IG HEAVY CHAIN V REGION 5-84. PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0505; HVMS84.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 71.7%; Score 439; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 7.9e-39;
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EVOLVESGGLVKPGSRSLRSLSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 60
Db 20 EVKLVSGLVQPGGSLKSLCAASGFTFSYTMGVRQTPKRLWAVYISGGSTYY 79
Qy 61 LDTVQGRFTISRDNKNTLYQMSSLSNEDTAMYCAR 98
Db 80 PDTVKGRTISRDNKNTLYQMSSLSNEDTAMYCAR 117

RESULT 3
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81234548.
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RA "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
RL [2]
RN SEQUENCE OF 17-136.
RP MEDLINE; 77100368.
RX Adetugbo K., Milstein C., Secher D.S.;
RA "Molecular analysis of spontaneous somatic mutants.";
RT Nature 265:299-304(1977).
RL [2]
RN [2]
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CC -----
DR EMBL; J00522; AAD15290.1; -.
DR PIR: A02066; GIMS21.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 16
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HVAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 71.7%; Score 438.5; DB 1; Length 136;
Best Local Similarity 72.5%; Pred. No. 1.1e-38;
Matches 87; Conservative 12; Mismatches 18; Indels 3; Gaps 2;

Qy 1 EVOLVESGGLVKPGSRSLRSLSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 60
Db 17 DVOLVESGGLVQPGGSRKLSLCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTLHY 76
Qy 61 LDTVQGRFTISRDNKNTLYQMSSLSNEDTAMYCAR-HNYGSFA--YWGQGTLVTVSA 117
Db 77 ADTVKGRFTISRDNKNTLYQMSSLSNEDTAMYCARWGNYPYAMDYWGQGTSTVTVSS 136

RESULT 4
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 81013859.
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR: A02051; M3HUM.
DR HSSP: P01772; 2IG2.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 70.8%; Score 433.5; DB 1; Length 122;
Best Local Similarity 66.4%; Pred. No. 3.1e-38;
Matches 81; Conservative 19; Mismatches 17; Indels 5; Gaps 1;

Qy 1 EVOLVESGGLVKPGSRSLRSLSCAASGFAFSSYDMSWVRQIPKRLWAKVSSGGSTYY 60
Db 1 QVELVESGGGVZPGSRSLRSLSCAASGFTFSNYAMHWVRQPPKGLWVAVISYGBBKYY 60

```

QY 61 LDTVOGRFTISRDNKNTLYLQSSLSNSEDYAMYYCARH-----NYGSFAYWGQGLTVTV 115
 Db 61 ABSVKGRTISRDBSKETLYLQMSLSRAETAVYYCARDRPLYGBYAFNFWGQGLTVTV 120

QY 116 SA 117

Db 121 SS 122

RESULT 5
 HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 914.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0504; HVMS91.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB333FF55DA893 CRC64;

Query Match 69.0%; Score 422.5; DB 1; Length 97;
 Best Local Similarity 84.7%; Pred. No. 3.3e-37;
 Matches 83; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSVWRQIPEKRLRWAKVSSGGSTYY 60
 Db 1 EVKLVSGLGLVPGGSLKLSAASGFTFSSYAMSVWRQTPKRLRWAVATISS-GGSTYY 59
 QY 61 LDTVOGRFTISRDNKNTLYLQSSLSNSEDYAMYYCAR 98
 Db 60 PDSVKGRTISRDNARNILYQSSLSRSEDYAMYYCAR 97

RESULT 6
 HV57_MOUSE STANDARD; PRT; 98 AA.
 AC P18528;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 6.96.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0501; HVMS96.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.

KW Immunoglobulin V region.
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 68.5%; Score 419; DB 1; Length 98;
 Best Local Similarity 82.7%; Pred. No. 7.6e-37;
 Matches 81; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSVWRQIPEKRLRWAKVSSGGSTYY 60
 Db 1 EVQLVESGGGLVPGGSLKLSAASGFTFSSYAMSVWRQTPKRLRWAVATISSGGSTYY 60
 QY 61 LDTVOGRFTISRDNKNTLYLQSSLSNSEDYAMYYCAR 98
 Db 61 PDSVKGRTISRDNKNTLYLQSSLSNSEDYAMYYCAR 98

RESULT 7
 HV3T_HUMAN STANDARD; PRT; 116 AA.
 ID HV3T_HUMAN
 AC P01781;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75059123.
 RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 type), subgroup H III. Architecture of the complete IgM-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [2]
 RP REVISION TO THE COMPOSITION OF 28-33.
 RA Hilschmann N.;
 RL Submitted (JUN-1975) to the PIR data bank.
 CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 CC PIR; A02064; M3HUGL.
 DR HSP; P01772; 2IG2.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 68.2%; Score 417.5; DB 1; Length 116;
 Best Local Similarity 70.7%; Pred. No. 1.3e-36;
 Matches 82; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVPGKSLRLSCAASGFAFSSYDMSVWRQIPEKRLRWAKVSSGGSTYY 60
 Db 1 EVQLVESGGDLVQPGKSLRLSCAASGFBBLGTMVWRQAPGKLEWVANIKZBGSZBY 60
 QY 61 LDTVOGRFTISRDNKNTLYLQSSLSNSEDYAMYYCARHNYGSFAYWGQGLTVTVS 116
 Db 61 VDSVKGRTISRDNKNTLYLQSSLSRVEDTALYYCAR-GWGGGDYWGQGLTVTVS 115

RESULT 8
 HV53_MOUSE STANDARD; PRT; 117 AA.
 ID HV53_MOUSE
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION RF PRECURSOR.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Melipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J0503; HVM5RF.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RP.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 67.3%; Score 412; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 5e-36; Mismatches 10; Indels 0; Gaps 0;
Matches 81; Conservative 7;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSYDMNWVRQIPEKRLWVAKVSSGGSTYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 DVLVESGGGLVKGLGSLKSCAASGFTSSYMSWVRQTPKRLVLAAINSNGSTYY 79
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYMYCAR 98
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 PTVKGRFTISRDNKNTLYLQMSLSKSEDYLYCAR 117
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
HV37_MOUSE
ID HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79223895.
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
   THAT BINDS GALACTAN.
DR PIR: A02077; AVMSX4.
DR HSSP: P01810; 2FBJ.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

Query Match 66.7%; Score 408.5; DB 1; Length 119;

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Best Local Similarity 66.9%; Pred. No. 1.2e-35;
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSYDMNWVRQIPEKRLWVAKVSSGGSTYY 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVLVESGGGLVPGGSLKSCAASGDFRYSWVRQAPKGKLEWIGEINPDSSSTINY 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYMYCAR-HNYGSFAYWGQCTLVTVSA 117
   :::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 TPCLKDKFIISRDNKNTLYLQMSKVRSEDYLYCARLHYGYGYAAYWGQCTLVTVSA 118
   ::::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
HV40_MOUSE
ID HV40_MOUSE STANDARD; PRT; 119 AA.
AC P01810;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP PRELIMINARY SEQUENCE.
RX MEDLINE; 79223895.
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE; 88217852.
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
   BINDS GALACTAN.
DR PIR: A02080; AVMSJ5.
DR PDB: 2FBJ; 15-OCT-90.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region; 3D-structure.
FT NON_TER 119 119
FT STRAND 3 7
FT STRAND 10 12
FT STRAND 14 15
FT STRAND 18 25
FT STRAND 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT STRAND 88 90
FT HELIX 92 100
FT STRAND 101 103
FT TURN 104 108
FT STRAND 112 116
FT STRAND 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;
SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match 66.7%; Score 408.5; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 1.2e-35;
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

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QY 1 EVOLVESGGGLVKPGSLRLSCAASGFAFSSYDMNSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 EVKLSEGGGLVQPGSLKSLSCAASGFAFSSYDMNSWVRQAPGKGLWGEIHPDSTINY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCAR-HNYGSPAYWCGTFLVTVA 117
DB 61 TPSLKDFIISRNAKNSLYLQMSKVRSEDALYCARHYGYWAYWCGTFLVTVA 118

RESULT 11
HV58_MOUSE STANDARD; PRT; 117 AA.
AC PI8529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpietro U.V., Lebecqec S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO506; HVMS57.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 66.7%; Score 408; DB 1; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.3e-35;
Matches 79; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVKPGSLRLSCAASGFAFSSYDMNSWVRQIPEKRLWAKVSSGGSTYY 60
DB 20 EVHLVESGGGLVQPGSLKSLSCVSGFTFNKYSWVRQTPKRLWVATISSGGLTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCAR 98
DB 80 PDSVKGRTISRDNAGNTLYLQMSLSRSEDAMYCAR 117

RESULT 12
HV3J_HUMAN STANDARD; PRT; 121 AA.
AC PV1771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RC SEQUENCE.
RX MEDLINE; 79124695.
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
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RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG HIL."
RL Biochemistry 18:553-560(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR; A02054; GIHJHL.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 66.5%; Score 407; DB 1; Length 121;
Best Local Similarity 64.5%; Pred. No. 1.7e-35;
Matches 78; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVKPGSLRLSCAASGFAFSSYDMNSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 QVKLVQAGGVQPGSLRLSLSCIASGFTFSNYGMIIWVRQAPGKGLWAVVIWNGSRYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARH---NYGSPAYWCGTFLTVS 116
DB 61 GDSVKGRFTISRDNKNTLYLQMSLSNSEDAMYCARDPDILTFASFYWGQGLTVTS 120
QY 117 A 117
DB 121 S 121

RESULT 13
HV3B_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RC SEQUENCE.
RX MEDLINE; 83273707.
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A02046; M3HUWE.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 66.4%; Score 406.5; DB 1; Length 114;
Best Local Similarity 65.8%; Pred. No. 1.8e-35;
Matches 77; Conservative 19; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVKPGSLRLSCAASGFAFSSYDMNSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 QVOLVDSGGGLVQPGSLRLSCSASGFTFSANDNMWVRQAPGKGLWLSFVGGSGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYCARHNYGSPAYWCGTFLTVSA 117
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:00:07 ; Search time 263.81 Seconds
(without alignments)
51.982 Million cell updates/sec

Title: US-09-016-061-6

Perfect score: 612
Sequence: 1 EVLVESGGLVKPGRSLRL.....RHNYGSFAYWGQTLTVTSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	440	71.9	116	4 Q9UL93	Q9UL93 homo sapien
2	429.5	70.2	437	11 Q9RLA4	Q9RLA4 mus musculus
3	429	70.1	121	4 Q9UL71	Q9UL71 homo sapien
4	428	69.9	113	4 Q9UL90	Q9UL90 homo sapien
5	424.5	69.4	118	4 Q9UL91	Q9UL91 homo sapien
6	423.5	69.2	118	4 Q9UL72	Q9UL72 homo sapien
7	418.5	68.4	147	4 Q9Y509	Q9Y509 homo sapien
8	413.5	67.6	122	4 Q9UL84	Q9UL84 homo sapien
9	393	64.2	131	4 Q9UL88	Q9UL88 homo sapien
10	381.5	62.3	298	11 Q9QVF0	Q9QVF0 mus musculus
11	374	61.1	95	4 Q9ULB6	Q9ULB6 homo sapien
12	357.5	58.4	124	4 Q9UL92	Q9UL92 homo sapien
13	339	55.4	104	4 Q9UL87	Q9UL87 homo sapien
14	332.5	54.3	124	6 Q9N0W4	Q9N0W4 oryctolagus
15	329.5	53.8	124	6 Q9N0W6	Q9N0W6 oryctolagus
16	324	52.9	125	4 Q9UL95	Q9UL95 homo sapien
17	321	52.5	112	4 Q9UGP3	Q9UGP3 homo sapien
18	319	52.1	117	11 Q9QXE9	Q9QXE9 mus musculus
19	310	50.7	117	11 Q9QXF0	Q9QXF0 mus musculus

20	307.5	50.2	118	11 Q9Z1C4	Q9Z1C4 mus musculus
21	303.5	49.6	116	4 Q9UL89	Q9UL89 homo sapien
22	300.5	49.1	150	4 Q95973	Q95973 homo sapien
23	300	49.0	119	4 Q9UL94	Q9UL94 homo sapien
24	299.5	48.9	110	11 Q9UL83	Q9UL83 mus musculus
25	296	48.4	109	11 Q9UL85	Q9UL85 mus musculus
26	293.5	48.0	109	11 Q9UL75	Q9UL75 mus musculus
27	293	47.9	119	4 Q9UL73	Q9UL73 homo sapien
28	289	47.2	117	11 Q9Z1C6	Q9Z1C6 mus musculus
29	277.5	45.3	122	4 Q9UL75	Q9UL75 homo sapien
30	273	44.6	150	4 Q9Y298	Q9Y298 homo sapien
31	273	44.6	157	4 Q95978	Q95978 homo sapien
32	272.5	44.5	110	11 Q9UL77	Q9UL77 mus musculus
33	270.5	44.2	114	11 Q9JL81	Q9JL81 mus musculus
34	268	43.8	77	4 Q9JL74	Q9JL74 homo sapien
35	260	42.5	102	11 Q9JL79	Q9JL79 mus musculus
36	256.5	41.9	77	4 Q9JL76	Q9JL76 homo sapien
37	256	41.8	81	4 Q9JL79	Q9JL79 mus musculus
38	254	41.5	78	4 Q9JL73	Q9JL73 homo sapien
39	252	41.2	82	4 Q9JL79	Q9JL79 mus musculus
40	250.5	40.9	77	4 Q9JL78	Q9JL78 homo sapien
41	249	40.7	121	4 Q9UL96	Q9UL96 homo sapien
42	247.5	40.4	416	4 Q9NPP6	Q9NPP6 homo sapien
43	245	40.0	81	4 Q9JL74	Q9JL74 homo sapien
44	239.5	39.1	86	4 Q9JL72	Q9JL72 homo sapien
45	235	38.4	79	4 Q9JL71	Q9JL71 homo sapien

ALIGNMENTS

RESULT 1

Q9UL93 PRELIMINARY; PRT; 116 AA.

AC Q9UL93;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035021; AAD56257.1; -;
 DR INTERPRO; IPR003006; -;
 DR PFAM; PF00047; ig; 1;
 FT NON_TER 1
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 71.9%; Score 440.; DB 4; Length 116;

Best Local Similarity 73.3%; Pred. No. 5.8e-39;

Matches 85; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 VOLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWEVAKVSGGGSYYL 61

Db 1 VOLVESGGGVQPGRLSLRLSCAASGFTSSYAMHWVRQAFKGLWVAVLSYGSNNKYA 60

QY 62 DTVQGRFTISRNNAKNTLYLQMSLSNSEDATMYTCARHNYSFAYWGQGLTVTSSA 117

Db 61 DSVKGRFTISRDNSKNTLYLQMSLSRAEDATMYTCAGGGGLGLCYWGQGLTVTVSS 116

RESULT 2


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Q9R1A4
ID Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT 437
FT SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;

Query Match 70.2%; Score 429.5; DB 11; Length 437;
Best Local Similarity 75.9%; Pred. No. 3.7e-37;
Matches 88; Conservative 6; Mismatches 19; Indels 3; Gaps 2;

QY 2 VOLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWAKVSSGGSTYYL 61
DB 1 VOLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWAKVSSGGSTYYL 59

QY 62 DTVQGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNGSFAYWGQGLTVTSA 117
DB 60 DSVKGRFTIYKDKRNLISLQMSLSNSEDAMYICARGDYS--AYWGPGLTVTSA 113

RESULT 3
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT 121
FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 70.1%; Score 429; DB 4; Length 121;
Best Local Similarity 67.8%; Pred. No. 8.7e-38;
Matches 82; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

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QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWAKVSSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNGSFAYWGQGLTVTSA 116
DB 61 ADSVKGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNGSFAYWGQGLTVTSA 120

QY 117 A 117
DB 121 S 121

RESULT 4
Q9UL90
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT 113
FT SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 69.9%; Score 428; DB 4; Length 113;
Best Local Similarity 70.9%; Pred. No. 1e-37;
Matches 83; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWAKVSSGGSTYY 60
DB 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDNMSWVRQIPEKRLWAKVSSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNGSFAYWGQGLTVTSA 117
DB 61 ADSVKGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNGSFAYWGQGLTVTSA 113

RESULT 5
Q9UL91
ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

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Db 1 EVQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 60
Qy 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 115
Db 61 ADSVKGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 120
Qy 116 SA 117
Db 121 SS 122

RESULT 9
Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 64.2%; Score 393; DB 4; Length 131;
Best Local Similarity 62.6%; Pred. No. 5.8e-34;
Matches 82; Conservative 11; Mismatches 24; Indels 14; Gaps 2;

Qy 1 EVQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 58
Db 1 EVQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 60
Qy 59 YLDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 106
Db 61 DYAAPVKGRLTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 120
Qy 107 WQGTGLTVTVA 117
Db 121 WQGTGLTVTSS 131

RESULT 10
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 64.2%; Score 393; DB 4; Length 131;
Best Local Similarity 62.6%; Pred. No. 5.8e-34;
Matches 82; Conservative 11; Mismatches 24; Indels 14; Gaps 2;

Qy 1 EVQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 58
Db 1 EVQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 60
Qy 59 YLDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 106
Db 61 DYAAPVKGRLTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 120
Qy 107 WQGTGLTVTVA 117
Db 121 WQGTGLTVTSS 131

RESULT 10
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;
```

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RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=SPLEEN;
RA Shinozaki N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036341; BAA88633.1; -.
DR HSP; P01607; IREI.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 62.3%; Score 381.5; DB 11; Length 298;
Best Local Similarity 62.7%; Pred. No. 2.6e-32;
Matches 74; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

Qy 1 EVQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 60
Db 40 QVQLQSGGGLVQPGGSLRLSCLCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 99
Qy 61 LDTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 117
Db 100 TFSLKDKFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 157

RESULT 11
Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE IMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -.
DR HSP; P01772; 2F84.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 61.1%; Score 374; DB 4; Length 95;
Best Local Similarity 74.7%; Pred. No. 3.9e-32;
Matches 71; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 2 VQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 61
Db 1 VQLVESGGVQVQPSRLSLSCAASGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 60
Qy 62 DTVQGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 96
Db 61 DSVKGRFTISRDNKNTLYLQMSLSNSEDYAMYYCARHNSGFTFSNGYGMHWVRQAPGKGLVWVAIAISNDGSNKEY 95

RESULT 12
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
```


Search completed: March 28, 2001, 07:26:53
Job time: 1606 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 06:26:00 ; Search time 183.85 Seconds
(without alignments)
21.761 Million cell updates/sec

Title: US-09-016-061-6

Perfect score: 632

Sequence: 1 EVQLVESGGGLVKPGRSLRL.....RHNGSFAYWGQGLTVTVA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	117	19 W76003	LM609 antibody hea
2	596	97.4	117	20 Y06381	Murine monoclonal
3	582	95.1	130	20 Y06379	Murine monoclonal
4	552	90.2	117	19 W76001	Vitaxin antibody h
5	531	86.8	123	19 W66099	anti-CD22 monoclon
6	510	83.3	136	11 R06251	Variable region of
7	508.5	83.1	139	15 R52773	Murine KC-4 immuno
8	508.5	83.1	139	15 R52791	Murine KC-4 immuno
9	501	81.9	117	19 W48865	Murine monoclonal
10	501	81.9	117	20 W86139	Protein sequence o
11	501	81.9	136	15 R56962	MAB A33 heavy chai
12	498	81.4	643	19 W73048	A33 chimeric recep

13	497	81.2	237	20 W95440	A33/212 single-cha
14	497	81.2	237	21 Y54836	Linked fusion prot
15	497	81.2	241	20 W95441	A33/218 single-cha
16	497	81.2	241	21 Y54837	Linked fusion prot
17	497	81.2	245	20 W97891	A33/218 single-cha
18	495	80.9	117	16 R79155	Human IgE receptor
19	495	80.9	117	18 W27357	Heavy chain variab
20	495	80.9	117	18 W27354	Heavy chain variab
21	494	80.7	117	16 R79157	Human IgE receptor
22	493	80.6	117	18 W27526	Heavy chain variab
23	493	80.6	239	20 W73874	Human antiFc epsil
24	493	80.6	242	20 W73876	Human antiFc epsil
25	487.5	79.7	139	18 W21656	Chimeric MAB 15 PC
26	486	79.4	138	13 R20064	MRK16-H chain. Ch
27	486	79.4	247	16 W11917	Murine MAB SK48-E2
28	485.5	79.3	118	19 W57576	Chimeric H chain S
29	485.5	79.3	118	20 W89627	Mouse humanised an
30	485.5	79.3	118	21 Y77502	Peptide seq ID No:
31	485.5	79.3	137	19 W57592	Chimeric antibody
32	485.5	79.3	137	20 W89625	Mouse humanised an
33	485.5	79.3	137	21 Y77513	Mouse antibody H c
34	485.5	79.3	139	15 R52823	Humanised murine K
35	485.5	79.3	139	16 R70471	Humanised anti-KC-
36	484.5	79.2	140	18 W21654	Mouse MAB 15 heavy
37	483.5	79.0	139	18 W21652	Humanised reshaped
38	481	78.6	121	18 W22951	Monoclonal antibody
39	481	78.6	121	20 W86118	Murine 340 Vh amin
40	480.5	78.5	118	18 W06208	Xenograft antibody
41	480	78.4	121	20 W86125	Protein sequence o
42	477	77.9	119	14 R32244	Humanised MAB heav
43	477	77.9	119	21 W27144	Mature heavy chain
44	477	77.9	119	21 Y87570	Humanised ABL 364
45	476.5	77.9	240	20 Y02472	A single chain ant

ALIGNMENTS

RESULT 1

W76003

ID W76003 standard; Protein; 117 AA.

XX

AC W76003;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 antibody heavy chain variable region protein fragment.

XX

DE Vitaxin; antibody; variable region; heavy chain; integrin;

XX

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX

OS macular degeneration; osteoporosis.

XX

Mus sp.

XX

PN W09833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

XX WPI; 1998-437472/37.

DR N-PSDB; V49822.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

This sequence represents the heavy chain variable region of murine monoclonal antibody LM609. LM609 is directed to integrin α -v beta-3. It selectively promotes apoptosis of vascular cells that have been stimulated to undergo angiogenesis, making it a tool for cancer diagnosis and therapy. The invention provides

CC cells that have been stimulated to undergo angiogenesis, making it
 CC a tool for cancer diagnosis and therapy. The invention provides
 CC humanised antibodies, especially humanised LM609. In such humanized
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse
 CC antibody is grafted onto a human antibody heavy chain to produce
 CC libraries from which a humanised murine antibody having the desired
 CC specificity is selected. By preserving the original CDR sequences
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see Y06371-72), the
 CC humanisation strategy ensures epitope conservation.

XX SQ Sequence 130 AA;

Query Match 95.1%; Score 582; DB 20; Length 130;
 Best Local Similarity 97.4%; Pred. No. 1.8e-48;
 Matches 111; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LVESGGLVKPGRSLRSLCAASGFATSSYDMSWROIPEKRLEWAKVSSGGSTYYLDT 63
 :||||| :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 leesggglvkgpgslkscaasgfafssydmswvrglpekrlewkvssggstyyldt 60

QY 64 VQGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNYGSFAYWGQTLVTVSA 117
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 vdgrftisrdnakntlylqmsslnsedtamycarhnygsfaywgqgtlvtvsa 114

RESULT 4

W76001 ID W76001 standard; Protein; 117 AA.

XX AC W76001;

XX 02-NOV-1998 (first entry)

XX Vitaxin antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;
 PI WPI; 1998-437472/37.
 DR N-PSDB; V49820.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 1; Fig 1a; 129pp; English.

XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

XX SQ Sequence 117 AA;

Query Match 90.2%; Score 552; DB 19; Length 117;
 Best Local Similarity 88.0%; Pred. No. 1.1e-45;
 Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQVLESGLVKPGRSLRSLCAASGFATSSYDMSWROIPEKRLEWAKVSSGGSTYY 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 qvqlvesgggvgvqgrslrslcaasgfafssydmswvrrqapqkglewakvssgggstyy 60

QY 61 LDTVOGRTISRDNKNTLYLQMSLSNSEDAMYICARHNYGSFAYWGQTLVTVSA 117
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 ldtvggrftisrdnskntlylqmsslnsedtavvycarhnygsfaywggttvtvss 117

RESULT 5

W66099 ID W66099 standard; Protein; 123 AA.

XX AC W66099;

XX 10-DEC-1998 (first entry)

XX anti-CD22 monoclonal antibody heavy chain variable region.

XX anti-CD22 monoclonal antibody heavy chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; immunodiagnosis; RFB4 IgG.

XX OS Mammalia.

XX Key Location/Qualifiers
 FT Misc-difference 121
 FT /note= "Encoded by gtc"

XX WO9841641-A1.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-US05453.

XX 20-MAR-1997; 97US-0041437.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Fitzgerald D, Kreitman R, Mansfield E, Pastan I;
 PI WPI; 1998-521227/44.
 DR N-PSDB; V07642.

XX Recombinant anti-CD22 antibodies and immuno-conjugates - of
 PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
 PT or a label; for inhibiting malignant B-cells

XX Claim 6; Fig 1; 71pp; English.

XX The invention claims for a recombinant immunoconjugate comprising
 CC of a therapeutic agent (e.g. Pseudomonas exotoxin) or a detectable
 CC label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)
 CC having the present variable heavy (VH) chain with a cysteine residue
 CC at amino acid 44 and a variable light (VL; W66098) chain with a
 CC cysteine residue at amino acid 100. The immunoconjugate is claimed
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and
 CC can be used in diagnostic kits.

CC humanized antibody A33 (ha33; see W48864 and W48866). The invention
 CC claims to provide a method for causing regression of a colorectal
 CC carcinoma or a gastric carcinoma by administering the radio-labelled
 CC chimeric ha33 or a radio-labelled binding fragment of ha33 to the
 CC patient.

XX Sequence 117 AA;

Query Match 81.9%; Score 501; DB 19; Length 117;
 Best Local Similarity 82.1%; Pred. No. 8.1e-41;
 Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWVAKVSSGGSTYY 60
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 evklvesggglvkpggsklscasgfaftsdmswvrtqpkrlwvatisggsgytyy 60
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LDTVOGRTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGLTVTVSA 117
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 ldsvkgrftisrdsarntlylqmslsrsdaltalycaptvtvpfaywgqglvtvsa 117

RESULT 10

W86139
 ID W86139 standard; Protein; 117 AA.

XX AC W86139;

DT 03-MAR-1999 (first entry)

XX Protein sequence of murine A33 Vh.

DE Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunoglobulin; therapeutic; streptokinase; A33.

XX Mus sp.

XX WO9852976-A1.

XX 26-NOV-1998.

XX 21-MAY-1998; 98WO-GB01473.

XX 14-APR-1998; 98GB-0007751.

PR 21-MAY-1997; 97GB-0010480.

PR 31-JUL-1997; 97GB-0016197.

PR 28-NOV-1997; 97GB-0025270.

PR 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FJ;

XX WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid
 XX sequence of the protein to eliminate potential epitopes for T-cells
 XX of a given species

XX Example 6; Fig 26; 77pp; English.

XX The invention relates to a method for the production of non-immunogenic
 XX proteins. The method comprises determining at least part of the amino
 XX acid sequence of the protein; (b) identifying in the amino acid sequence
 XX one or more potential epitopes for T-cells (T-cell epitopes) of the given
 XX species; and (c) modifying the amino acid sequence to eliminate at least
 XX one of the T-cell epitopes identified in step (b) thereby to eliminate or
 XX reduce the immunogenicity of the protein when exposed to the immune
 XX system of the given species. A method of analysing a pre-existing protein
 XX to predict the basis for immunogenic responses is also provided. The
 XX methods can be used particularly for reducing the immunogenicity of
 XX immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 XX products can be used for diagnosis and therapy. The present sequence

CC represents the protein sequence of murine A33 Vh.

XX Sequence 117 AA;

Query Match 81.9%; Score 501; DB 20; Length 117;
 Best Local Similarity 82.1%; Pred. No. 8.1e-41;
 Matches 96; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDMSWVRQIPEKRLWVAKVSSGGSTYY 60
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 evklvesggglvkpggsklscasgfaftsdmswvrtqpkrlwvatisggsgytyy 60
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LDTVOGRTISRDNKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGLTVTVSA 117
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 ldsvkgrftisrdsarntlylqmslsrsdaltalycaptvtvpfaywgqglvtvsa 117

RESULT 11

R56962
 ID R56962 standard; Protein; 136 AA.

XX AC R56962;

XX 13-FEB-1995 (first entry)

DE MAb A33 heavy chain.

XX Polymerase chain reaction; primer; amplify; PCR; variable region; light;
 KW heavy; chains; VL; VH; humanised; antibody; vectors; expression; human;
 KW secretion; A33; Fab'(gamma4deltaCys); pCG16; ompa signal; C-kappa;
 KW pSKompA; pMRR055; CH1 domains; hinge; deltaCys; pMRR022; pRO109;
 KW antigen; diagnosis; treatment; colorectal cancer; metastases.

XX Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /note= "Signal peptide"

FT Misc-difference 5

FT /label= Leu, Phe

FT Misc-difference 8

FT /label= Val, Ile

FT Protein 20..136

FT /note= "MAb A33 heavy chain"

FT Region 50..54

FT /label= CDR1

FT Region 69..85

FT /label= CDR2

FT Region 118..125

FT /label= CDR3

XX WO9413805-A.

XX 23-JUN-1994.

XX 10-DEC-1993; 93WO-GB02529.

XX 10-DEC-1992; 92GB-0025853.

PR 22-JUL-1993; 93GB-0015249.

XX (CLLT) CELLTech LTD.

XX Adair JR, King DJ, Owens RJ;

XX WPI; 1994-217881/26.

DR N-PSDB; Q68650.

XX Humanised antibodies raised against A33 antigen - are used for
 PT diagnosis or treatment of colorectal tumours and metastases
 XX Example 1; Fig 3(11); 90pp; English.


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XX 23-MAR-1999 (first entry)
XX A33/212 single-chain Fv fragment.
XX Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
XX multichain protein; immunoglobulin; single chain antibody Fv; cancer;
XX aggregation.
XX Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..107
XX Peptide /note= "A33 V1 region"
XX Peptide 108..121
XX Peptide /note= "peptide linker 212"
XX Peptide 122..237
XX /note= "A33 Vh region"
XX US5856456-A.
XX 05-JAN-1999.
XX 07-APR-1994; 94US-0224591.
XX 07-APR-1994; 94US-0224591.
XX 20-NOV-1992; 92US-0980529.
XX 15-JAN-1993; 93US-0002845.
XX (ENZO-) ENZON INC.
XX Filpula DR, Whitlow MD;
XX WPI: 1999-105193/09.
XX N-PSDB; V99765.
XX DNA encoding fusion polypeptide including protease resistant linker
XX - for making single-chain Fv antibody fragments, e.g for diagnosis
XX and treatment of cancer
XX Disclosure; Fig 12; 39pp; English.
XX The invention is directed to a novel peptide linker useful for connecting
XX polypeptide constituents into a novel linked fusion polypeptide. The
XX peptide linker includes at least one XP motif (where x is a charged
XX amino acid) and includes any of these sequences (GSTSGXPGSGSGSGSTKG;
XX GSTSGXPSGSGSTKG; or GSTSGSEKKG) to inhibit its proteolysis by
XX subtilisin or trypsin. DNA molecules encoding fusion polypeptides
XX containing two polypeptides, derived from the same multichain protein of
XX the immunoglobulin (Ig) superfamily and a peptide linker as above, are
XX particularly used to prepare single chain antibody Fv fragments (scFv),
XX potentially useful for diagnosis and treatment of cancer. The fusion
XX polypeptide containing the specified linkers is proteolytically stable
XX (associated with positioning of the P residue) and resistant to
XX aggregation, while residue X improves solubility. The present sequence
XX represents the amino acid sequence of a A33/212 scFv fragment.
XX Sequence 237 AA;
XX Query Match 81.2%; Score 497; DB 20; Length 237;
XX Best Local Similarity 81.9%; Pred. No. 4.3e-40;
XX Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
XX 1 EVLVESGGGLVKPGRSLRSLCAASGFATSSVDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 122 evklvesggglvkpggsklscasgfaistydmswvrtqptekrliewatissggsyty 181
XX 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDATMYCYCARHNYGSFAYWGOGTLTVTS 116
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 182 ldsvkgrftisrdsarntlylqmslsrsedatlyycaptvtvpfaywgqgtlvtvs 237
XX RESULT 15
XX ID W95441 standard; Protein; 241 AA.
XX AC W95441;
XX DT 23-MAR-1999 (first entry)
XX DE A33/212 single-chain Fv fragment.
XX KW Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
XX
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RESULT 14
Y54836
ID Y54836 standard; Protein; 237 AA.
XX AC Y54836;
XX DT 08-FEB-2000 (first entry)
XX DE Linked fusion protein A33/212 sFv sequence.
XX KW Fusion protein; linker; linked fusion polypeptide; multichain protein;
XX protein complex; antibody.
XX OS Synthetic.
XX PN US5990275-A.
XX PD 23-NOV-1999.
XX PF 10-SEP-1997; 97US-0926789.
XX PR 07-APR-1994; 94US-0224591.
XX PR 20-NOV-1992; 92US-0980529.
XX PR 15-JAN-1993; 93US-0002845.
XX PA (ENZO-) ENZON INC.
XX PI Filpula DR, Whitlow MD;
XX DR WPI: 2000-022812/02.
XX DR N-PSDB; 237397.
XX PT Peptide linkers, linked fusion polypeptides containing the linkers and
XX their preparation
XX PS Example; Fig 12; 42pp; English.
XX This sequence represents a linked fusion protein containing the
XX amino acid linker of the invention. The linkers are used for connecting
XX constituent polypeptides to form novel linked fusion polypeptides.
XX Polypeptides derived from any protein can be connected, in particular
XX multichain protein or protein complexes e.g. enzymes, members of the
XX immunoglobulin superfamily, hormones, DNA-binding proteins. The linker
XX provides fusion proteins which have greater stability and are less
XX susceptible to aggregation.
XX Sequence 237 AA;
XX Query Match 81.2%; Score 497; DB 21; Length 237;
XX Best Local Similarity 81.9%; Pred. No. 4.3e-40;
XX Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
XX 1 EVLVESGGGLVKPGRSLRSLCAASGFATSSVDMSWVRQIPEKRLIEWAKVSSGGSTYY 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 122 evklvesggglvkpggsklscasgfaistydmswvrtqptekrliewatissggsyty 181
XX 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDATMYCYCARHNYGSFAYWGOGTLTVTS 116
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 182 ldsvkgrftisrdsarntlylqmslsrsedatlyycaptvtvpfaywgqgtlvtvs 237
XX RESULT 15
XX ID W95441 standard; Protein; 241 AA.
XX AC W95441;
XX DT 23-MAR-1999 (first entry)
XX DE A33/212 single-chain Fv fragment.
XX KW Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
```

multichain protein; immunoglobulin; single chain antibody Fv; cancer; aggregation.

Synthetic.

Synthetic.

Key

Key	Location/Qualifiers
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Peptide

```

/note= "A33 vl region"

```

Peptide
108..125

./note="

Peptide

US5856456-A.

05-JAN-1999.

07-APR-1994; 94US-0224591.

07-APR-1994; 94US-0224591.

20-NOV-1995

15-JAN-1993; 93US-0002845.

(ENZO-) ENZON INC.

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Filpula DR, Whitlow MD;

1004

WPI; 1999-105193/09.
N-DEP. 100766

N-PSDB; V99766.

DNA analysis

- for making single-chain Fv antibody fragments, e.g for diagnosis and treatment of cancer

.....

Disclosure

100

The invent

polypeptide constituents into a novel linked fusion polypeptide. The peptide linker includes at least one XP motif (where X is a charged amino acid) and includes any of these sequences (GSTSGXPGSGSGEGRK; GSTSGXPGSGEGRK; or GSTGSRSEKG) to inhibit its proteolysis by subtilisin or trypsin. DNA molecules encoding fusion polypeptides containing two polypeptides, derived from the same multichain protein of the immunoglobulin (Ig) superfamily and a peptide linker as above, are particularly used to prepare single chain antibody Fv fragments (scFv), potentially useful for diagnosis and treatment of cancer. The fusion polypeptide containing the specified linkers is proteolytically stable (associated with positioning of the P residue) and resistant to aggregation, while residue X improves solubility. The present sequence represents the amino acid sequence of a A33/218 scFv fragment.

Sequence 241 AA;

Query Match

Query Match 81.2%; Score 497; DB 20; Length 241;

Best Local Similarity 81.9%; Pred. No. 4.4e-40;

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126 evklivesggglvkpggslklscasgafafstvdmswrrtpekrlewatissqgsytyv 185

QY 61 LDTVQGRFTISRDNAKNTLYLQMSSLNSED[.]TAMYYCARHNYGSEFAYWCGQTLVTVS 116

Db 186 ldsvkgrftisrdsarntlylqmsslrseatalyycaptvvpfaywgqgltlvts 241

Search completed: March 28, 2001, 06:34:20

Job time: 500 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:26:26 ; Search time 269.55 Seconds
(without alignments)
7.794 Million cell updates/sec

Title: US-09-016-061-6
Perfect score: 612
Sequence: 1 EVOLVESGGLVKPGRSLRL.....RHNYGFAYWGQGLTVTSA 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497	81.2	237	2	US-08-224-591-16
2	497	81.2	237	2	US-08-926-789-16
3	497	81.2	241	2	US-08-224-591-18
4	497	81.2	241	2	US-08-926-789-18
5	496	81.0	136	1	US-08-253-877C-57
6	496	81.0	136	1	US-08-432-164A-57
7	486	79.4	247	4	PCT-US94-07659-2
8	485.5	79.3	139	1	US-08-129-930B-96
9	477	77.9	119	1	US-08-053-171-14
10	477	77.9	119	1	US-08-053-171-17
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12	476	77.8	119	2	US-08-815-190A-13
13	476	77.8	119	2	US-08-475-000-16
14	476	77.8	119	2	US-08-483-199-16
15	476	77.8	119	2	US-08-484-508-16
16	476	77.8	125	1	US-08-331-398A-65
17	476	77.8	125	2	US-08-331-397B-65
18	476	77.8	125	2	US-08-759-804A-64
19	476	77.8	138	1	US-08-053-171-7
20	476	77.8	138	1	US-08-053-171-11
21	468.5	76.6	443	4	PCT-US96-13152-4
22	465	76.0	119	1	US-08-053-171-12
23	464	75.8	113	3	US-08-974-899-6
24	464	75.8	118	2	US-08-379-057-30
25	463	75.7	158	2	US-08-653-402B-6
26	463	75.7	158	2	US-08-653-402B-10
27	462	75.5	138	2	US-08-379-057-14
28	461.5	75.4	122	2	US-07-934-373C-21

29	461.5	75.4	122	3	US-08-437-642B-21	Sequence 21, Appl
30	461.5	75.4	122	4	PCT-US93-07832-21	Sequence 21, Appl
31	461	75.3	125	1	US-08-478-039-99	Sequence 99, Appl
32	461	75.3	125	1	US-08-476-349A-99	Sequence 99, Appl
33	460.5	75.2	135	4	PCT-US95-07302-8	Sequence 8, Appl
34	456.5	74.6	122	4	PCT-US93-08435-12	Sequence 12, Appl
35	456.5	74.6	122	4	PCT-US93-08435-43	Sequence 43, Appl
36	456.5	74.6	123	1	US-08-356-272-3	Sequence 3, Appl
37	456.5	74.6	223	2	US-08-190-199A-63	Sequence 63, Appl
38	456.5	74.6	236	2	US-08-190-199A-65	Sequence 65, Appl
39	455	74.3	119	1	US-07-988-925-11	Sequence 11, Appl
40	455	74.3	119	2	US-08-362-780-11	Sequence 11, Appl
41	454.5	74.3	118	4	PCT-US93-08435-10	Sequence 10, Appl
42	454	74.2	239	2	US-08-553-497A-18	Sequence 18, Appl
43	453.5	74.1	118	1	US-08-326-362-2	Sequence 2, Appl
44	453.5	74.1	122	4	PCT-US93-08435-14	Sequence 14, Appl
45	453.5	74.1	130	1	US-08-398-613A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-224-591-16
; Sequence 16, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-224-591-16

Query Match 81.2%; Score 497; DB 2; Length 237;
Best Local Similarity 81.9%; Pred. No. 6.5e-43;
Matches 95; Conservative 12; Indels 0; Gaps 0;

QY 1 EVOLVESGGLVKPGRSLRLSCAASGFATSSYDMSWVRQIPKRLKLEWVAKVSSGGGTTY 60

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; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-224-591-18

Query Match 81.2%; Score 497; DB 2; Length 241;
Best Local Similarity 81.9%; Pred. No. 6.7e-43;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0

QY 1 EVLVESGGGLVKGPSRLSLRSCAASGFSAFSSDMSWVRQIPKRLRWAKVSSGGGSTYY 60
   ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 126 EVLVESGGGLVKGPGGSLKLSCAASGFSAFSTDMSWVRQTPKRLRWATISSGGSVYY 180
   ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
QY 61 LDTVQGRFTISRNAKNTLYLQWSSLNSEDATMYICARHNYGSFAYWGQGLTVTS 116
   ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 186 LDSVKGRFTISRDSARNTLYLQWSSLRSSEDTALYYCAPTTVPFAYWGQGLTVTS 241
   ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

RESULT 4
US-08-926-789-18
; Sequence 18, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 08/002,845
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-926-789-18

Query Match 81.2%; Score 497; DB 2; Length 241;
Best Local Similarity 81.9%; Pred. No. 6.7e-43;
Matches 95; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVPGKSLRSLSCAASGFAPFSSYDMSWVRQIPEKRLKLEWAKVSSGGSTYY 60
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 126 EVLVESGGGLVPGKSLRSLSCAASGFAPFSTYDMSWVRQIPEKRLKLEWATISSGGSTYY 185

Qy 61 LDTVGRETISRDNKNTLYLQMSLSNSEDATMYICARHNYGSFAYWGQGLTVTVS 116
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 186 LDSVKGREFTISRDSRNTLYLQMSLSRSEDATLYICAPTIVVPFAYWGQGLTVTVS 241

RESULT 5
US-08-253-877C-57
; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE: 15-JAN-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-926-789-18
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; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match 81.0%; Score 496; DB 1; Length 136;
Best Local Similarity 81.2%; Pred. No. 4.4e-43;
Matches 95; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EVLVESGGGLVPGKSLRSLSCAASGFAPFSSYDMSWVRQIPEKRLKLEWAKVSSGGSTYY 60
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 20 EVLVESGGGLVPGKSLRSLSCAASGFAPFSTYDMSWVRQIPEKRLKLEWATISSGGSTYY 79

Qy 61 LDTVGRETISRDNKNTLYLQMSLSNSEDATMYICARHNYGSFAYWGQGLTVTVS 117
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 80 LDSVKGREFTISRDSRNTLYLQMSLSRSEDATLYICAPTIVVPFAYWGQGLTVTVS 136

RESULT 6
US-08-452-164A-57
; Sequence 57, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-4117
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
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QY TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-57

Query Match 81.0%; Score 496; DB 2; Length 136;
Best Local Similarity 81.2%; Pred. No. 4.4e-43;
Matches 95; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVKPGKRSRLSCAASGFASFSSYDMSWVRQIPKRLKLEWAKVSSGGGTY 60
Db 20 EVKLVSGLLVKPGGSLKSLCAASGFASFSSYDMSWVRQIPKRLKLEWATISSGGSYTY 79
QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNYGSFAYWGQGLTIVTVA 117
Db 80 LDSVKGRTISRDNKNTLYLQMSLSRSEDALYICAPTIVVPFAYWGQGLTIVTVA 136

RESULT 7

PCT-US94-07659-2

Sequence 2, Application PC/TUS9407659

GENERAL INFORMATION:

APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurlle, Mark
APPLICANT: Jackson, Jeffrey R.

TITLE OF INVENTION: Recombinant and Humanized IL-1 beta

TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory

TITLE OF INVENTION: Disorders in Man

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation - Corp.

ADDRESSEE: Intellectual Property

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07659

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/090,534

FILING DATE: 09-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50171-1

TELEPHONE: (610) 270-5024

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-07659-2

Query Match 79.4%; Score 486; DB 4; Length 247;
Best Local Similarity 80.7%; Pred. No. 8.8e-42;
Matches 96; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVKPGKRSRLSCAASGFASFSSYDMSWVRQIPKRLKLEWAKVSSGGGTY 60
Db 20 EVKLVSGLLVKPGGSLKSLCAASGFASFSSYDMSWVRQIPKRLKLEWATISSGGGTY 79
QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNYGSFAYWGQGLTIVTVA 117
Db 80 PDTVKGRTISRDNKNTLYLQMSLSKSEDAMYHCARGVRRGYFDVWGAGTTVTVSS 138

RESULT 8

US-08-129-930B-96

Sequence 96, Application US/08129930B

Patent No. 5804187

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.

APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.

APPLICANT: Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Broad

TITLE OF INVENTION: Carcinoma Specificity, and Kit and

TITLE OF INVENTION: Diagnostic Vaccination and

TITLE OF INVENTION: Therapeutic Methods

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: V. AMZEL & ASSOC.

STREET: 2055 No. 5804187th Broadway, Suite 201

CITY: Walnut Creek

STATE: California

COUNTRY: USA

ZIP: 94596

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/129,930B

FILING DATE: September 30, 1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Amzel Ph.D., Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: CRFCC-008A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 521-1333

TELEFAX: (510) 521-3541

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:

LENGTH: 139 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-129-930B-96

Query Match 79.3%; Score 485.5; DB 1; Length 139;
Best Local Similarity 78.3%; Pred. No. 5.1e-42;
Matches 94; Conservative 10; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVKPGKRSRLSCAASGFASFSSYDMSWVRQIPKRLKLEWAKVSSGGGTY 60
Db 20 EVQWVESGGGLVQPGGSLKSLCAASGFASFSSYDMSWVRQIPKRLKLEWAEISSGGNYAY 79
QY 61 LDTVOGRFTISRDNKNTLYLQMSLSNSEDAMYICARHNYGSFAYWGQGLTIVTVA 117
Db 80 QDTVKGRTISRDNKNTLYLQMSLSRAEDTAVYYCAREDDYGIPANFAYWGQGLTIVTSS 139

RESULT 9

US-08-053-171-14

Sequence 14, Application US/08053171

Patent No. 5562903

APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-1261110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
OTHER INFORMATION: Heavy chain region"
US-08-331-398A-65

Query Match 77.8%; Score 476; DB 1; Length 125;
Best Local Similarity 79.8%; Pred. No. 4.le-41;
Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 2;
QY 1 EVLVESGGGLVKPGRSLRLSCAASGFAFSSYDMHWVRQIPEKRLIEWAKVSSGGSTYY 60
Db 1 EVKLVESGGGLVQPGGSLKSCATSGFTSDYIMYWVRQTPKEKRLIEWAYISNGGGSTYY 60
QY 61 LDTVGRTTISRDNKNTLYLQMSLSNSEDYAMYICARH-NYGS-FAYWGQGLVTVSA 117
Db 61 PDTVGRTTIDRDNKNTLYLQMSRLKSEDYAMYICARGLSDGSWFAYWGQGLVTVSS 119

Search completed: March 28, 2001, 06:39:01
Job time: 755 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:25 ; Search time 801.32 Seconds
(without alignments)
19.447 Million cell updates/sec

Title: US-09-016-061-8
Perfect score: 561
Sequence: 1 DIVLTQSPATLSVTPEDSVS.....COQSGSWPHTFGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	561	100.0	107	11	US-08-790-540-8
2	561	100.0	107	11	US-08-790-540A-8
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4	561	100.0	107	11	US-08-791-391A-8
5	561	100.0	107	14	US-09-016-061-8
6	561	100.0	107	17	US-09-339-922A-8
7	530	94.5	109	1	PCT-US98-25828-45
8	530	94.5	109	13	US-08-986-016-45
9	529	94.3	107	8	US-08-484-537-62
10	529	94.3	107	17	US-09-325-000-21
11	529	94.3	127	8	US-08-484-537-83
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					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 45, Appli
					Sequence 45, Appli
					Sequence 62, Appli
					Sequence 21, Appli
					Sequence 83, Appli

12	521	92.9	127	17	US-09-325-000-70	Sequence 70, Appli
13	519	92.5	107	3	US-07-881-109-7	Sequence 7, Appli
14	519	92.5	107	3	US-07-881-109A-7	Sequence 7, Appli
15	519	92.5	107	7	US-08-313-198-7	Sequence 7, Appli
16	519	92.5	107	11	US-08-720-323-7	Sequence 7, Appli
17	519	92.5	107	15	US-09-160-911-9	Sequence 9, Appli
18	519	92.5	108	11	US-08-720-323-73	Sequence 73, Appli
19	519	92.5	108	16	US-09-232-290-27	Sequence 27, Appli
20	516	92.0	107	3	US-07-804-464A-1	Sequence 1, Appli
21	516	92.0	107	3	US-07-808-464-1	Sequence 1, Appli
22	516	92.0	107	4	US-08-082-842-1	Sequence 1, Appli
23	516	92.0	107	5	US-08-107-669B-1	Sequence 1, Appli
24	516	92.0	107	5	US-08-107-669C-1	Sequence 1, Appli
25	516	92.0	107	8	US-08-472-788-1	Sequence 1, Appli
26	516	92.0	107	8	US-08-477-531A-1	Sequence 1, Appli
27	516	92.0	107	14	US-09-097-980A-1	Sequence 1, Appli
28	516	92.0	107	14	US-09-097-980B-1	Sequence 1, Appli
29	516	92.0	107	16	US-09-245-202A-1	Sequence 1, Appli
30	516	92.0	107	16	US-09-245-202A-1	Sequence 1, Appli
31	501	89.3	108	1	PCT-US98-04987-7	Sequence 7, Appli
32	501	89.3	108	22	US-60-039-609-7	Sequence 7, Appli
33	498	88.8	108	10	US-08-617-835-5	Sequence 5, Appli
34	491	87.5	259	18	US-09-419-788-29	Sequence 29, Appli
35	470	83.8	107	11	US-08-791-391-4	Sequence 4, Appli
36	470	83.8	107	11	US-08-791-391A-4	Sequence 4, Appli
37	470	83.8	107	14	US-09-016-061-4	Sequence 4, Appli
38	470	83.8	107	17	US-09-339-922A-4	Sequence 4, Appli
39	465	82.9	108	1	PCT-US99-02949-1	Sequence 1, Appli
40	465	82.9	108	14	US-09-026-291-1	Sequence 1, Appli
41	465	82.9	108	14	US-09-026-291-1	Sequence 1, Appli
42	465	82.9	108	16	US-09-247-352-1	Sequence 1, Appli
43	465	82.9	108	18	US-09-466-635-1	Sequence 1, Appli
44	465	82.9	214	1	PCT-US99-02949-4	Sequence 4, Appli
45	465	82.9	214	14	US-09-026-291-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-790-540-8
; Sequence 8, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-8

Query Match      100.0%; Score 561; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
Db 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
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QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||
Db 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||

RESULT 2
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match      100.0%; Score 561; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
Db 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||
Db 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||

RESULT 3
US-08-790-540A-8
; Sequence 8, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540A-8

Query Match      100.0%; Score 561; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
Db 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||
Db 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||

RESULT 4
US-08-791-391A-8
; Sequence 8, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391-8

Query Match      100.0%; Score 561; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
Db 1 DIVLTQSPATLSVTPGDVSVLSLCOASQSIHNLHWYQOKSHSPRLLIKYRSQISGIPS 60
    |||||||
QY 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
    |||||||
Db 61 RFGSGSGTDFALSIINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-8

Query Match 100.0%; Score 561; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIHNLHWYQKSHSPRLIKYRSQISGIPS 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIHNLHWYQKSHSPRLIKYRSQISGIPS 60
QY 61 RFGSGSGTDFALSIHNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
|||||
Db 61 RFGSGSGTDFALSIHNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107

RESULT 5
US-09-016-061-8
Sequence 8, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-8
Query Match 100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIHNLHWYQKSHSPRLIKYRSQISGIPS 60
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Db 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIHNLHWYQKSHSPRLIKYRSQISGIPS 60
QY 61 RFGSGSGTDFALSIHNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
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Db 61 RFGSGSGTDFALSIHNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
RESULT 6
US-09-339-922A-8
Sequence 8, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-09-339-922A-8

Query Match 100.0%; Score 561; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIHNLHWYQKSHSPRLIKYRSQISGIPS 60
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Db 1 DIVLTQSPATLSVTPGDSVSLSCQASQSIHNLHWYQKSHSPRLIKYRSQISGIPS 60
QY 61 RFGSGSGTDFALSIHNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107
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Db 61 RFGSGSGTDFALSIHNSVETEDFGMYFCQSGSWPHTFGGTTKLEIK 107

RESULT 7
PCT-US98-25828-45
Sequence 45, Application PC/TUS9825828A
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
FILE REFERENCE: TSRI 598.0
CURRENT APPLICATION NUMBER: PCT/US98/25828A
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 08/986,016
EARLIER FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 109
TYPE: PRT
ORGANISM: Murine hybridoma LM609
PCT-US98-25828-45

Query Match 94.5%; Score 530; DB 1; Length 109;
Best Local Similarity 92.5%; Pred. No. 3.1e-46;

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RESULT          9
US-08-484-537-62
; Sequence 62, Application US/08484537
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:

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Query Match          94.3%; Score 529; DB 8; Length 127;
Best Local Similarity 93.5%; Pred. No. 4.6e-46;
Matches 100: Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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RESULT 12
US-09-325-000-70
: Sequence 70. Application US/09325000

APPLICANT: Queen, Cary L.
 APPLICANT: Co, Man Sung
 APPLICANT: Schneider, William P.
 APPLICANT: Landolfi, Nicholas F.
 APPLICANT: Coelingh, Kathleen L.
 APPLICANT: Selick, Harold E.
 TITLE OF INVENTION: Improved Humanized Immunoglobulins
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/325,000
 FILING DATE: 01-JUN-1999
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-325-000-70

Query Match 92.9%; Score 521; DB 17; Length 127;
Best Local Similarity 91.6%; Pred. No. 3e-45;
Matches 98; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
Db 21 DIVLTQSPATLSVTPGDSVSLSCRASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 80
QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 81 RFSGSGGTDFLTVNGVETEDFGMYFCQHTNSWPHTFGGKLEIK 127

RESULT 13
US-07-881-109-7
; Sequence 7, Application US/07881109
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Keck, Peter C.
; TITLE OF INVENTION: CHIMERIC MULTIVALENT PROTEIN ANALOGUES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,109
; FILING DATE: 08-MAY-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CBM92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-881-109A-7

Query Match 92.5%; Score 519; DB 3; Length 107;
Best Local Similarity 92.5%; Pred. No. 3.9e-45;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGGTDFTLINSVETEDFGMYFCQSGNSWPYTFGGGKLEIK 107

RESULT 15
US-08-313-198-7
; Sequence 7, Application US/08313198
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US-07-881-109-7

Query Match 92.5%; Score 519; DB 3; Length 107;
Best Local Similarity 92.5%; Pred. No. 3.9e-45;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGGTDFTLINSVETEDFGMYFCQSGNSWPYTFGGGKLEIK 107

RESULT 14
US-07-881-109A-7
; Sequence 7, Application US/07881109A
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Keck, Peter C.
; TITLE OF INVENTION: CHIMERIC MULTIVALENT PROTEIN ANALOGUES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,109A
; FILING DATE: 08-MAY-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CBM92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-881-109A-7

Query Match 92.5%; Score 519; DB 3; Length 107;
Best Local Similarity 92.5%; Pred. No. 3.9e-45;
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPATLSVTPGDSVSLSCQASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQISNHLHWYQOKSHSPRLLIKYSQISGIPS 60
QY 61 RFSGSGGTDFALINSVETEDFGMYFCQSGSWPHTFGGKLEIK 107
Db 61 RFSGSGGTDFTLINSVETEDFGMYFCQSGNSWPYTFGGGKLEIK 107

RESULT 15
US-08-313-198-7
; Sequence 7, Application US/08313198
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PCT/US93/04338)

GENERAL INFORMATION:
APPLICANT: Huston, James S.
ATTORNEY: Keck, Peter C.
TITLE OF INVENTION: CHIMERIC MULTIVALENT PROTEIN ANALOGUES
TITLE OF INVENTION: CHIMERIC AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,198
FILING DATE: 07-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,109
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CBM92-01A
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-198-7

	Query Match	92.5%	Score 519;	DB 7;	Length 107;
	Best Local Similarity	92.5%;	pred. No. 3.9e-45;		
	Matches	99;	Conservative	4;	Mismatches 4; Indels 0; Gaps 0;
QY	1	DIVLTQSPATLSVTPGGDSVLSLCSQAQSGISNHLHWYQOKSHESPRLLLIKYRSQTSIGIPS	60		
Db	1	DIVLTQSPATLSVTPGGDSVLSLCSQAQSGISNHLHWYQOKSHESPRLLLIKYASQTSIGIPS	60		
QY	61	RFSGSGSGTDFTALSIINSVETEDFGMYFCQSGSWPHTFGGCKTLEIK	107		
Db	61	RFSGSGSGTDFTLISINSVETEDFGMYFCQSGNSWPYTFGGCKTLEIK	107		

Search completed: March 28, 2001, 06:55:27
Job time: 1471 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	486.5	86.7	109	5	US-09-445-602A-6	Sequence 6, Appli
2	345.5	61.5	237	5	US-09-607-756-2	Sequence 2, Appli
3	341.5	60.9	108	5	US-09-711-485-150	Sequence 150, Appl
4	339	60.4	111	5	US-09-385-673-14	Sequence 14, Appl
5	338	60.2	128	4	US-08-454-899C-31	Sequence 31, Appl
6	336.5	60.0	108	5	US-09-530-237-2	Sequence 2, Appli
7	334.5	59.6	109	5	US-09-726-258-47	Sequence 47, Appl
8	334.5	59.6	116	5	US-09-753-436-66	Sequence 66, Appl
9	334	59.5	124	4	US-08-454-899C-71	Sequence 71, Appl
10	333	59.4	107	5	US-09-711-485-125	Sequence 125, Appl
11	332.5	59.3	107	5	US-09-500-299-2	Sequence 2, Appli
12	332.5	59.3	331	5	US-09-500-299-14	Sequence 14, Appl
13	332	59.2	107	5	US-09-373-403-25	Sequence 25, Appl
14	332	59.2	330	5	US-09-445-576-32	Sequence 32, Appl
15	332	59.2	331	5	US-09-445-576-33	Sequence 33, Appl
16	332	59.2	592	5	US-09-445-576-34	Sequence 34, Appl
17	331.5	59.1	298	5	US-09-318-661-2	Sequence 2, Appli
18	331	59.0	105	5	US-09-147-443C-52	Sequence 52, Appl
19	331	59.0	105	5	US-09-147-443C-56	Sequence 56, Appl
20	330.5	58.9	131	5	US-09-523-095A-10	Sequence 10, Appl
21	330.5	58.9	245	5	US-09-523-095A-40	Sequence 40, Appl
22	330.5	58.9	271	5	US-09-523-095A-34	Sequence 34, Appl
23	330.5	58.9	274	5	US-09-523-095A-32	Sequence 32, Appl
24	330	58.8	106	4	US-08-454-899C-10	Sequence 10, Appl
25	330	58.8	111	5	US-09-716-028-7	Sequence 7, Appli
26	330	58.8	240	5	US-09-711-485-147	Sequence 147, Appl
27	330	58.8	240	5	US-09-711-485-148	Sequence 148, Appl

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RESULT. 5
US-08-454-899C-31
US-08-454-899C-31
Sequence 31, Application US/08454899C
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Tempest, Philip R.
; TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
; FILE REFERENCE: 10274-007001
; CURRENT APPLICATION NUMBER: US/08/454, 899C
; CURRENT FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/004,798
; PRIOR FILING DATE: 1993-01-12
; PRIOR APPLICATION NUMBER: PCT/US94/00266
; PRIOR FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 31-
; LENGTH: 128
; TYPE: PRT

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R4-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; US-09-726-258-47

Query Match          59.6%; Score 334.5; DB 5; Length 109;
Best Local Similarity 57.4%; Pred. No. 2.8e-27;
Matches 62; Conservative 24; Mismatches 21; Indels 1; Gaps

QY      1 DIVLTQSPATLSVTPGDSVSLSCASQISNHLHWYQQKSHESPLLIIKYRSQSI-SGIP 59
       || :|||::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 DIQMOTSPSSLASVGDRVTITCRASKTISKYLAWYQPKRAPKLLIYSGSTLESGVP 60

QY      60 SRFSGSGGTDFALINSVEDEFGWYFCQSGSWPHTFGGGTKLEIK 107
       ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      61 SRFSGSGGTDFLTISSLQPEDFATYYCQHNEYP LTFGGGTKVEIK 108

RESULT      8
US-09-753-436-66
; Sequence 66, Application US/09753436
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemary
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,436
; FILING DATE:
; CLASSIFICATION: /
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/382,289
; FILING DATE:
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-753-436-66

Query Match 59.6%; Score 334.5; DB 5; Length 116;
Best Local Similarity 58.0%; Pred. No. 3e-27;
Matches 65; Conservative 16; Mismatches 26; Indels 5; Gaps 1;

QY 1 DIVLTQSPATLSVTPGDGVSLSQASQSI-----SNHLHWYQKSHESPRLLIKYRSQSI 55
DB 5 DIVMTQSPSLPTGPPEASISCRSSQSLVHSNGDYLHWYLOKPGQSPQLLIYKVSNR 64
QY 56 SGIPRSFGSGSGTDFALNSINVTEDFGMYFCQSGSWPHTFGGKLEIK 107
DB 65 SGVPDRFSGSGSGTDFTLKISRVEADVGVIYCSQSTHVPYTFGGTKVEIK 116

RESULT 9
US-08-454-899C-71
Sequence 71, Application US/08454899C
GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
APPLICANT: Carr, Frank J.
APPLICANT: Tempest, Philip R.
TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
FILE REFERENCE: 10274-007001
CURRENT APPLICATION NUMBER: US/08/454,899C
CURRENT FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR FILING DATE: 1993-01-12
PRIOR APPLICATION NUMBER: PCT/US94/00266
PRIOR FILING DATE: 1994-01-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Fastseq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 124
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: light chain variable region
US-08-454-899C-71

Query Match 59.5%; Score 334; DB 4; Length 124;
Best Local Similarity 58.1%; Pred. No. 3.6e-27;
Matches 61; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
QY 2 IVLTQSPATLSVTPGDGVSLSQASQSI-----SNHLHWYQKSHESPRLLIKYRSQSI 61
DB 20 IVMTQSPDLSAVLSGERVTINCKASQSVTNDVAVYQKSPKLLIYASNRYTGVDPDR 79
QY 62 FSGSGSGTDFALNSINVTEDFGMYFCQSGSWPHTFGGKLEI 106
DB 80 FSGSGYGTDFTFITSSVQAEDVAVIYCOQDYSSPYTFGGGKLEI 124

RESULT 10
US-09-711-485-125
Sequence 125, Application US/09711485
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroli, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-125

Query Match 59.4%; Score 333; DB 5; Length 107;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:35 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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- 2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
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- 22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	14	US-09-016-061-48
2	52	100.0	10	17	US-09-339-922A-48
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4	45	86.5	10	17	US-09-339-922A-34
5	45	86.5	117	11	US-08-790-540-2
6	45	86.5	117	11	US-08-790-540A-2
7	45	86.5	117	11	US-08-791-391-2
8	45	86.5	117	11	US-08-791-391A-2
9	45	86.5	117	14	US-09-016-061-2
10	45	86.5	117	17	US-09-339-922A-2
11	42	80.8	115	10	US-08-621-899-8

12	42	80.8	117	18	US-09-438-136-246
13	42	80.8	123	9	US-08-571-755-15
14	42	80.8	123	14	US-09-054-847-12
15	42	80.8	83	22	US-60-160-209-3496
16	41	78.8	97	1	PCT-US00-07946-638
17	41	78.8	97	19	US-09-534-717-638
18	41	78.8	103	22	US-60-160-203-5859
19	41	78.8	103	22	US-60-160-209-4300
20	41	78.8	112	22	US-60-195-053-2430
21	41	78.8	116	22	US-60-160-203-4816
22	41	78.8	116	22	US-60-195-053-2431
23	41	78.8	120	11	US-08-743-788-48
24	41	78.8	120	11	US-08-743-788-49
25	41	78.8	120	11	US-08-743-788-55
26	41	78.8	120	22	US-60-195-053-2432
27	41	78.8	131	13	US-08-973-065A-25
28	41	78.8	131	13	US-08-973-065B-25
29	40	76.9	10	14	US-09-016-061-50
30	40	76.9	10	17	US-09-339-922A-50
31	40	76.9	117	1	PCT-US98-25828-56
32	40	76.9	117	11	US-08-790-540-6
33	40	76.9	117	11	US-08-790-540A-6
34	40	76.9	117	11	US-08-791-391-6
35	40	76.9	117	11	US-08-791-391A-6
36	40	76.9	117	13	US-08-986-016-56
37	40	76.9	117	14	US-09-016-061-6
38	40	76.9	117	17	US-09-339-922A-6
39	40	76.9	130	1	PCT-US98-25828-44
40	40	76.9	130	13	US-08-986-016-44
41	40	76.9	247	4	US-08-090-534-2
42	39	75.0	10	14	US-09-016-061-52
43	39	75.0	10	17	US-09-339-922A-52
44	39	75.0	100	22	US-60-192-739-3178
45	39	75.0	100	22	US-60-194-243-2280

ALIGNMENTS

RESULT 1
US-09-016-061-48
; Sequence 48, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-48

Query Match 100.0%; Score 52; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 1 GTTFSSYDMS 10

RESULT 2
US-09-339-922A-48
; Sequence 48, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-48

Query Match 100.0%; Score 52; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 1 GTTFSSYDMS 10

RESULT 3
US-09-016-061-34
; Sequence 34, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-34

Query Match 86.5%; Score 45; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 1 GTTFSSYDMS 10

RESULT 4
US-09-339-922A-34
; Sequence 34, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-34

Query Match 86.5%; Score 45; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 1 GTTFSSYDMS 10

RESULT 5
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

```

; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540-2

Query Match      86.5%; Score 45; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYDMS 35

RESULT 6
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

```

US-08-790-540A-2

Query Match      86.5%; Score 45; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYDMS 35

RESULT 7
US-08-791-391A-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match      86.5%; Score 45; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYDMS 35

RESULT 8
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP

```

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 86.5%; Score 45; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 9
US-09-016-061-2
Sequence 2, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-2

Query Match 86.5%; Score 45; DB 14; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 10
US-09-339-922A-2
Sequence 2, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: grafted
OTHER INFORMATION: antibody variable region
US-09-339-922A-2

Query Match 86.5%; Score 45; DB 17; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | | | | |
Db 26 GTTFSSYDMS 35

RESULT 11
US-08-621-899-8
Sequence 8, Application US/08621899
GENERAL INFORMATION:
APPLICANT: IWASA, SUSUMU
APPLICANT: TADA, HIROKO
APPLICANT: WATANABE, TAKESHI
TITLE OF INVENTION: CHIMERIC ANTIBODIES AND THEIR USE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,899
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810704
; FILING DATE: 18-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41485
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: BALB/c mouse
; TISSUE TYPE: spleen
; CELL TYPE: B cell hybridoma
; CELL LINE: FIBI-11
; US-08-621-899-8

```

```

Query Match      80.8%; Score 42; DB 10; Length 115;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 GTTFSSYDMS 10
   | |||:||||
Db 26 GTFSYDMS 35

```

RESULT 12

```
US-09-438-136-246
```

```
; Sequence 246, Application US/09/438136
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: CARR, Francis Joseph
; ADAIR, Fiona Suzanne
; HAMILTON, Anita Anne
; CARTER, Graham

```

```
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
```

```
; NON-IMMUNOGENIC PROTEINS
```

```
; NUMBER OF SEQUENCES: 254
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Hale and Dorr L.L.P.
```

```
; STREET: 60 State Street
```

```
; CITY: Boston
```

```
; STATE: Massachusetts
```

```
; COUNTRY: United States
```

```
; ZIP: 02109
```

```
; COMPUTER READABLE FORM:
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```
; MEDIUM TYPE: Floppy disk
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```
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/438,136
```

```
; FILING DATE: 10-Nov-1999
```

```
; CLASSIFICATION: <Unknown>
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: WO PCT/GB98/01473
```

```
; FILING DATE: 21-MAY-1998
```

```
; APPLICATION NUMBER: GB 9710480.6
```

```
; FILING DATE: 21-MAY-1997
```

```
; APPLICATION NUMBER: GB 9716197.0
```

```
; FILING DATE: 31-JUL-1997
```

```
; APPLICATION NUMBER: GB 9725270.4
```

```

; FILING DATE: 28-NOV-1997
; APPLICATION NUMBER: GB 9807751.4
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/067,235
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102286.395CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 246:
; US-09-438-136-246

```

```

Query Match      80.8%; Score 42; DB 18; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 GTTFSSYDMS 10
   | |||:||||
Db 26 GTTFSTYDMS 35

```

RESULT 13

```
US-08-571-755-15
```

```
; Sequence 15, Application US/08571755
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Thompson, Julia E
```

```
; APPLICANT: Vaughan, Tristan J
```

```
; APPLICANT: Williams, Andrew J
```

```
; APPLICANT: Green, Jonathan A
```

```
; APPLICANT: Jackson, Ronald H
```

```
; APPLICANT: Bacon, Louise
```

```
; APPLICANT: Johnson, Kevin S
```

```
; APPLICANT: Field, Raymond P
```

```
; APPLICANT: Wilton, Alison J
```

```
; APPLICANT: Tempest, Philip R
```

```
; TITLE OF INVENTION: Specific binding members for human transforming
```

```
; TITLE OF INVENTION: growth factor beta; materials and methods.
```

```
; NUMBER OF SEQUENCES: 92
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
```

```
; STREET: 6300 Sears Tower, 233 South Wacker Drive
```

```
; CITY: Chicago
```

```
; STATE: Illinois
```

```
; COUNTRY: USA
```

```
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0; Version #1.25 (EPO)
```

```
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/571,755
```

```
; FILING DATE: 13-DEC-1995
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: GB 9520486.3
```

```
; FILING DATE: 06-OCT-1995
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/244,597
```

```
; FILING DATE: 01-JUN-1994
```

```
; APPLICATION NUMBER: US 08/350,260
```

```
; FILING DATE: 05-DEC-1994
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: David W. Clough
```

```
; REGISTRATION NUMBER: 36,107
```

```
; REFERENCE/DOCKET NUMBER: 28111/32975
```


TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-571-755-15

Query Match 80.8%; Score 42; DB 9; Length 123;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| | | | |
Db 26 GLTFSSYDM 34

RESULT 14
US-09-054-847-12
; Sequence 12, Application US/09054847
; GENERAL INFORMATION:
; APPLICANT: Thomson, Julia E
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Williams, Andrew J
; APPLICANT: Green, Jonathan A
; APPLICANT: Jackson, Ronald H
; APPLICANT: Bacon, Louise
; APPLICANT: Johnson, Kevin S
; APPLICANT: Wilton, Alison J
; APPLICANT: Tempest, Philip R
; APPLICANT: Pope, Anthony R
; TITLE OF INVENTION: Specific binding members for human
; TITLE OF INVENTION: transforming growth factor beta; materials and methods
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,847
; FILING DATE: 03-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/02450
; FILING DATE: 07-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9520486.3
; FILING DATE: 06-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9601081.4
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-054-847-12

Query Match 80.8%; Score 42; DB 14; Length 123;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| | | | |
Db 26 GLTFSSYDM 34

RESULT 15
US-60-160-209-3496
; Sequence 3496, Application US/60160209
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
; FILE REFERENCE: CL000113
; CURRENT APPLICATION NUMBER: US/60/160,209
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4646
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3496
; LENGTH: 83
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-209-3496

Query Match 78.8%; Score 41; DB 22; Length 83;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| | | | |
Db 12 GFTFSSYDM 20

Search completed: March 28, 2001, 06:55:35
Job time: 1479 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:02 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-48

Perfect score: 52

Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

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2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*

3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*

4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*

5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*

6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	73.1	87	1	PCT-US01-03537-53
2	38	73.1	89	1	PCT-US01-03537-48
3	38	73.1	98	1	PCT-US01-03537-38
4	38	73.1	98	1	PCT-US01-03537-39
5	38	73.1	98	1	PCT-US01-03537-44
6	38	73.1	98	1	PCT-US01-03537-45
7	38	73.1	98	5	US-09-297-344-4
8	38	73.1	124	5	US-09-518-737-2
9	37	71.2	11	5	US-09-623-611-67
10	37	71.2	88	1	PCT-US01-03537-51
11	37	71.2	89	1	PCT-US01-03537-49
12	37	71.2	98	1	PCT-US01-03537-40
13	37	71.2	98	5	US-09-430-048-35
14	37	71.2	98	5	US-09-430-048-36
15	37	71.2	108	5	US-09-780-035-28
16	37	71.2	112	5	US-09-430-048-14
17	37	71.2	112	5	US-09-430-048-15
18	37	71.2	112	5	US-09-194-356A-8
19	37	71.2	113	5	PCT-US01-03537-80
20	37	71.2	116	5	US-09-385-673-15
21	37	71.2	117	5	US-09-780-035-67
22	37	71.2	118	5	PCT-US01-03537-85
23	37	71.2	120	1	PCT-US01-03537-92
24	37	71.2	121	1	US-09-194-356A-9
25	37	71.2	121	5	PCT-US01-03537-82
26	37	71.2	123	1	PCT-US01-03537-81
27	37	71.2	124	1	PCT-US01-03537-81

28	37	71.2	124	1	PCT-US01-03537-89	Sequence 89, Appl
29	37	71.2	125	1	PCT-US01-03537-76	Sequence 76, Appl
30	37	71.2	127	1	PCT-US01-03537-87	Sequence 87, Appl
31	37	71.2	128	1	PCT-US01-03537-77	Sequence 77, Appl
32	37	71.2	128	1	PCT-US01-03537-79	Sequence 79, Appl
33	37	71.2	130	5	US-09-341-711-53	Sequence 53, Appl
34	37	71.2	130	5	US-09-341-711-54	Sequence 54, Appl
35	37	71.2	235	5	US-09-780-035-30	Sequence 30, Appl
36	37	71.2	238	5	US-09-430-048-24	Sequence 24, Appl
37	36	69.2	120	4	US-08-907-146-25	Sequence 25, Appl
38	36	69.2	146	4	US-08-907-146-15	Sequence 15, Appl
39	35	67.3	677	4	US-08-686-968C-58	Sequence 58, Appl
40	35	67.3	677	4	US-08-686-968C-193	Sequence 193, App
41	34	65.4	117	1	PCT-US01-03537-83	Sequence 83, Appl
42	34	65.4	125	1	PCT-US01-03537-84	Sequence 84, Appl
43	34	65.4	128	5	US-09-147-443C-54	Sequence 54, Appl
44	34	65.4	138	5	US-09-403-107-144	Sequence 144, App
45	34	65.4	138	5	US-09-403-107-150	Sequence 150, App

ALIGNMENTS

RESULT 1
PCT-US01-03537-53
; Sequence 53, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-53

Query Match 73.1%; Score 38; DB 1; Length 87;
Best Local Similarity 80.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 15 GTTFSSYDMS 24

RESULT 2
PCT-US01-03537-48
; Sequence 48, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

```

; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-48

```

```

Query Match          73.1%; Score 38; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 0.66;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

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Qy 1 GTTFSSYDMS 10
   | | | | | | | |
Db 17 GTTFSSYDMS 26

```

```

RESULT 3
PCT-US01-03537-38
; Sequence 38, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-38

```

```

Query Match          73.1%; Score 38; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

```

```

Qy 1 GTTFSSYDMS 10
   | | | | | | | |
Db 26 GTTFSSYDMS 35

```

```

RESULT 4
PCT-US01-03537-39
; Sequence 39, Application PC/TUS0103537

```

```

; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-39

```

```

Query Match          73.1%; Score 38; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

```

```

Qy 1 GTTFSSYDMS 10
   | | | | | | | |
Db 26 GTTFSSYDMS 35

```

```

RESULT 5
PCT-US01-03537-44
; Sequence 44, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-44

```

```

Query Match          73.1%; Score 38; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

```

```

Qy 1 GTTFSSYDMS 10

```


; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-611-67

Query Match 71.2%; Score 37; DB 5; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 2 GFTFSYAMS 11

RESULT 10
US-09-623-611-74
; Sequence 74, Application US/09623611
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: V-like Domain Binding Molecules
; FILE REFERENCE: 674537-2002
; CURRENT APPLICATION NUMBER: US/09/623,611
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/AU99/00136
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: AU PP 2210
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-611-74

Query Match 71.2%; Score 37; DB 5; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 9 GFTFSYAMS 18

RESULT 11
PCT-US01-03537-51
; Sequence 51, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-51

Query Match 71.2%; Score 37; DB 1; Length 88;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 17 GFTFSYAMS 26

RESULT 12
PCT-US01-03537-49
; Sequence 49, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-49

Query Match 71.2%; Score 37; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 17 GFTFSYAMS 26

RESULT 13
PCT-US01-03537-40
; Sequence 40, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(98)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US01-03537-40

Query Match 71.2%; Score 37; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 26 GTTFSSYAMS 35

RESULT 14
US-09-430-048-35
; Sequence 35, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-35

Query Match 71.2%; Score 37; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 26 GTTFSSYAMS 35

RESULT 15
US-09-430-048-36
; Sequence 36, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36

; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-36

Query Match 71.2%; Score 37; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
| | | | | | |
Db 26 GTTFSSYAMS 35

Search completed: March 28, 2001, 06:57:02
Job time: 1551 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:35 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues
Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US08_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
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10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
13: /cgnl_7/ptodata/1/paa/US089_COMB.pep.*
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15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
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17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	14	US-09-016-061-50
2	58	100.0	10	17	US-09-339-922A-50
3	48	82.8	10	14	US-09-016-061-34
4	48	82.8	10	17	US-09-339-922A-34
5	48	82.8	117	11	US-08-790-540-2
6	48	82.8	117	11	US-08-790-540A-2
7	48	82.8	117	11	US-08-791-391-2
8	48	82.8	117	11	US-08-791-391A-2
9	48	82.8	117	14	US-09-016-061-2
10	48	82.8	117	17	US-09-339-922A-2
11	45	77.6	115	10	US-08-621-899-8

12	45	77.6	117	18	US-09-438-136-246
13	44	75.9	83	22	US-60-160-209-3496
14	44	75.9	97	1	PCT-US00-07946-638
15	44	75.9	97	19	US-09-534-717-638
16	44	75.9	103	22	US-60-160-203-5859
17	44	75.9	103	22	US-60-160-209-4300
18	44	75.9	112	22	US-60-195-053-4816
19	44	75.9	116	22	US-60-160-203-4230
20	44	75.9	116	22	US-60-195-053-2431
21	44	75.9	120	11	US-08-743-788-48
22	44	75.9	120	11	US-08-743-788-49
23	44	75.9	120	11	US-08-743-788-55
24	44	75.9	120	22	US-60-195-053-2432
25	44	75.9	131	13	US-08-973-065A-25
26	44	75.9	131	13	US-08-973-065B-25
27	43	74.1	117	1	PCT-US98-25828-56
28	43	74.1	117	11	US-08-790-540-6
29	43	74.1	117	11	US-08-790-540A-6
30	43	74.1	117	11	US-08-791-391-6
31	43	74.1	117	11	US-08-791-391A-6
32	43	74.1	117	13	US-08-986-016-56
33	43	74.1	117	14	US-09-016-061-6
34	43	74.1	117	17	US-09-339-922A-6
35	43	74.1	130	1	PCT-US98-25828-44
36	43	74.1	130	13	US-08-986-016-44
37	43	74.1	247	4	US-08-090-534-2
38	43	74.1	505	18	US-09-417-507-37648
39	42	72.4	10	14	US-09-016-061-52
40	42	72.4	10	17	US-09-339-922A-52
41	42	72.4	115	1	PCT-US00-20131A-2
42	42	72.4	117	18	US-09-438-136-250
43	42	72.4	119	4	US-08-090-534-6
44	42	72.4	239	1	PCT-US00-20131A-6
45	41	70.7	77	22	US-60-182-467-1616

ALIGNMENTS

RESULT 1
US-09-016-061-50
; Sequence 50, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-50

Query Match 100.0%; Score 58; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 1 GFTWSSYDMS 10

RESULT 2
US-09-339-922A-50
; Sequence 50, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-50

Query Match 100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 1 GFTWSSYDMS 10

RESULT 3
US-09-016-061-34
; Sequence 34, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-34

Query Match 82.8%; Score 48; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 1 GFTWSSYDMS 10

RESULT 4
US-09-339-922A-34
; Sequence 34, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-34

Query Match 82.8%; Score 48; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 1 GFTWSSYDMS 10

RESULT 5
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
```


;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: US/08/790,540
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IX 2405
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-790-540-2

Query Match 82.8%; Score 48; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMS 35

RESULT 6
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-790-540A-2

Query Match 82.8%; Score 48; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMS 35

RESULT 7
US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match 82.8%; Score 48; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMS 35

RESULT 8
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 82.8%; Score 48; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMS 35

RESULT 9
US-09-016-061-2
Sequence 2, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791.391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-2

Query Match 82.8%; Score 48; DB 14; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMS 35

RESULT 10
US-09-339-922A-2
Sequence 2, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: grafted
OTHER INFORMATION: antibody variable region
US-09-339-922A-2

Query Match 82.8%; Score 48; DB 17; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSSYDMS 35

RESULT 11
US-08-621-899-8
Sequence 8, Application: US/08621899
GENERAL INFORMATION:
APPLICANT: IWASA, SUSUMU
APPLICANT: TADA, HIROKO
APPLICANT: WATANABE, TAKESHI
TITLE OF INVENTION: CHIMERIC ANTIBODIES AND THEIR USE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/621,899
;; FILING DATE: 18-DEC-1991
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/810704
;; FILING DATE: 18-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: RESNICK, DAVID S.
;; REGISTRATION NUMBER: 34235
;; REFERENCE/DOCKET NUMBER: 41485
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 523-3400
;; TELEFAX: (617) 523-6440
;; TELEX: 200291 STRE UR
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 115 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; ORIGINAL SOURCE:
;; ORGANISM: BALB/c mouse
;; TISSUE TYPE: spleen
;; CELL TYPE: B cell hybridoma
;; CELL LINE: FIB1-11
US-08-621-899-8

Query Match 77.6%; Score 45; DB 10; Length 115;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSYDMS 35

RESULT 12

US-09-438-136-246
;; Sequence 246, Application US/09438136
;; GENERAL INFORMATION:
;; APPLICANT: CARR, Francis Joseph
;; ADAIR, Fiona Suzanne
;; HAMILTON, Anita Anne
;; CARTER, Graham
;; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
;; NON-IMMUNOGENIC PROTEINS
;; NUMBER OF SEQUENCES: 254
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hale and Dorr L.L.P.
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: United States
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/438,136
;; FILING DATE: 10-Nov-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/GB98/01473
;; FILING DATE: 21-MAY-1998
;; APPLICATION NUMBER: GB 9710480.6
;; FILING DATE: 21-MAY-1997
;; APPLICATION NUMBER: GB 9716197.0
;; FILING DATE: 31-JUL-1997
;; APPLICATION NUMBER: GB 9725270.4

;; FILING DATE: 28-NOV-1997
;; APPLICATION NUMBER: GB 9807751.4
;; FILING DATE: 14-APR-1998
;; APPLICATION NUMBER: US 60/067,235
;; FILING DATE: 02-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baker, Hollie L.
;; REGISTRATION NUMBER: 31,321
;; REFERENCE/DOCKET NUMBER: 102286.395CON
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 526-6000
;; INFORMATION FOR SEQ ID NO: 246:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-438-136-246

Query Match 77.6%; Score 45; DB 18; Length 117;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 26 GFTFSYDMS 35

RESULT 13

US-60-160-209-3496
;; Sequence 3496, Application US/60160209
;; GENERAL INFORMATION:
;; APPLICANT: BONAZZI, VIVIAN
;; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: C1000113
;; CURRENT APPLICATION NUMBER: US/60/160,209
;; CURRENT FILING DATE: 1999-10-19
;; NUMBER OF SEQ ID NOS: 4646
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3496
;; LENGTH: 83
;; TYPE: PRT
;; ORGANISM: HUMAN
US-60-160-209-3496

Query Match 75.9%; Score 44; DB 22; Length 83;
Best Local Similarity 88.9%; Pred. No. 6.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
Db 12 GFTFSYDM 20

RESULT 14

PCT-US00-07946-638
;; Sequence 638, Application PC/TUS00007946
;; GENERAL INFORMATION:
;; APPLICANT: Jochen, Salfeld et al.
;; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Product
;; FILE REFERENCE: BBI-093CPPC
;; CURRENT APPLICATION NUMBER: PCT/US00/07946
;; CURRENT FILING DATE: 2000-03-24
;; EARLIER FILING DATE: 60/126,603
;; EARLIER FILING DATE: March 25, 1999
;; NUMBER OF SEQ ID NOS: 675
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 638
;; LENGTH: 97

; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07946-638

Query Match 75.9%; Score 44; DB 1; Length 97;
Best Local Similarity 88.9%; Pred. No. 7.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
 | | | | |
Db 26 GFTFSSYDM 34

RESULT 15
US-09-534-717-638
; Sequence 638, Application US/09534717
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-638

Query Match 75.9%; Score 44; DB 19; Length 97;
Best Local Similarity 88.9%; Pred. No. 7.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDM 9
 | | | | |
Db 26 GFTFSSYDM 34

Search completed: March 28, 2001, 06:55:35
Job time: 1479 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:02 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Pending_Patents_AA_New:*
1: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep:*
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3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	70.7	87	1	PCT-US01-03537-53
2	41	70.7	89	1	PCT-US01-03537-48
3	41	70.7	98	1	PCT-US01-03537-38
4	41	70.7	98	1	PCT-US01-03537-39
5	41	70.7	98	1	PCT-US01-03537-44
6	41	70.7	98	1	PCT-US01-03537-45
7	41	70.7	98	5	US-09-297-344-4
8	41	70.7	124	5	US-09-518-737-2
9	40	69.0	11	5	US-09-623-611-67
10	40	69.0	18	5	US-09-623-611-74
11	40	69.0	88	1	PCT-US01-03537-51
12	40	69.0	89	1	PCT-US01-03537-49
13	40	69.0	98	1	PCT-US01-03537-40
14	40	69.0	98	5	US-09-430-048-35
15	40	69.0	98	5	US-09-430-048-36
16	40	69.0	108	5	US-09-780-035-28
17	40	69.0	112	5	US-09-430-048-14
18	40	69.0	112	5	US-09-430-048-15
19	40	69.0	113	5	US-09-194-356A-8
20	40	69.0	116	1	PCT-US01-03537-80
21	40	69.0	117	5	US-09-385-673-15
22	40	69.0	118	5	US-09-780-035-67
23	40	69.0	120	1	PCT-US01-03537-85
24	40	69.0	121	1	PCT-US01-03537-92
25	40	69.0	121	5	US-09-194-356A-9
26	40	69.0	123	1	PCT-US01-03537-82
27	40	69.0	124	1	PCT-US01-03537-81

28	40	69.0	124	1	PCT-US01-03537-89	Sequence 89, Appl
29	40	69.0	125	1	PCT-US01-03537-76	Sequence 76, Appl
30	40	69.0	127	1	PCT-US01-03537-87	Sequence 87, Appl
31	40	69.0	128	1	PCT-US01-03537-77	Sequence 77, Appl
32	40	69.0	128	1	PCT-US01-03537-79	Sequence 79, Appl
33	40	69.0	130	5	US-09-341-711-53	Sequence 53, Appl
34	40	69.0	130	5	US-09-341-711-54	Sequence 54, Appl
35	40	69.0	235	5	US-09-780-035-30	Sequence 30, Appl
36	40	69.0	238	5	US-09-430-048-24	Sequence 24, Appl
37	39	67.2	120	4	US-08-907-146-25	Sequence 25, Appl
38	39	67.2	146	4	US-08-907-146-15	Sequence 15, Appl
39	38	65.5	335	5	US-09-719-108-10	Sequence 10, Appl
40	37	63.8	80	5	US-09-107-433-2852	Sequence 83, Appl
41	37	63.8	117	1	PCT-US01-03537-83	Sequence 84, Appl
42	37	63.8	125	1	PCT-US01-03537-84	Sequence 54, Appl
43	37	63.8	128	5	US-09-147-443C-54	Sequence 144, App
44	37	63.8	138	5	US-09-403-107-144	Sequence 150, App
45	37	63.8	138	5	US-09-403-107-150	

ALIGNMENTS

RESULT 1
PCT-US01-03537-53
; Sequence 53, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-53

Query Match 70.7%; Score 41; DB 1; Length 87;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 GFTWSSYDMS 10
|||:|||||
Db 15 GFTFSSYTMS 24

RESULT 2
PCT-US01-03537-48
; Sequence 48, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

```

; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-48

```

```

Query Match          70.7%; Score 41; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

```

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Qy 1 GFTWSSYDMS 10
    |||:||||||
Db 17 GFTFSSYDMS 26

```

```

RESULT 3
PCT-US01-03537-38
; Sequence 38, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-38

```

```

Query Match          70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 1 GFTWSSYDMS 10
    |||:||||||
Db 26 GFTFSSYDMS 35

```

```

RESULT 4
PCT-US01-03537-39
; Sequence 39, Application PC/TUS0103537

```

```

; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-39

```

```

Query Match          70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 1 GFTWSSYDMS 10
    |||:||||||
Db 26 GFTFSSYDMS 35

```

```

RESULT 5
PCT-US01-03537-44
; Sequence 44, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-44

```

```

Query Match          70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

```

```

Qy 1 GFTWSSYDMS 10

```

```
Db 26 GFTFSSYMS 35
    III:III:II
RESULT 6
PCT-US01-03537-45
; Sequence 45, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larrosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 09/497,625
; PRIOR APPLICATION NUMBER: 2000-02-03
; PRIOR FILING DATE: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-45

Query Match 70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
    III:III:II
Db 26 GFTFSSYMS 35

RESULT 7
US-09-297-344-4
; Sequence 4, Application US/09297344
; GENERAL INFORMATION:
; APPLICANT: Deen, Keith C.
; APPLICANT: Dillon, Susan B.
; APPLICANT: Porter, Terence C.
; APPLICANT: Sweet, Raymond A.
; TITLE OF INVENTION: Human Monoclonal Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,344
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,149
; FILING DATE: 01-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5968
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-297-344-4

Query Match 70.7%; Score 41; DB 5; Length 98;
Best Local Similarity 70.0%; Pred. No. 2.7;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
    III:III:II
Db 26 GFTFSSYMS 35

RESULT 8
US-09-518-737-2
; Sequence 2, Application US/09518737
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHISA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2

Query Match 70.7%; Score 41; DB 5; Length 124;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
    III:III:II
Db 26 GFTFSSYMS 35

RESULT 9
US-09-623-611-67
; Sequence 67, Application US/09623611
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: V-like Domain Binding Molecules
; FILE REFERENCE: 674537-2002
; CURRENT APPLICATION NUMBER: US/09/623,611
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/AU99/00136
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: AU PP 2210
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; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-611-67

Query Match 69.0%; Score 40; DB 5; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.51;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|||||
Db 2 GFTFSSYAMS 11

RESULT 10
US-09-623-611-74
; Sequence 74, Application US/09623611
; GENERAL INFORMATION:
; APPLICANT: Cola, et al.
; TITLE OF INVENTION: V-like Domain Binding Molecules
; FILE REFERENCE: 674537-2002
; CURRENT APPLICATION NUMBER: US/09/623,611
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/AU99/00136
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: AU PP 2210
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-611-74

Query Match 69.0%; Score 40; DB 5; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.81;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|||||
Db 9 GFTFSSYAMS 18

RESULT 11
PCT-US01-03537-51
; Sequence 51, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-51

Query Match 69.0%; Score 40; DB 1; Length 88;
Best Local Similarity 80.0%; Pred. No. 3.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|||||
Db 17 GFTFSSYAMS 26

RESULT 12
PCT-US01-03537-49
; Sequence 49, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-49

Query Match 69.0%; Score 40; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 3.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
|||:|||||
Db 17 GFTFSSYAMS 26

RESULT 13
PCT-US01-03537-40
; Sequence 40, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(98)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US01-03537-40

Query Match 69.0%; Score 40; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 3.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|||:||||||
Db 26 GFTFSYAMS 35

RESULT 14
US-09-430-048-35
; Sequence 35, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430.048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-35

Query Match 69.0%; Score 40; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 3.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|||:||||||
Db 26 GFTFSYAMS 35

RESULT 15
US-09-430-048-36
; Sequence 36, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430.048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36

; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-36

Query Match 69.0%; Score 40; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 3.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
|||:||||||
Db 26 GFTFSYAMS 35

Search completed: March 28, 2001, 06:57:02
Job time: 1551 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:35 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues
Total number of hits satisfying chosen parameters: 8981110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1:	/cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
2:	/cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3:	/cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4:	/cgnl_7/ptodata/1/paa/US08_COMB.pep.*
5:	/cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6:	/cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7:	/cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8:	/cgnl_7/ptodata/1/paa/US084_COMB.pep.*
9:	/cgnl_7/ptodata/1/paa/US085_COMB.pep.*
10:	/cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11:	/cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12:	/cgnl_7/ptodata/1/paa/US088_COMB.pep.*
13:	/cgnl_7/ptodata/1/paa/US089_COMB.pep.*
14:	/cgnl_7/ptodata/1/paa/US090_COMB.pep.*
15:	/cgnl_7/ptodata/1/paa/US091_COMB.pep.*
16:	/cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17:	/cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18:	/cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19:	/cgnl_7/ptodata/1/paa/US095_COMB.pep.*
20:	/cgnl_7/ptodata/1/paa/US096_COMB.pep.*
21:	/cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22:	/cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	14	US-09-016-061-52
2	53	100.0	10	17	US-09-339-922A-52
3	47	88.7	10	14	US-09-016-061-34
4	47	88.7	10	17	US-09-339-922A-34
5	47	88.7	117	11	US-08-790-540-2
6	47	88.7	117	11	US-08-790-540A-2
7	47	88.7	117	11	US-08-791-391-2
8	47	88.7	117	11	US-08-791-391A-2
9	47	88.7	117	14	US-09-016-061-2
10	47	88.7	117	17	US-09-339-922A-2
11	45	84.9	117	18	US-09-438-136-250

12	44	83.0	115	10	US-08-621-899-8
13	44	83.0	117	18	US-09-438-136-246
14	43	81.1	83	22	US-60-160-209-3496
15	43	81.1	97	1	PCT-US00-07946-638
16	43	81.1	97	19	US-09-534-717-638
17	43	81.1	103	22	US-60-160-203-5859
18	43	81.1	103	22	US-60-160-209-4300
19	43	81.1	112	22	US-60-195-053-2430
20	43	81.1	116	22	US-60-160-203-4816
21	43	81.1	116	22	US-60-195-053-2431
22	43	81.1	120	11	US-08-743-788-48
23	43	81.1	120	11	US-08-743-788-49
24	43	81.1	120	11	US-08-743-788-55
25	43	81.1	120	22	US-60-195-053-2432
26	43	81.1	131	13	US-08-973-065A-25
27	43	81.1	131	13	US-08-973-065B-25
28	42	79.2	10	14	US-09-016-061-50
29	42	79.2	10	17	US-09-339-922A-50
30	42	79.2	117	1	PCT-US98-25828-56
31	42	79.2	117	11	US-08-790-540-6
32	42	79.2	117	11	US-08-790-540A-6
33	42	79.2	117	11	US-08-791-391-6
34	42	79.2	117	11	US-08-791-391A-6
35	42	79.2	117	13	US-08-986-016-56
36	42	79.2	117	14	US-09-016-061-6
37	42	79.2	117	17	US-09-339-922A-6
38	42	79.2	121	18	US-09-438-136-113
39	42	79.2	130	1	PCT-US98-25828-44
40	42	79.2	130	13	US-08-986-016-44
41	42	79.2	247	4	US-08-090-534-2
42	41	77.4	115	1	PCT-US00-20131A-2
43	41	77.4	119	4	US-08-090-534-6
44	41	77.4	239	1	PCT-US00-20131A-6
45	40	75.5	77	22	US-60-182-467-1616

ALIGNMENTS

RESULT 1
US-09-016-061-52
; Sequence 52, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/016,061
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-52

Query Match 100.0%; Score 53; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
DB 1 GFTFLSYDMS 10

RESULT 2
US-09-339-922A-52
; Sequence 52, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-52

Query Match 100.0%; Score 53; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
DB 1 GFTFLSYDMS 10

RESULT 3
US-09-016-061-34
; Sequence 34, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-34

Query Match 88.7%; Score 47; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
DB 1 GFTFLSYDMS 10

RESULT 4
US-09-339-922A-34
; Sequence 34, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-34

Query Match 88.7%; Score 47; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
DB 1 GFTFLSYDMS 10

RESULT 5
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/790,540
;; FILING DATE:
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IX 2405
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-790-540-2

Query Match 88.7%; Score 47; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 26 GFTFSSYDMS 35

RESULT 6
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-790-540A-2

Query Match 88.7%; Score 47; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 26 GFTFSSYDMS 35

RESULT 7
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match 88.7%; Score 47; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 26 GFTFSSYDMS 35

RESULT 8
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 88.7%; Score 47; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTFFLSYDMS 10
DB 26 GTFFSSYDMS 35

RESULT 9
US-09-016-061-2
Sequence 2, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-2

Query Match 88.7%; Score 47; DB 14; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTFFLSYDMS 10
DB 26 GTFFSSYDMS 35

RESULT 10
US-09-339-922A-2
Sequence 2, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
TITLE OF INVENTION: Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: grafted
OTHER INFORMATION: antibody variable region
US-09-339-922A-2

Query Match 88.7%; Score 47; DB 17; Length 117;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTFFLSYDMS 10
DB 26 GTFFSSYDMS 35

RESULT 11
US-09-438-136-250
Sequence 250, Application US/09438136
GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
ADAIR, Fiona Suzanne
HAMILTON, Anita Anne
CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
NON-IMMUNOGENIC PROTEINS
NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr L.L.P.
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438.136
FILING DATE: 10-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB98/01473
FILING DATE: 21-MAY-1998
APPLICATION NUMBER: GB 9710480.6
FILING DATE: 21-MAY-1997
APPLICATION NUMBER: GB 9716197.0
FILING DATE: 31-JUL-1997
APPLICATION NUMBER: GB 9725270.4
FILING DATE: 28-NOV-1997
APPLICATION NUMBER: GB 9807751.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/067,235
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.395CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
INFORMATION FOR SEQ ID NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 250:
US-09-438-136-250

Query Match 84.9%; Score 45; DB 18; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:||||
DB 26 GFTFTYDMS 35

RESULT 12
US-08-621-899-8
Sequence 8, Application US/08621899
GENERAL INFORMATION:
APPLICANT: IWASA, SUSUMU
APPLICANT: TADA, HIROKO
APPLICANT: WATANABE, TAKESHI
TITLE OF INVENTION: CHIMERIC ANTIBODIES AND THEIR USE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,899
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810704
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.

REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 41485
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: BALB/c mouse
TISSUE TYPE: spleen
CELL TYPE: B cell hybridoma
CELL LINE: FIB1-11
US-08-621-899-8

Query Match 83.0%; Score 44; DB 10; Length 115;
Best Local Similarity 80.0%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:||||
DB 26 GFTFSNYDMS 35

RESULT 13
US-09-438-136-246
Sequence 246, Application US/09438136
GENERAL INFORMATION:
APPLICANT: CARR, Francis Joseph
ADAIR, Fiona Suzanne
HAMILTON, Anita Anne
CARTER, Graham
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
NON-IMMUNOGENIC PROTEINS
NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr L.L.P.
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,136
FILING DATE: 10-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB98/01473
FILING DATE: 21-MAY-1998
APPLICATION NUMBER: GB 9710480.6
FILING DATE: 21-MAY-1997
APPLICATION NUMBER: GB 9716197.0
FILING DATE: 31-JUL-1997
APPLICATION NUMBER: GB 9725270.4
FILING DATE: 28-NOV-1997
APPLICATION NUMBER: GB 9807751.4
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/067,235
FILING DATE: 02-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.395CON

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-438-136-246

Query Match 83.0%; Score 44; DB 18; Length 117;
Best Local Similarity 80.0%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
DB 26 GFTFSSYDMS 35

RESULT 14
US-60-160-209-3496
; Sequence 3496, Application US/60160209
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIAN
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
; FILE REFERENCE: CL000113
; CURRENT APPLICATION NUMBER: US/60/160,209
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4646
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3496
; LENGTH: 83
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-209-3496

Query Match 81.1%; Score 43; DB 22; Length 83;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
|||||
DB 12 GFTFSSYDM 20

RESULT 15
PCT-US00-07946-638
; Sequence 638, Application PC/TUS0007946
; GENERAL INFORMATION:
; APPLICANT: Jochen, Saifeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CPC
; CURRENT APPLICATION NUMBER: PCT/US00/07946
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07946-638

Query Match 81.1%; Score 43; DB 1; Length 97;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 28, 2001, 06:55:35
Job time: 1479 sec

QY 1 GFTFLSYDM 9
|||||
DB 26 GFTFSSYDM 34

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:02 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New: *

1: /cgnl_1/ptodata/2/paa/PCT_NEW_COMB.pep.*

2: /cgnl_1/ptodata/2/paa/US06_NEW_COMB.pep.*

3: /cgnl_1/ptodata/2/paa/US07_NEW_COMB.pep.*

4: /cgnl_1/ptodata/2/paa/US08_NEW_COMB.pep.*

5: /cgnl_1/ptodata/2/paa/US09_NEW_COMB.pep.*

6: /cgnl_1/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	75.5	87	1	PCT-US01-03537-53
2	40	75.5	89	1	PCT-US01-03537-48
3	40	75.5	98	1	PCT-US01-03537-38
4	40	75.5	98	1	PCT-US01-03537-39
5	40	75.5	98	1	PCT-US01-03537-44
6	40	75.5	98	1	PCT-US01-03537-45
7	40	75.5	98	5	US-09-297-344-4
8	40	75.5	124	5	US-09-518-737-2
9	39	73.6	11	5	US-09-623-611-67
10	39	73.6	18	5	US-09-623-611-74
11	39	73.6	88	1	PCT-US01-03537-51
12	39	73.6	89	1	PCT-US01-03537-49
13	39	73.6	98	1	PCT-US01-03537-40
14	39	73.6	98	5	US-09-430-048-35
15	39	73.6	98	5	US-09-430-048-36
16	39	73.6	108	5	US-09-780-035-28
17	39	73.6	112	5	US-09-430-048-14
18	39	73.6	112	5	US-09-430-048-15
19	39	73.6	113	5	US-09-194-356A-8
20	39	73.6	116	1	PCT-US01-03537-80
21	39	73.6	117	5	US-09-385-673-15
22	39	73.6	118	5	US-09-780-035-67
23	39	73.6	120	1	PCT-US01-03537-85
24	39	73.6	121	1	PCT-US01-03537-92
25	39	73.6	121	5	US-09-194-356A-9
26	39	73.6	123	1	PCT-US01-03537-82
27	39	73.6	124	1	PCT-US01-03537-81

28	39	73.6	124	1	PCT-US01-03537-89	Sequence 89, Appl
29	39	73.6	125	1	PCT-US01-03537-76	Sequence 76, Appl
30	39	73.6	127	1	PCT-US01-03537-87	Sequence 87, Appl
31	39	73.6	128	1	PCT-US01-03537-77	Sequence 77, Appl
32	39	73.6	128	1	PCT-US01-03537-79	Sequence 79, Appl
33	39	73.6	130	5	US-09-341-711-53	Sequence 53, Appl
34	39	73.6	130	5	US-09-341-711-54	Sequence 54, Appl
35	39	73.6	235	5	US-09-780-035-30	Sequence 30, Appl
36	39	73.6	238	5	US-09-430-048-24	Sequence 24, Appl
37	38	71.7	120	4	US-08-907-146-25	Sequence 25, Appl
38	38	71.7	146	4	US-08-907-146-15	Sequence 15, Appl
39	37	69.8	137	5	US-09-648-624A-2	Sequence 2, Appl
40	36	67.9	117	1	PCT-US01-03537-83	Sequence 83, Appl
41	36	67.9	125	1	PCT-US01-03537-84	Sequence 84, Appl
42	36	67.9	125	5	US-09-147-443C-30	Sequence 30, Appl
43	36	67.9	125	5	US-09-147-443C-46	Sequence 46, Appl
44	36	67.9	128	5	US-09-147-443C-54	Sequence 54, Appl
45	36	67.9	138	5	US-09-403-107-144	Sequence 144, App

ALIGNMENTS

RESULT 1
PCT-US01-03537-53
; Sequence 53, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-53

Query Match 75.5%; Score 40; DB 1; Length 87;
Best Local Similarity 80.0%; Pred No. 0.76;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 GFTFLSYDMS 10
Db 15 GFTFLSYDMS 24

RESULT 2
PCT-US01-03537-48
; Sequence 48, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052005
CURRENT APPLICATION NUMBER: PCT/US01/03537
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 89
TYPE: PRT
ORGANISM: Mus musculus
PCT-US01-03537-48

Query Match 75.5%; Score 40; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 0.77;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| |||
Db 17 GFTFSYGMMS 26

RESULT 3
PCT-US01-03537-38
Sequence 38, Application PC/TUS0103537
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052005
CURRENT APPLICATION NUMBER: PCT/US01/03537
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 98
TYPE: PRT
ORGANISM: Mus musculus
PCT-US01-03537-38

Query Match 75.5%; Score 40; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| |||
Db 26 GFTFSYTMMS 35

RESULT 4
PCT-US01-03537-39
Sequence 39, Application PC/TUS0103537

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052005
CURRENT APPLICATION NUMBER: PCT/US01/03537
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 98
TYPE: PRT
ORGANISM: Mus musculus
PCT-US01-03537-39

Query Match 75.5%; Score 40; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
||||| ||| |||
Db 26 GFTFSYTMMS 35

RESULT 5
PCT-US01-03537-44
Sequence 44, Application PC/TUS0103537
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052005
CURRENT APPLICATION NUMBER: PCT/US01/03537
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 98
TYPE: PRT
ORGANISM: Mus musculus
PCT-US01-03537-44

Query Match 75.5%; Score 40; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10

```
Db 26 GFTFSSYMS 35
||||| |||
RESULT 6
PCT-US01-03537-45
; Sequence 45, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-45

Query Match 75.5%; Score 40; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GFTFLSYDMS 10
||||| |||
Db 26 GFTFSSYMS 35

RESULT 7
US-09-297-344-4
; Sequence 4, Application US/09297344
; GENERAL INFORMATION:
; APPLICANT: Deen, Keith C.
; APPLICANT: Dillon, Susan B.
; APPLICANT: Porter, Terence C.
; APPLICANT: Sweet, Raymond A.
; TITLE OF INVENTION: Human Monoclonal Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,344
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,149
; FILING DATE: 01-NOV-1997

Query Match 75.5%; Score 40; DB 1; Length 124;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GFTFLSYDMS 10
||||| |||
Db 26 GFTFSSYMS 35

RESULT 8
US-09-518-737-2
; Sequence 2, Application US/09518737
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIISA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2

Query Match 75.5%; Score 40; DB 5; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.84;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 0;

QY 1 GFTFLSYDMS 10
||||| |||
Db 26 GFTFSSYEMN 35

RESULT 9
US-09-623-611-67
; Sequence 67, Application US/09623611
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: V-like Domain Binding Molecules
; FILE REFERENCE: 674537-2002
; CURRENT APPLICATION NUMBER: US/09/623,611
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/AU99/00136
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: AU PP 2210
```

; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-611-67

Query Match 73.6%; Score 39; DB 5; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 2 GFTFSSYAMS 11

RESULT 10
PCT-US01-03537-49
; Sequence 74, Application US/09623611
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: V-like Domain Binding Molecules
; FILE REFERENCE: 674537-2002
; CURRENT APPLICATION NUMBER: US/09/623,611
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/AU99/00136
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: AU PP 2210
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-611-74

Query Match 73.6%; Score 39; DB 5; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 9 GFTFSSYAMS 18

RESULT 11
PCT-US01-03537-51
; Sequence 51, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-51

Query Match 73.6%; Score 39; DB 1; Length 88;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 17 GFTFSSYAMS 26

RESULT 12
PCT-US01-03537-49
; Sequence 49, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-49

Query Match 73.6%; Score 39; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
Db 17 GFTFSSYAMS 26

RESULT 13
PCT-US01-03537-40
; Sequence 40, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(98)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US01-03537-40

Query Match 73.6%; Score 39; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
Db 26 GFTFSYAMS 35

RESULT 14
US-09-430-048-35
; Sequence 35, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: MILLER, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-35

Query Match 73.6%; Score 39; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
Db 26 GFTFSYAMS 35

RESULT 15
US-09-430-048-36
; Sequence 36, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: MILLER, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36

; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-36

Query Match 73.6%; Score 39; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||||
Db 26 GFTFSYAMS 35

Search completed: March 28, 2001, 06:57:02
Job time: 1551 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:35 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WYAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:
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4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
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6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	55	100.0	10	14	US-09-016-061-54
2	55	100.0	10	17	US-09-339-922A-54
3	50	90.9	10	14	US-09-016-061-36
4	50	90.9	10	17	US-09-339-922A-36
5	50	90.9	117	1	PCT-US98-25828-56
6	50	90.9	117	11	US-08-790-540-2
7	50	90.9	117	11	US-08-790-540-6
8	50	90.9	117	11	US-08-790-540A-2
9	50	90.9	117	11	US-08-790-540A-6
10	50	90.9	117	11	US-08-791-391-2
11	50	90.9	117	11	US-08-791-391-6

12	50	90.9	117	11	US-08-791-391A-2	Sequence 2, Appl
13	50	90.9	117	11	US-08-791-391A-6	Sequence 6, Appl
14	50	90.9	117	13	US-08-986-016-56	Sequence 56, Appl
15	50	90.9	117	14	US-09-016-061-2	Sequence 2, Appl
16	50	90.9	117	14	US-09-016-061-6	Sequence 6, Appl
17	50	90.9	117	17	US-09-339-922A-2	Sequence 2, Appl
18	50	90.9	117	17	US-09-339-922A-6	Sequence 6, Appl
19	50	90.9	130	1	PCT-US98-25828-44	Sequence 44, Appl
20	50	90.9	130	13	US-08-986-016-44	Sequence 44, Appl
21	43	78.2	98	18	US-09-497-625-44	Sequence 44, Appl
22	43	78.2	138	8	US-08-485-044-2	Sequence 2, Appl
23	43	78.2	140	16	US-09-286-240-4	Sequence 4, Appl
24	42	76.4	119	4	US-08-090-534-6	Sequence 6, Appl
25	42	76.4	123	17	US-09-381-497-2	Sequence 2, Appl
26	42	76.4	247	4	US-08-090-534-2	Sequence 2, Appl
27	41	74.5	110	1	PCT-US96-06804-10	Sequence 10, Appl
28	41	74.5	110	1	PCT-US96-06804A-10	Sequence 10, Appl
29	41	74.5	110	8	US-08-440-621A-10	Sequence 10, Appl
30	41	74.5	110	8	US-08-440-621B-10	Sequence 10, Appl
31	41	74.5	110	8	US-08-440-621C-10	Sequence 10, Appl
32	41	74.5	110	8	US-08-440-621D-10	Sequence 10, Appl
33	41	74.5	110	8	US-08-440-621E-10	Sequence 10, Appl
34	41	74.5	110	8	US-08-462-045-10	Sequence 10, Appl
35	41	74.5	110	8	US-08-462-045B-10	Sequence 10, Appl
36	41	74.5	110	8	US-08-465-270-10	Sequence 10, Appl
37	41	74.5	110	8	US-08-465-270C-10	Sequence 10, Appl
38	41	74.5	110	8	US-08-465-270D-10	Sequence 10, Appl
39	41	74.5	110	8	US-08-465-270E-10	Sequence 10, Appl
40	41	74.5	110	18	US-09-426-819-10	Sequence 10, Appl
41	41	74.5	116	1	PCT-US96-06804-25	Sequence 25, Appl
42	41	74.5	116	1	PCT-US96-06804A-25	Sequence 25, Appl
43	41	74.5	116	8	US-08-440-621A-25	Sequence 25, Appl
44	41	74.5	116	8	US-08-440-621B-25	Sequence 25, Appl
45	41	74.5	116	8	US-08-440-621C-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-54
; Sequence 54, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-54

Query Match 100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 |||||
Db 1 WVAKVSGGG 10

RESULT 2

US-09-339-922A-54
; Sequence 54, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-54

Query Match 100.0%; Score 55; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
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Db 1 WVAKVSGGG 10

RESULT 3

US-09-016-061-36
; Sequence 36, Application US/09016061
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; FILE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-36

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 |||||
Db 1 WVAKVSGGG 10

RESULT 4

US-09-339-922A-36
; Sequence 36, Application US/09339922A
; GENERAL INFORMATION:

; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-36

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
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Db 1 WVAKVSGGG 10

RESULT 5

PCT-US98-25828-56
; Sequence 56, Application PC/TUS9825828A
; GENERAL INFORMATION:

; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 56
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-56

Query Match          90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
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Db 47 WVAKVSGGG 56

RESULT 6
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540-2

Query Match          90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
    ||||| |||||
Db 47 WVAKVSGGG 56

RESULT 7
US-08-790-540-6
; Sequence 6, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540-6

Query Match          90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
    ||||| |||||
Db 47 WVAKVSGGG 56

RESULT 8
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-790-540A-2

Query Match          90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
Db 47 WVAKVSGGG 56

RESULT 9
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-790-540A-6

Query Match          90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
Db 47 WVAKVSGGG 56

RESULT 10
US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
|||||
DB 47 WVAKVSGGG 56

RESULT 12

US-08-791-391A-2
Sequence 2, Application US/08791391A

GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
|||||
DB 47 WVAKVSGGG 56

RESULT 13

US-08-791-391A-6

Sequence 6, Application US/08791391A

GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791.391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1482
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 90.9%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
|||||
DB 47 WVAKVSGGG 56

RESULT 14

US-08-986-016-56
Sequence 56, Application US/08986016A

GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Rader, Christoph
TITLE OF INVENTION: Humanization of Murine Antibody
FILE REFERENCE: Tsri 598.0
CURRENT APPLICATION NUMBER: US/08/986,016A
CURRENT FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 117

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-56

Query Match 90.9%; Score 50; DB 13; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10

Db 47 WYAKVSSGGG 56

RESULT 15
US-09-016-061-2
; Sequence 2, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-2

Query Match 90.9%; Score 50; DB 14; Length 117;
Best/Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WYAKVSSGGG 10
Db 47 WYAKVSSGGG 56

Search completed: March 28, 2001, 06:55:35
Job time: 1479 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:02 ; Search time 79'56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WVAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pcp.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pcp.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pcp.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pcp.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pcp.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	78.2	98	1	PCT-US01-03537-44
2	39	70.9	87	1	PCT-US01-03537-53
3	39	70.9	98	1	PCT-US01-03537-41
4	38	69.1	88	1	PCT-US01-03537-51
5	38	69.1	120	1	PCT-US00-26619-17
6	38	69.1	124	5	US-09-518-737-2
7	37	67.3	89	1	PCT-US01-03537-49
8	37	67.3	98	1	PCT-US01-03537-38
9	37	67.3	98	1	PCT-US01-03537-39
10	37	67.3	409	5	US-09-720-841-6
11	35	63.6	1102	6	US-60-259-128-4912
12	34	61.8	191	5	US-09-107-433-3931
13	34	61.8	250	1	PCT-US00-26619-8
14	34	61.8	259	6	US-60-258-016-34
15	34	61.8	347	5	US-09-489-039A-11579
16	33	60.0	98	1	PCT-US01-03537-45
17	33	60.0	124	1	PCT-US01-03537-89
18	33	60.0	218	5	US-09-489-039A-10326
19	33	60.0	300	5	US-09-188-082-4
20	33	60.0	301	5	US-09-188-082-14
21	33	60.0	553	5	US-09-188-082-16
22	32	58.2	111	5	US-09-489-039A-10282
23	32	58.2	120	5	US-09-482-352A-8
24	32	58.2	162	5	US-09-489-039A-9372
25	31	56.4	114	5	US-09-716-028-11
26	31	56.4	118	5	US-09-465-587-284
27	31	56.4	119	4	US-08-478-684G-11

28	31	56.4	170	5	US-09-522-433A-27	Sequence 27, Appl
29	31	56.4	170	5	US-09-522-433B-27	Sequence 27, Appl
30	31	56.4	229	5	US-09-716-028-21	Sequence 21, Appl
31	31	56.4	233	5	US-09-716-028-26	Sequence 26, Appl
32	31	56.4	248	5	US-09-716-028-23	Sequence 23, Appl
33	31	56.4	309	5	US-09-489-039A-7532	Sequence 7532, Ap
34	31	56.4	342	5	US-09-489-039A-7914	Sequence 7914, Ap
35	31	56.4	357	5	US-09-404-296A-10	Sequence 10, Appl
36	31	56.4	424	5	US-09-107-433-5202	Sequence 5202, Ap
37	31	56.4	451	5	US-09-716-028-18	Sequence 18, Appl
38	31	56.4	537	5	US-09-489-039A-14149	Sequence 14149, A
39	31	56.4	602	5	US-09-489-039A-11694	Sequence 11694, A
40	31	56.4	729	6	US-60-266-847-22	Sequence 22, Appl
41	31	56.4	735	5	US-09-636-791A-13	Sequence 13, Appl
42	31	56.4	1744	5	US-09-488-725A-2185	Sequence 2185, Ap
43	30	54.5	62	5	US-09-595-298A-1602	Sequence 1602, Ap
44	30	54.5	67	5	US-09-595-298A-1600	Sequence 1600, Ap
45	30	54.5	77	5	US-09-316-633-332	Sequence 332, App

ALIGNMENTS

RESULT 1
PCT-US01-03537-44
; Sequence 44, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-44

Query Match 78.2%; Score 43; DB 1; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGGG 10
||| : ||||
Db 47 WVAITSSGGG 56

RESULT 2
PCT-US01-03537-53
; Sequence 53, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

```

; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-53

```

```

Query Match          70.9%; Score 39; DB 1; Length 87;
Best Local Similarity 60.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 WVAKVSGGG 10
   ||| : |||
DB 36 WWAYISGGG 45

```

```

RESULT 3
PCT-US01-03537-41
; Sequence 41, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Theresa
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-41

```

```

Query Match          70.9%; Score 39; DB 1; Length 98;
Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 WVAKVSGGG 10
   ||| : |||
DB 47 WWAYISGGG 56

```

```

RESULT 4
PCT-US01-03537-51
; Sequence 51, Application PC/TUS0103537

```

```

; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows, Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-51

```

```

Query Match          69.1%; Score 38; DB 1; Length 88;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 WVAKVSGG 9
   ||| : |||
DB 38 WVASISGG 46

```

```

RESULT 5
PCT-US00-26619-17
; Sequence 17, Application PC/TUS0026619
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Chmura, Albert
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Engineering Antibodies That Bind Irreversibly
; FILE REFERENCE: 023070-099120PC
; CURRENT APPLICATION NUMBER: PCT/US00/26619
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,194
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/208,684
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: V-H sequence of
; OTHER INFORMATION: CHA255
PCT-US00-26619-17

```

```

Query Match          69.1%; Score 38; DB 1; Length 120;
Best Local Similarity 70.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 WVAKVSGGG 10
   ||| : |||
DB 47 WVATLSGGG 56

```

RESULT 6
US-09-518-737-2
; Sequence 2, Application US/09518737
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2

Query Match 69.1%; Score 38; DB 5; Length 124;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 1 WVAKVSGG 9
Db 47 WVASISGG 55

RESULT 7
PCT-US01-03537-49
; Sequence 49, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-49

Query Match 67.3%; Score 37; DB 1; Length 89;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 1 WVAKVSGG 9
Db 38 WVASISGG 46

RESULT 8
PCT-US01-03537-38
; Sequence 38, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-38

Query Match 67.3%; Score 37; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

Qy 1 WVAKVSGG 9
Db 47 WVASISGG 55

RESULT 9
PCT-US01-03537-39
; Sequence 39, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-39

Query Match 67.3%; Score 37; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 5.3;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
|||: |||

Db 47 WVAISSGG 55

RESULT 10

US-09-720-841-6
; Sequence 6, Application US/09720841
; GENERAL INFORMATION:
; APPLICANT: Biotica Technology Limited
; APPLICANT: Leadlay, Peter F
; APPLICANT: Pfizer, Inc.
; APPLICANT: Staunton, James
; APPLICANT: Cortes, Jesus
; APPLICANT: McArthur, Hamish AI
; TITLE OF INVENTION: Polyketides and their synthesis
; FILE REFERENCE: IS/CP578/585
; CURRENT APPLICATION NUMBER: US/09/720,841
; CURRENT FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: GB 9814006.4
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Streptomyces nogalater
US-09-720-841-6

Query Match 67.3%; Score 37; DB 5; Length 409;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
|||: |||

Db 198 WVAQLSSGG 206

RESULT 11

US-60-259-128-4912
; Sequence 4912, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4912
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4912

Query Match 63.6%; Score 35; DB 6; Length 1102;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 10
|||: |||

Db 657 WVAIKSISG 666

RESULT 12

US-09-107-433-3931
; Sequence 3931, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: CTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3931:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...191
; SEQUENCE DESCRIPTION: SEQ ID NO: 3931:
US-09-107-433-3931

Query Match 61.8%; Score 34; DB 5; Length 191;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAKVSGG 9
|||: |||

Db 137 WVAQKSGG 145

RESULT 13

PCT-US00-26619-8
; Sequence 8, Application PC/TUS0026619
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Chmura, Albert
; TITLE OF INVENTION: The Regents of the University of California
; Engineering Antibodies That Bind Irreversibly
; FILE REFERENCE: 023070-099120PC
; CURRENT APPLICATION NUMBER: PCT/US00/26619
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,194
; PRIOR FILING DATE: 1999-09-27

PROR APPLICATION NUMBER: US 60/208,684
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 250
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: polypeptide
OTHER INFORMATION: sequence of unmodified heavy chain of CHA255
PCT-US00-26619-8

Query Match 61.8%; Score 34; DB 1; Length 250;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WVAKVKGSGG 10
|| ||||
Db 49 WTTTSLGGG 58

RESULT 14
US-60-258-016-34
Sequence 34, Application US/60258016
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET ENZYMES,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET ENZYMES,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001037-PROV
CURRENT APPLICATION NUMBER: US/60/258.016
CURRENT FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 259
TYPE: PRT
ORGANISM: Human
US-60-258-016-34

Query Match 61.8%; Score 34; DB 6; Length 259;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAKVKGSGG 10
|| ||||
Db 186 WVDVKNKGK 195

RESULT 15
US-09-489-039A-11579
Sequence 11579, Application US/09489039A
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11579
LENGTH: 347
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11579

Query Match 61.8%; Score 34; DB 5; Length 347;

Best Local Similarity 50.0%; Pred. No. 64;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WVAKVKGSGG 10
|| ||||
Db 334 WLSAVPAGGG 343
Search completed: March 28, 2001, 06:57:02
Job time: 1351 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:35 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYPTDVTQV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgnl_7/ptodata/1/paa/PTUS_COMB.pep.*
2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
13: /cgnl_7/ptodata/1/paa/US089_COMB.pep.*
14: /cgnl_7/ptodata/1/paa/US090_COMB.pep.*
15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	14	US-09-016-061-56
2	56	100.0	10	17	US-09-339-922A-56
3	56	100.0	17	17	US-09-339-922A-104
4	52	92.9	87	18	US-09-497-625-53
5	52	92.9	98	18	US-09-497-625-41
6	52	92.9	120	10	US-08-617-835-2
7	52	92.9	120	11	US-08-743-788-43
8	52	92.9	120	11	US-08-743-788-47
9	52	92.9	120	11	US-08-743-788-48
10	52	92.9	120	11	US-08-743-788-49
11	52	92.9	120	11	US-08-743-788-50

12	52	92.9	120	11	US-08-743-788-55
13	52	92.9	121	11	US-08-743-788-39
14	52	92.9	125	7	US-08-331-396C-65
15	52	92.9	125	7	US-08-331-396D-64
16	52	92.9	158	10	US-08-653-402-6
17	52	92.9	158	10	US-08-653-402-10
18	49	87.5	123	17	US-09-381-497-2
19	48	85.7	88	18	US-09-497-625-51
20	48	85.7	89	18	US-09-497-625-48
21	48	85.7	108	3	US-07-881-109-26
22	48	85.7	108	3	US-07-881-109A-26
23	48	85.7	108	7	US-08-313-198-26
24	48	85.7	108	11	US-08-720-323-26
25	48	85.7	119	4	US-08-090-534-6
26	48	85.7	121	15	US-09-134-197-3
27	48	85.7	121	18	US-09-438-136-90
28	48	85.7	121	18	US-09-438-136-92
29	48	85.7	121	18	US-09-438-136-113
30	48	85.7	121	18	US-09-438-136-125
31	48	85.7	121	18	US-09-438-136-126
32	48	85.7	121	18	US-09-438-136-133
33	48	85.7	130	7	US-08-398-614A-22
34	48	85.7	130	7	US-08-398-616A-22
35	48	85.7	130	12	US-08-804-444-22
36	48	85.7	130	14	US-09-012-116-19
37	48	85.7	130	15	US-09-121-952A-19
38	48	85.7	130	15	US-09-122-513A-19
39	48	85.7	130	16	US-09-234-182A-19
40	48	85.7	130	18	US-09-489-394-19
41	48	85.7	135	9	US-08-579-378A-16
42	48	85.7	135	9	US-08-579-378A-20
43	48	85.7	247	4	US-08-090-534-2
44	48	85.7	251	12	US-08-804-444-30
45	48	85.7	251	14	US-09-012-116-27

ALIGNMENTS

RESULT 1
US-09-016-061-56
; Sequence 56, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-56

Query Match 100.0%; Score 56; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
| | | | | | | | | |
Db 1 STYYPDTVQG 10

RESULT 2

US-09-339-922A-56
; Sequence 56, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
US-09-339-922A-56

Query Match 100.0%; Score 56; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
| | | | | | | | | |
Db 1 STYYPDTVQG 10

RESULT 3

US-09-339-922A-104
; Sequence 104, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
US-09-339-922A-104

Query Match 100.0%; Score 56; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
| | | | | | | | | |
Db 8 STYYPDTVQG 17

RESULT 4

US-09-497-625-53
; Sequence 53, Application US/09497625
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625-53

Query Match 92.9%; Score 52; DB 18; Length 87;
Best Local Similarity 90.0%; Pred. No. 0.024; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;

Qy 1 STYYPDTVQG 10
| | | | | | | | | |
Db 46 STYYPDTVKG 55

RESULT 5

US-09-497-625-41
; Sequence 41, Application US/09497625
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625-41

Query Match 92.9%; Score 52; DB 18; Length 98;
Best Local Similarity 90.0%; Pred. No. 0.027;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||:|
Db 57 STYYPDTVKG 66

RESULT 6

US-08-617-835-2
; Sequence 2, Application US/08617835
; GENERAL INFORMATION:
; APPLICANT: STIRPE Firenze, BOLOGNESI Andrea,
; APPLICANT: MELE Antonio, DE SANTIS Rita
; TITLE OF INVENTION: RIBOSOME INACTIVATING PROTEINS
; TITLE OF INVENTION: EXTRACTED FROM SEEDS OF SAPONARIA OCYMOIDES AND VACCARIA
; TITLE OF INVENTION: PYRAMIDATA, THEIR PREPARATION AND IMMUNOTOXINS CONTAINING
; TITLE OF INVENTION: THEM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABELMAN, FRAYNE & SCHWAB
; STREET: 150 East 42nd Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017-5612
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch.
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WS4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,835
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02969
; FILING DATE: 06-SEP-1994
; APPLICATION NUMBER: IT FI 93 A 000171
; FILING DATE: 06-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT FI 93 A 000172
; FILING DATE: 06-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JAY S. CINAMON
; REGISTRATION NUMBER: 24,156
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-949-9022
; TELEFAX: 212-949-9190
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-617-835-2

Query Match 92.9%; Score 52; DB 10; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||:|
Db 57 STYYPDTVKG 66

RESULT 7

US-08-743-788-43

; Sequence 43, Application US/08743788
; GENERAL INFORMATION:
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Tarran
; APPLICANT: SALDANA, Jose
; TITLE OF INVENTION: Humanized Monoclonal Antibody
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,788
; FILING DATE: 05-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96177154.3
; FILING DATE: 25-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95117407.7
; FILING DATE: 06-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-743-788-43

Query Match 92.9%; Score 52; DB 11; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||:|
Db 57 STYYPDTVKG 66

RESULT 8

US-08-743-788-47
; Sequence 47, Application US/08743788
; GENERAL INFORMATION:
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Tarran
; APPLICANT: SALDANA, Jose
; TITLE OF INVENTION: Humanized Monoclonal Antibody
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,788
;; FILING DATE: 05-NOV-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 96177154.3
;; FILING DATE: 25-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95117407.7
;; FILING DATE: 06-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lebovitz, Richard M.
;; REGISTRATION NUMBER: 37,067
;; REFERENCE/DOCKET NUMBER: MERCK 1819
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-243-6333
;; TELEFAX: 703-243-6410
;; INFORMATION FOR SEQ ID NO: 47:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 120 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..120
;; OTHER INFORMATION: /note= "Mab 15 heavy chain variable
;; region, VH15 version"
US-08-743-788-47

Query Match 92.9%; Score 52; DB 11; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPPDTVQG 10
Db 57 STYPPDTVKG 66

RESULT 9
US-08-743-788-48
;; Sequence 48, Application US/08743788
;; GENERAL INFORMATION:
;; APPLICANT: BENDIG, Mary
;; APPLICANT: JONES, Tarran
;; APPLICANT: SALDANA, Jose
;; TITLE OF INVENTION: Humanized Monoclonal Antibody
;; NUMBER OF SEQUENCES: 55
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
;; STREET: 2200 Clarendon Blvd.
;; CITY: Arlington
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22201
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,788
;; FILING DATE: 05-NOV-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 96177154.3

;; FILING DATE: 25-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95117407.7
;; FILING DATE: 06-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lebovitz, Richard M.
;; REGISTRATION NUMBER: 37,067
;; REFERENCE/DOCKET NUMBER: MERCK 1819
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-243-6333
;; TELEFAX: 703-243-6410
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 120 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..120
;; OTHER INFORMATION: /note= "Reshaped MAB 15, heavy
;; chain variabel region, RVHa version"
US-08-743-788-48

Query Match 92.9%; Score 52; DB 11; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPPDTVQG 10
Db 57 STYPPDTVKG 66

RESULT 10
US-08-743-788-49
;; Sequence 49, Application US/08743788
;; GENERAL INFORMATION:
;; APPLICANT: BENDIG, Mary
;; APPLICANT: JONES, Tarran
;; APPLICANT: SALDANA, Jose
;; TITLE OF INVENTION: Humanized Monoclonal Antibody
;; NUMBER OF SEQUENCES: 55
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
;; STREET: 2200 Clarendon Blvd.
;; CITY: Arlington
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22201
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,788
;; FILING DATE: 05-NOV-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 96177154.3
;; FILING DATE: 25-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95117407.7
;; FILING DATE: 06-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lebovitz, Richard M.
;; REGISTRATION NUMBER: 37,067
;; REFERENCE/DOCKET NUMBER: MERCK 1819

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
OTHER INFORMATION: /note= "Reshaped Mab 15, heavy
OTHER INFORMATION: chain variable region, RVHb version"
US-08-743-788-49

Query Match 92.9%; Score 52; DB 11; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVQ 10
|||||||:|
Db 57 STYYPDVTQVG 66

RESULT 11

US-08-743-788-50
Sequence 50, Application US/08743788
GENERAL INFORMATION:
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Tarran
APPLICANT: SALDANA, Jose
TITLE OF INVENTION: Humanized Monoclonal Antibody
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd.
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,788
FILING DATE: 05-NOV-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96177154.3
FILING DATE: 25-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95117407.7
FILING DATE: 06-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1819
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
OTHER INFORMATION: /note= "Reshaped Mab 15, heavy
OTHER INFORMATION: chain variable region, RVHC version"
US-08-743-788-50

Query Match 92.9%; Score 52; DB 11; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVQ 10
|||||||:|
Db 57 STYYPDVTQVG 66

RESULT 12

US-08-743-788-55
Sequence 55, Application US/08743788
GENERAL INFORMATION:
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Tarran
APPLICANT: SALDANA, Jose
TITLE OF INVENTION: Humanized Monoclonal Antibody
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd.
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,788
FILING DATE: 05-NOV-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96177154.3
FILING DATE: 25-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95117407.7
FILING DATE: 06-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1819
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-743-788-55

Query Match 92.9%; Score 52; DB 11; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVOG 10
Db 57 STYYPDTVKG 66

RESULT 13
US-08-743-788-39
; Sequence 39, Application US/08743788
; GENERAL INFORMATION:
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Tarran
; APPLICANT: SALDANA, Jose
; TITLE OF INVENTION: Humanized Monoclonal Antibody
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millien, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,788
; FILING DATE: 05-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96177154.3
; FILING DATE: 25-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95117407.7
; FILING DATE: 06-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-743-788-39

Query Match 92.9%; Score 52; DB 11; Length 121;
Best Local Similarity 90.0%; Pred. No. 0.035; 0; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0

QY 1 STYYPDTVOG 10
Db 57 STYYPDTVKG 66

RESULT 14
US-08-331-396C-65
; Sequence 65, Application US/08331396C
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,
; .TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396C
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-1261300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..125
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
; OTHER INFORMATION: Heavy chain region"
US-08-331-396C-65

Query Match 92.9%; Score 52; DB 7; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.036; 0; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0

QY 1 STYYPDTVOG 10
Db 57 STYYPDTVKG 66

RESULT 15
US-08-331-396D-64
; Sequence 64, Application US/08331396D
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody
; .TITLE OF INVENTION: Fragments, Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,396D
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126130US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..125
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
US-08-331-396D-64

Query Match 92.9%; Score 52; DB 7; Length 125;
Best Local Similarity 90.0%; Pred. No. 0.036;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
|
Db 57 STYYPDTVKG 66

Search completed: March 28, 2001, 06:55:36
Job time: 1480 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:02 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYVPDVTQV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgnl_7/prodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_7/prodata/2/paa/US06_NEW_COMB.pep.*
3: /cgnl_7/prodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/prodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/prodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	92.9	87	1	PCT-US01-03537-53
2	52	92.9	98	1	PCT-US01-03537-41
3	48	85.7	88	1	PCT-US01-03537-51
4	48	85.7	89	1	PCT-US01-03537-48
5	48	85.7	130	5	US-09-726-258-19
6	48	85.7	251	5	US-09-726-258-27
7	45	80.4	98	1	PCT-US01-03537-44
8	44	78.6	30	5	US-09-568-341-6
9	44	78.6	89	1	PCT-US01-03537-49
10	44	78.6	98	1	PCT-US01-03537-38
11	44	78.6	98	1	PCT-US01-03537-39
12	44	78.6	98	1	PCT-US01-03537-45
13	44	78.6	120	5	US-09-482-352A-8
14	44	78.6	124	5	US-09-518-737-2
15	44	78.6	300	5	US-09-188-082-4
16	44	78.6	301	5	US-09-188-082-14
17	44	78.6	553	5	US-09-188-082-16
18	41	73.2	124	1	PCT-US01-03537-81
19	40	71.4	17	5	US-09-430-048-38
20	40	71.4	17	5	US-09-780-035-21
21	40	71.4	17	5	US-09-780-035-26
22	40	71.4	98	5	US-09-430-048-35
23	40	71.4	98	5	US-09-430-048-36
24	40	71.4	108	5	US-09-780-035-28
25	40	71.4	112	5	US-09-430-048-14
26	40	71.4	112	5	US-09-430-048-15
27	40	71.4	113	5	US-09-194-356A-8

28 40 71.4 116 1 PCT-US01-03537-80 Sequence 80, Appl
29 40 71.4 117 1 PCT-US01-03537-83 Sequence 83, Appl
30 40 71.4 117 5 US-09-385-673-15 Sequence 15, Appl
31 40 71.4 118 5 US-09-780-035-67 Sequence 67, Appl
32 40 71.4 120 1 PCT-US01-03537-85 Sequence 85, Appl
33 40 71.4 121 1 PCT-US01-03537-92 Sequence 92, Appl
34 40 71.4 121 5 US-09-194-356A-9 Sequence 9, Appl
35 40 71.4 124 1 PCT-US01-03537-89 Sequence 89, Appl
36 40 71.4 125 1 PCT-US01-03537-76 Sequence 76, Appl
37 40 71.4 125 1 PCT-US01-03537-84 Sequence 84, Appl
38 40 71.4 127 1 PCT-US01-03537-87 Sequence 87, Appl
39 40 71.4 128 1 PCT-US01-03537-77 Sequence 77, Appl
40 40 71.4 128 1 PCT-US01-03537-78 Sequence 78, Appl
41 40 71.4 128 1 PCT-US01-03537-79 Sequence 79, Appl
42 40 71.4 130 5 US-09-341-711-54 Sequence 54, Appl
43 40 71.4 235 5 US-09-780-035-30 Sequence 30, Appl
44 40 71.4 238 5 US-09-430-048-24 Sequence 24, Appl
45 39 69.6 120 5 US-09-530-237-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
PCT-US01-03537-53
; Sequence 53, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-53

Query Match 92.9% ; Score 52; DB 1; Length 87;
Best Local Similarity 90.0% ; Pred. No. 0.0037;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYVPDVTQV 10
Db 46 STYVPDVTQV 55

RESULT 2
PCT-US01-03537-41
; Sequence 41, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

```

; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-41

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```

Query Match      92.9%; Score 52; DB 1; Length 98;
Best Local Similarity 90.0%; Pred. No. 0.0042;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 STYYPDVTQVG 10
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Db 57 STYYPDVTQVG 66

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RESULT 3
PCT-US01-03537-51
; Sequence 51, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-51

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```

Query Match      85.7%; Score 48; DB 1; Length 88;
Best Local Similarity 80.0%; Pred. No. 0.02;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 STYYPDVTQVG 10
   |||||:|:|
Db 47 STYYPDVTQVG 56

```

```

RESULT 4
PCT-US01-03537-48
; Sequence 48, Application PC/TUS0103537

```

```

; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-48

Query Match      85.7%; Score 48; DB 1; Length 89;
Best Local Similarity 80.0%; Pred. No. 0.02;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTQVG 10
   |||||:|:|
Db 48 STYYPDVTQVG 57

RESULT 5
US-09-726-258-19
; Sequence 19, Application US/09726258
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:

```


NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-726-258-19

Query Match 85.7%; Score 48; DB 5; Length 130;
Best Local Similarity 80.0%; Pred. No. 0.031;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 57 STYYPDSVKG 66
|||||:|

RESULT 6
US-09-726-258-27
Sequence 27, Application US/09726258
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahtokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-726-258-27

Query Match 85.7%; Score 48; DB 5; Length 251;
Best Local Similarity 80.0%; Pred. No. 0.063;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 80 STYYPDSVKG 89
|||||:|

RESULT 7
PCT-US01-03537-44
Sequence 44, Application PC/TUS0103537
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052005
CURRENT APPLICATION NUMBER: PCT/US01/03537
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 98
TYPE: PRT
ORGANISM: Mus musculus
PCT-US01-03537-44

Query Match 80.4%; Score 45; DB 1; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.08;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 57 NTYYPDSVKG 66
|||||:|

RESULT 8
US-09-568-341-6
Sequence 6, Application US/09568341
GENERAL INFORMATION:
APPLICANT: TRANSGENE SA
TITLE OF INVENTION: Antitumoral complexes
FILE REFERENCE: Antitumoral complexes
CURRENT APPLICATION NUMBER: US/09/368,341
CURRENT FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-09-568-341-6

Query Match 78.6%; Score 44; DB 5; Length 30;
Best Local Similarity 80.0%; Pred. No. 0.034;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
|||||:|

Db 10 STYSDTVQK 19

```
RESULT 9
PCT-US01-03537-49
; Sequence 49, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 09/497,625
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-49
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Query Match 78.6%; Score 44; DB 1; Length 89;
Best Local Similarity 77.8%; Pred. No. 0.11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQK 10
Db 49 TYYPDSVKG 57
|||||:|

```
RESULT 10
PCT-US01-03537-38
; Sequence 38, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 09/497,625
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-38
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Query Match 78.6%; Score 44; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQK 10
Db 58 TYYPDSVKG 66
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RESULT 11
PCT-US01-03537-39
; Sequence 39, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-39
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Query Match 78.6%; Score 44; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQK 10
Db 58 TYYPDSVKG 66
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```
RESULT 12
PCT-US01-03537-45
; Sequence 45, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
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; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-45

Query Match 78.6%; Score 44; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYYPDTVOG 10
| | | | | : | |
Db 58 TYYPDSVKG 66

RESULT 13

US-09-482-352A-8
; Sequence 8, Application US/09482352A
; GENERAL INFORMATION:
; APPLICANT: DE PRAT GAY, Gonzalo
; APPLICANT: GOLDBAUM, Fernando
; APPLICANT: CERUTTI, Maria Laura
; TITLE OF INVENTION: SEQUENCE-SPECIFIC, HIGH AFFINITY ANTI-DNA MONOCLONAL ANTIBODIES
; FILE REFERENCE: 2038/48555
; CURRENT APPLICATION NUMBER: US/09/482,352A
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: amino acid sequence of the variable region of the heavy chain of
; OTHER INFORMATION: the mouse monoclonal antibody ED-8
US-09-482-352A-8

Query Match 78.6%; Score 44; DB 5; Length 120;
Best Local Similarity 77.8%; Pred. No. 0.15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYYPDTVOG 10
| | | | | : | |
Db 59 TYYPDSVKG 67

RESULT 14

US-09-518-737-2
; Sequence 2, Application US/09518737
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHISA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2

Query Match 78.6%; Score 44; DB 5; Length 124;
Best Local Similarity 77.8%; Pred. No. 0.16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYYPDTVOG 10
| | | | | : | |
Db 58 TYYPDSVKG 66

RESULT 15

US-09-188-082-4
; Sequence 4, Application US/09188082
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-188-082-4

Query Match 78.6%; Score 44; DB 5; Length 300;
Best Local Similarity 77.8%; Pred. No. 0.41;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYYPDTVOG 10
| | | | | : | |
Db 58 TYYPDSVKG 66

Search completed: March 28, 2001, 06:57:03
Job time: 1552 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:36 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STVYLDVTEG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgnl_7/ptodata/1/paa/US08_COMB.pep.*
- 5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
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- 19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
- 20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	53	100.0	10	US-09-016-061-58
2	53	100.0	10	US-09-339-922A-58
3	50	94.3	10	US-09-016-061-38
4	50	94.3	10	US-09-339-922A-38
5	50	94.3	17	US-09-339-922A-102
6	50	94.3	117	PCT-US98-25828-56
7	50	94.3	117	US-08-790-540-2
8	50	94.3	117	US-08-790-540A-6
9	50	94.3	117	US-08-790-540A-2
10	50	94.3	117	US-08-790-540A-6
11	50	94.3	117	US-08-791-391-2

12	50	94.3	117	11	US-08-791-391-6	Sequence 6, Appl
13	50	94.3	117	11	US-08-791-391A-2	Sequence 2, Appl
14	50	94.3	117	11	US-08-791-391A-6	Sequence 6, Appl
15	50	94.3	117	13	US-08-986-016-56	Sequence 56, Appl
16	50	94.3	117	14	US-09-016-061-2	Sequence 2, Appl
17	50	94.3	117	14	US-09-016-061-6	Sequence 6, Appl
18	50	94.3	117	17	US-09-339-922A-2	Sequence 2, Appl
19	50	94.3	117	17	US-09-339-922A-6	Sequence 6, Appl
20	50	94.3	130	1	PCT-US98-25828-44	Sequence 44, Appl
21	50	94.3	130	13	US-08-986-016-44	Sequence 44, Appl
22	44	83.0	124	18	US-09-497-625-81	Sequence 81, Appl
23	43	81.1	10	14	US-09-016-061-56	Sequence 56, Appl
24	43	81.1	10	17	US-09-339-922A-56	Sequence 56, Appl
25	43	81.1	17	17	US-09-339-922A-104	Sequence 104, App
26	43	81.1	30	17	US-09-336-093-4	Sequence 4, Appl
27	43	81.1	30	19	US-09-557-465-4	Sequence 4, Appl
28	42	79.2	87	18	US-09-497-625-53	Sequence 53, Appl
29	42	79.2	98	18	US-09-497-625-41	Sequence 41, Appl
30	42	79.2	120	10	US-08-617-835-2	Sequence 2, Appl
31	42	79.2	120	11	US-08-743-788-43	Sequence 43, Appl
32	42	79.2	120	11	US-08-743-788-47	Sequence 47, Appl
33	42	79.2	120	11	US-08-743-788-48	Sequence 48, Appl
34	42	79.2	120	11	US-08-743-788-49	Sequence 49, Appl
35	42	79.2	120	11	US-08-743-788-50	Sequence 50, Appl
36	42	79.2	120	11	US-08-743-788-55	Sequence 55, Appl
37	42	79.2	121	11	US-08-743-788-39	Sequence 39, Appl
38	42	79.2	125	7	US-08-331-396C-65	Sequence 65, Appl
39	42	79.2	125	7	US-08-331-396D-64	Sequence 64, Appl
40	42	79.2	127	3	US-07-868-983-3	Sequence 3, Appl
41	42	79.2	158	10	US-08-653-402-6	Sequence 6, Appl
42	42	79.2	158	10	US-08-653-402-10	Sequence 10, Appl
43	41	77.4	13	18	US-09-438-136-51	Sequence 51, Appl
44	41	77.4	13	18	US-09-438-136-77	Sequence 77, Appl
45	41	77.4	117	11	US-08-752-693A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-016-061-58
; Sequence 58, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-58

Query Match          100.0%; Score 53; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 1 STYYLDTVEG 10
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RESULT 2
US-09-339-922A-58
; Sequence 58, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-58

Query Match          100.0%; Score 53; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 1 STYYLDTVEG 10
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RESULT 3
US-09-016-061-38
; Sequence 38, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-38

Query Match          94.3%; Score 50; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0033;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 1 STYYLDTVEG 10
|||||

RESULT 4
US-09-339-922A-38
; Sequence 38, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-38

Query Match          94.3%; Score 50; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0033;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 1 STYYLDTVEG 10
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RESULT 5
US-09-339-922A-102
; Sequence 102, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
```

SEQ ID NO 102
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-102

Query Match 94.3%; Score 50; DB 17; Length 17;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
Db 8 STYLDTVQV 17
|||||

RESULT 6
PCT-US98-25828-56
Sequence 56, Application PC/TUS9825828A
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
FILE REFERENCE: TSRI 598.0
CURRENT APPLICATION NUMBER: PCT/US98/25828A
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 08/986,016
EARLIER FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 117
TYPE: PRT
ORGANISM: Murine hybridoma LM609
PCT-US98-25828-56

Query Match 94.3%; Score 50; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
Db 57 STYLDTVQV 66
|||||

RESULT 7
US-08-790-540-2
Sequence 2, Application US/08790540
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540-2

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
Db 57 STYLDTVQV 66
|||||

RESULT 8
US-08-790-540-6
Sequence 6, Application US/08790540
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-540-6

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYLDTVQV 10
Db 57 STYLDTVQV 66
|||||

```
RESULT 9
US-08-790-540A-2
; Sequence 2, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790.540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66

RESULT 10
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790.540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66
```

```
RESULT 11
US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66
```

RESULT 12
US-08-791-391-6
; Sequence 6, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391-6

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66
|||||||:|

RESULT 13
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-2

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYLDTVEG 10
Db 57 STYYLDTVQG 66
|||||||:|

RESULT 14
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-391A-6

Query Match 94.3%; Score 50; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 57 STYYLDTVQG 66

RESULT 15
US-08-986-016-56
; Sequence 56, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsri 598.0
; CURRENT APPLICATION NUMBER: US/08/986.016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-56

Query Match 94.38; Score 50; DB 13; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.055;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 57 STYYLDTVQG 66

Search completed: March 28, 2001, 06:55:36
Job time: 1480 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:03 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYYLDVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	44	83.0	124	1	PCT-US01-03537-81
2	43	81.1	730	5	US-09-568-341-6
3	42	79.2	87	1	PCT-US01-03537-53
4	42	79.2	98	1	PCT-US01-03537-41
5	40	75.5	17	5	US-09-430-048-38
6	40	75.5	17	5	US-09-780-035-21
7	40	75.5	17	5	US-09-780-035-26
8	40	75.5	98	5	US-09-430-048-35
9	40	75.5	98	5	US-09-430-048-36
10	40	75.5	108	5	US-09-780-035-28
11	40	75.5	112	5	US-09-430-048-14
12	40	75.5	112	5	US-09-430-048-15
13	40	75.5	113	5	US-09-194-356A-8
14	40	75.5	116	1	PCT-US01-03537-80
15	40	75.5	117	1	PCT-US01-03537-83
16	40	75.5	117	5	US-09-385-673-15
17	40	75.5	118	5	US-09-780-035-67
18	40	75.5	120	1	PCT-US01-03537-85
19	40	75.5	121	1	PCT-US01-03537-92
20	40	75.5	121	5	US-09-194-356A-9
21	40	75.5	124	1	PCT-US01-03537-89
22	40	75.5	125	1	PCT-US01-03537-76
23	40	75.5	125	1	PCT-US01-03537-84
24	40	75.5	127	1	PCT-US01-03537-87
25	40	75.5	128	1	PCT-US01-03537-77
26	40	75.5	128	1	PCT-US01-03537-78
27	40	75.5	128	1	PCT-US01-03537-79

28 40 75.5 130 5 US-09-341-711-54 Sequence 54, Appl
29 40 75.5 235 5 US-09-780-035-30 Sequence 30, Appl
30 40 75.5 238 5 US-09-430-048-24 Sequence 24, Appl
31 39 73.6 120 5 US-09-530-237-1 Sequence 1, Appl
32 38 71.7 88 1 PCT-US01-03537-51 Sequence 51, Appl
33 38 71.7 89 1 PCT-US01-03537-48 Sequence 48, Appl
34 38 71.7 130 5 US-09-726-258-19 Sequence 19, Appl
35 38 71.7 251 5 US-09-726-258-27 Sequence 27, Appl
36 37 69.8 19 5 US-09-532-106-4 Sequence 4, Appl
37 37 69.8 27 5 US-09-532-106-21 Sequence 21, Appl
38 37 69.8 123 1 PCT-US01-03537-82 Sequence 82, Appl
39 37 69.8 571 5 US-09-489-039A-10805 Sequence 10805, A
40 36 67.9 121 5 US-09-716-028-4 Sequence 4, Appl
41 36 67.9 133 5 US-09-214-027A-21 Sequence 21, Appl
42 35 66.0 17 4 US-08-478-684G-2 Sequence 2, Appl
43 35 66.0 17 5 US-09-780-035-27 Sequence 27, Appl
44 35 66.0 89 1 PCT-US01-03537-50 Sequence 50, Appl
45 35 66.0 98 1 PCT-US01-03537-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
PCT-US01-03537-81
; Sequence 81, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03537-81

Query Match 83.0% Score 44; DB 1; Length 124;
Best Local Similarity 80.0%; Pred.No. 0.031;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDVEG 10
|||||:||||
Db 57 STYYADSVEG 66

RESULT 2
US-09-568-341-6
; Sequence 6, Application US/09568341
; GENERAL INFORMATION:
; APPLICANT: TRANSGENE SA
; TITLE OF INVENTION: Antitumoral complexes
; FILE REFERENCE: Antitumoral complexes
; CURRENT APPLICATION NUMBER: US/09/568,341
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-368-341-6

Query Match 81.1%; Score 43; DB 5; Length 30;
Best Local Similarity 80.0%; Pred. No. 0.01;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
 |||||:|
Db 10 STYYSDTVKG 19

RESULT 3
PCT-US01-03537-53
; Sequence 53, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-53

Query Match 79.2%; Score 42; DB 1; Length 87;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
 |||||:|
Db 46 STYYSDTVKG 55

RESULT 4
PCT-US01-03537-41
; Sequence 41, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-41

Query Match 79.2%; Score 42; DB 1; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
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Db 57 STYYSDTVKG 66

RESULT 5
US-09-430-048-38
; Sequence 38, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-38

Query Match 75.5%; Score 40; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.022;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVG 10
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Db 8 STYYADSVKG 17

RESULT 6
US-09-780-035-21
; Sequence 21, Application US/09780035
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tarig et al.
; TITLE OF INVENTION: ANTIBODIES THAT BIND HUMAN INTERLEUKIN-18 AND METHODS
; TITLE OF INVENTION: OF MAKING AND USING
; FILE REFERENCE: BBI-149
; CURRENT APPLICATION NUMBER: US/09/780,035
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,608
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-035-21

Query Match 75.5%; Score 40; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.022;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDIVTEG 10
| | | | : | : |
Db 8 STYADSVKG 17

RESULT 7
US-09-780-035-26
; Sequence 26, Application US/097800035
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tarig et al.
; TITLE OF INVENTION: ANTIBODIES THAT BIND HUMAN INTERLEUKIN-18 AND METHODS
; FILE REFERENCE: BBI-149
; CURRENT APPLICATION NUMBER: US/09/780,035
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,608
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-035-26

Query Match 75.5%; Score 40; DB 5; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.022;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDIVTEG 10
| | | | : | : |
Db 8 STYADSVKG 17

RESULT 8
US-09-430-048-35
; Sequence 35, Application US/094300048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-35

Query Match 75.5%; Score 40; DB 5; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDIVTEG 10
| | | | : | : |
Db 57 STYADSVKG 66

RESULT 9
US-09-430-048-36

Sequence 36, Application US/094300048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-36

Query Match 75.5%; Score 40; DB 5; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDIVTEG 10
| | | | : | : |
Db 57 STYADSVKG 66

RESULT 10
US-09-780-035-28
; Sequence 28, Application US/097800035
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tarig et al.
; TITLE OF INVENTION: ANTIBODIES THAT BIND HUMAN INTERLEUKIN-18 AND METHODS
; FILE REFERENCE: BBI-149
; CURRENT APPLICATION NUMBER: US/09/780,035
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,608
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-035-28

Query Match 75.5%; Score 40; DB 5; Length 108;
Best Local Similarity 70.0%; Pred. No. 0.17;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYLDIVTEG 10
| | | | : | : |
Db 47 STYADSVKG 56

RESULT 11
US-09-430-048-14
; Sequence 14, Application US/094300048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430,048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

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; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-14

Query Match          75.5%; Score 40; DB 5; Length 112;
Best Local Similarity 70.0%; Pred. No. 0.18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
Db 57 STYYADSVKG 66

RESULT 12
US-09-430-048-15
; Sequence 15, Application US/09430048
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/09/430.048
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-048-15

Query Match          75.5%; Score 40; DB 5; Length 112;
Best Local Similarity 70.0%; Pred. No. 0.18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
Db 57 STYYADSVKG 66

RESULT 13
US-09-194-356A-8
; Sequence 8, Application US/09194356A
; GENERAL INFORMATION:
; APPLICANT: NERI, DARIO
; APPLICANT: CARNEMOLLA, BARBARA
; APPLICANT: SIRI, ANNALISA
; APPLICANT: BALZA, ENRICA
; APPLICANT: CASTELLANI, PATRIZIA
; APPLICANT: ZARDI, LUCIANO
; APPLICANT: WINTER, GREGORY PAUL
; APPLICANT: NERI, GIOVANNI
; APPLICANT: BORSI, LAURA
; APPLICANT: PINI, ALESSANDRO
; TITLE OF INVENTION: ANTIBODIES TO THE ED-B DOMAIN OF FIBRONECTIN, THEIR
; FILE REFERENCE: SCH-1732
; CURRENT APPLICATION NUMBER: US/09/194,356A
; CURRENT FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: PCT/GB97/01412
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 9610967.3
; PRIOR FILING DATE: 1996-05-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 8
; LENGTH: 113
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-194-356A-8

Query Match          75.5%; Score 40; DB 5; Length 113;
Best Local Similarity 70.0%; Pred. No. 0.18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
Db 57 STYYADSVKG 66

RESULT 14
PCT-US01-03537-80
; Sequence 80, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005.
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03537-80

Query Match          75.5%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
Db 57 STYYADSVKG 66

RESULT 15
PCT-US01-03537-83
; Sequence 83, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
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; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03537-83

Query Match 75.58; Score 40; DB 1; Length 117;
Best Local Similarity 70.08; Pred. No. 0.19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVVEG 10
||| |:
Db 57 STYYADSVKG 66

Search completed: March 28, 2001, 06:57:03
Job time: 1552 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:36 ; Search time 80i.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARHNHGSFAY 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues
Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
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22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	14	US-09-016-061-60
2	58	100.0	10	17	US-09-339-922A-60
3	52	89.7	10	14	US-09-016-061-40
4	52	89.7	10	17	US-09-339-922A-40
5	52	89.7	117	1	PCT-US98-25828-54
6	52	89.7	117	1	PCT-US98-25828-56
7	52	89.7	117	11	US-08-790-540-2
8	52	89.7	117	11	US-08-790-540-6
9	52	89.7	117	11	US-08-790-540A-2
10	52	89.7	117	11	US-08-790-540A-6
11	52	89.7	117	11	US-08-791-391-2

12	52	89.7	117	11	US-08-791-391-6	Sequence 6, Appl
13	52	89.7	117	11	US-08-791-391A-2	Sequence 2, Appl
14	52	89.7	117	11	US-08-791-391A-6	Sequence 6, Appl
15	52	89.7	117	13	US-08-986-016-54	Sequence 54, Appl
16	52	89.7	117	13	US-08-986-016-56	Sequence 56, Appl
17	52	89.7	117	14	US-09-016-061-2	Sequence 2, Appl
18	52	89.7	117	14	US-09-016-061-6	Sequence 6, Appl
19	52	89.7	117	17	US-09-339-922A-2	Sequence 2, Appl
20	52	89.7	117	17	US-09-339-922A-6	Sequence 6, Appl
21	52	89.7	118	1	PCT-US98-25828-50	Sequence 50, Appl
22	52	89.7	118	1	PCT-US98-25828-51	Sequence 51, Appl
23	52	89.7	118	1	PCT-US98-25828-52	Sequence 52, Appl
24	52	89.7	118	1	PCT-US98-25828-53	Sequence 53, Appl
25	52	89.7	118	13	US-08-986-016-50	Sequence 50, Appl
26	52	89.7	118	13	US-08-986-016-51	Sequence 51, Appl
27	52	89.7	118	13	US-08-986-016-52	Sequence 52, Appl
28	52	89.7	119	13	US-08-986-016-53	Sequence 53, Appl
29	52	89.7	130	1	PCT-US98-25828-44	Sequence 44, Appl
30	52	89.7	130	13	US-08-986-016-44	Sequence 44, Appl
31	51	87.9	10	14	US-09-016-061-94	Sequence 94, Appl
32	51	87.9	10	17	US-09-339-922A-96	Sequence 96, Appl
33	49	84.5	10	14	US-09-016-061-62	Sequence 62, Appl
34	49	84.5	10	17	US-09-339-922A-62	Sequence 62, Appl
35	47	81.0	10	14	US-09-016-061-96	Sequence 96, Appl
36	47	81.0	10	17	US-09-339-922A-94	Sequence 94, Appl
37	46	79.3	10	14	US-09-016-061-64	Sequence 64, Appl
38	46	79.3	10	14	US-09-016-061-66	Sequence 66, Appl
39	46	79.3	10	17	US-09-339-922A-64	Sequence 64, Appl
40	46	79.3	10	17	US-09-339-922A-66	Sequence 66, Appl
41	45	77.6	10	14	US-09-016-061-68	Sequence 68, Appl
42	45	77.6	10	14	US-09-016-061-70	Sequence 70, Appl
43	45	77.6	10	14	US-09-016-061-72	Sequence 72, Appl
44	45	77.6	10	14	US-09-016-061-74	Sequence 74, Appl
45	45	77.6	10	14	US-09-016-061-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-09-016-061-60
; Sequence 60, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-60

Query Match      100.0%; Score 58; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 1 ARNHGSPAY 10

RESULT 2
US-09-339-922A-60
; Sequence 60, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-60

Query Match      100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 1 ARNHGSPAY 10

RESULT 3
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-60

Query Match      89.7%; Score 52; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0043;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 1 ARNHGSPAY 10

RESULT 4
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match      89.7%; Score 52; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0043;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 1 ARNHGSPAY 10

RESULT 5
PCT-US98-25828-54
; Sequence 54, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 54
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-54

Query Match 89.7%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
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Db 97 ARHNYGSFAY 106

RESULT 6
PCT-US98-25828-56
; Sequence 56, Application PCT/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-56

Query Match 89.7%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
 ||||:|||||
Db 97 ARHNYGSFAY 106

RESULT 7
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-6

Query Match 89.7%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAY 10
 ||||:|||||
Db 97 ARHNYGSFAY 106

RESULT 9
US-08-790-540A-2
; Sequence 2, Application US/08790540A

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-2

Query Match 89.7%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAY 10
 ||||:|||||
Db 97 ARHNYGSFAY 106

RESULT 8
US-08-790-540-6
; Sequence 6, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-6

Query Match 89.7%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAY 10
 ||||:|||||
Db 97 ARHNYGSFAY 106

RESULT 9
US-08-790-540A-2
; Sequence 2, Application US/08790540A

GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/790,540A
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 89.7%; Score 52; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 97 ARHNGSFAY 106

RESULT 10
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 89.7%; Score 52; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 97 ARHNGSFAY 106

RESULT 11
US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match 89.7%; Score 52; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
Db 97 ARHNGSFAY 106

RESULT 12

Db 97 ARHNYGSFAY 106

RESULT 15
US-08-986-016-54
; Sequence 54, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsr1 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING-DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-54

Query Match 89.7%; Score 52; DB 13; Length 117;
Best Local Similarity 90.0%; Pred. NO. 0.053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFAY 10

|||||

Db 97 ARHNYGSFAY 106

Search completed: March 28, 2001, 06:55:36
Job time: 1480 sec

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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:03 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pap.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pap.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pap.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pap.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pap.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	196	5	US-09-741-669-368
2	38	65.5	265	5	US-09-732-091-44
3	36	62.1	237	5	US-09-488-725A-3328
4	35	60.3	566	1	PCT-US01-01394-80
5	35	60.3	772	5	US-09-488-725A-2926
6	35	60.3	788	5	US-09-488-725A-6498
7	34	58.6	231	5	US-09-172-952-32
8	34	58.6	231	5	US-09-172-952-33
9	34	58.6	231	5	US-09-557-735-32
10	34	58.6	231	5	US-09-557-735-33
11	34	58.6	238	5	US-09-172-952-18
12	34	58.6	238	5	US-09-557-735-18
13	34	58.6	285	5	US-09-489-039A-12402
14	34	58.6	482	6	US-60-269-308-4703
15	33	56.9	290	5	US-09-201-228A-326
16	33	56.9	426	5	US-09-489-039A-13845
17	33	56.9	780	5	US-09-489-039A-13670
18	32	55.2	102	1	PCT-US00-32990-16
19	32	55.2	136	5	US-09-489-039A-9897
20	32	55.2	278	5	US-09-201-228A-1069
21	32	55.2	679	6	US-60-257-931-3490
22	32	55.2	679	6	US-60-253-625-2662
23	32	55.2	679	6	US-60-269-308-4512
24	32	55.2	776	5	US-09-489-039A-10778
25	31	53.4	74	1	PCT-US00-30086-11
26	31	53.4	94	5	US-09-557-917-14
27	31	53.4	94	5	US-09-557-917-45

28	31	53.4	94	5	US-09-557-917-48	Sequence 48, Appl
29	31	53.4	94	5	US-09-557-917-77	Sequence 77, Appl
30	31	53.4	94	5	US-09-557-917-84	Sequence 84, Appl
31	31	53.4	94	5	US-09-557-917-90	Sequence 90, Appl
32	31	53.4	94	5	US-09-557-917-101	Sequence 101, Appl
33	31	53.4	254	6	US-60-257-931-3589	Sequence 3589, Ap
34	31	53.4	254	6	US-60-253-625-2761	Sequence 2761, Ap
35	31	53.4	254	6	US-60-269-308-4611	Sequence 4611, Ap
36	31	53.4	291	1	PCT-US00-30086-2	Sequence 2, Appl1
37	31	53.4	465	6	US-60-257-931-3140	Sequence 3140, Ap
38	31	53.4	465	6	US-60-253-625-2533	Sequence 2533, Ap
39	31	53.4	465	6	US-60-269-308-4162	Sequence 4162, Ap
40	31	53.4	681	1	PCT-US00-30086-4	Sequence 4, Appl1
41	31	53.4	787	5	US-09-107-433-4612	Sequence 4612, Ap
42	31	53.4	1770	5	US-09-488-725A-2247	Sequence 2247, Ap
43	31	53.4	1848	5	US-09-488-725A-5819	Sequence 5819, Ap
44	30	51.7	13	5	US-09-635-434-4	Sequence 4, Appl1
45	30	51.7	73	1	PCT-US01-01322-605	Sequence 605, App

ALIGNMENTS

RESULT 1
US-09-741-669-368
; Sequence 368, Application US/09741669
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; proliferation of E. coli
; FILE REFERENCE: ELITEA 009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-368

Query Match 67.2%; Score 39; DB 5; Length 196;
Best Local Similarity 75.0%; Pred. No. 1.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
|||||
Db 105 HNHGSFKH 112

RESULT 2
US-09-732-091-44
; Sequence 44, Application US/09732091
; GENERAL INFORMATION:
; APPLICANT: Tian, Jing-Hui
; APPLICANT: Jackson, W. James
; APPLICANT: Walker, Richard I.
; TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
; thereof
; FILE REFERENCE: 7969-088
; CURRENT APPLICATION NUMBER: US/09/732,091
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter sp.

US-09-732-091-44

Query Match 65.5%; Score 38; DB 5; Length 265;
Best Local Similarity 75.0%; Pred. No. 3.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RHNGSFAY 10
|:|||||
Db 8 HHGSMAY 15

RESULT 3

US-09-488-725A-3528
; Sequence 3528, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3528
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3528

Query Match 62.1%; Score 36; DB 5; Length 237;
Best Local Similarity 44.4%; Pred. No. 7.9;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFAY 10
:|||||:
Db 177 KHHGAYQF 185

RESULT 4

PCT-US01-01394-80
; Sequence 80, Application PC/TUS0101394
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 21 human secreted proteins
; FILE REFERENCE: PS729PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01394
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/226,278
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 566
; TYPE: PRT

; ORGANISM: Homo sapiens
PCT-US01-01394-80

Query Match 60.3%; Score 35; DB 1; Length 566;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10
||:|||||
Db 75 ARYCHGFGY 84

RESULT 5

US-09-488-725A-2926
; Sequence 2926, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2926
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2926

Query Match 60.3%; Score 35; DB 5; Length 772;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10
||:|||||
Db 220 ARYCHGFGY 229

RESULT 6

US-09-488-725A-6498
; Sequence 6498, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 6498
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6498

Query Match 60.38; Score 35; DB 5; Length 788;
Best Local Similarity 60.08; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSPAY 10
||: |||||
Db 236 ARYCHGFGY 245

RESULT 7
US-09-172-952-32
; Sequence 32, Application US/09172952
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Yias-Ec
US-09-172-952-32

Query Match 58.68; Score 34; DB 5; Length 231;
Best Local Similarity 62.58; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPAY 10
||: |||||
Db 169 HSHGPFAP 176

RESULT 8
US-09-172-952-33
; Sequence 33, Application US/09172952
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Yias-HI
US-09-172-952-33

Query Match 58.68; Score 34; DB 5; Length 231;
Best Local Similarity 62.58; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPAY 10
||: |||||
Db 169 HSHGPFAP 176

RESULT 9
US-09-557-735-32
; Sequence 32, Application US/09557735
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/557,735
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/172,952
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Yias-Ec
US-09-557-735-32

Query Match 58.68; Score 34; DB 5; Length 231;
Best Local Similarity 62.58; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPAY 10
||: |||||
Db 169 HSHGPFAP 176

RESULT 10
US-09-557-735-33
; Sequence 33, Application US/09557735
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/557,735
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/172,952
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Yias-HI
US-09-557-735-33

Query Match 58.68; Score 34; DB 5; Length 231;
Best Local Similarity 62.58; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPAY 10
||: |||||
Db 169 HSHGPFAP 176

RESULT 11
US-09-172-952-18
; Sequence 18, Application US/09172952
; GENERAL INFORMATION:

; APPLICANT: Hoch, James
 ; APPLICANT: Dartois, Veronique
 ; TITLE OF INVENTION: METABOLIC SELECTION METHODS
 ; FILE REFERENCE: 234/191
 ; CURRENT APPLICATION NUMBER: US/09/172,952
 ; CURRENT FILING DATE: 1998-10-14
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Yias-Ko
 US-09-172-952-18

Query Match 58.6%; Score 34; DB 5; Length 238;
 Best Local Similarity 62.5%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
 I:|:| I:
 DB 169 HSHGPFAY 176

RESULT 12
 US-09-557-735-18
 ; Sequence 18, Application US/09557735
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoch, James
 ; APPLICANT: Dartois, Veronique
 ; TITLE OF INVENTION: METABOLIC SELECTION METHODS
 ; FILE REFERENCE: 234/191
 ; CURRENT APPLICATION NUMBER: US/09/557,735
 ; CURRENT FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/172,952
 ; PRIOR FILING DATE: 1998-10-14
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Yias-Ko
 US-09-557-735-18

Query Match 58.6%; Score 34; DB 5; Length 238;
 Best Local Similarity 62.5%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
 I:|:| I:
 DB 169 HSHGPFAY 176

RESULT 13
 US-09-489-039A-12402
 ; Sequence 12402, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 12402
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12402

Query Match 58.6%; Score 34; DB 5; Length 285;
 Best Local Similarity 62.5%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFAY 10
 I:|:| I:
 DB 223 HSHGPFAY 230

RESULT 14
 US-60-269-308-4703
 ; Sequence 4703, Application US/60269308
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, RW
 ; APPLICANT: Ohlsen, KL
 ; APPLICANT: Zyskind, JW
 ; APPLICANT: Trawick, JD
 ; APPLICANT: Wall, D
 ; TITLE OF INVENTION: Identification of Essential Genes in *Staphylococcus aureus*, *Ps*
 ; TITLE OF INVENTION: *aeruginosa*, *Klebsiella pneumoniae*, *Salmonella typhimurium*, an
 ; FILE REFERENCE: ELITRA.017PRS
 ; CURRENT APPLICATION NUMBER: US/60/269,308
 ; CURRENT FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 4774
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4703
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: *Enterococcus faecalis*
 US-60-269-308-4703

Query Match 58.6%; Score 34; DB 6; Length 482;
 Best Local Similarity 75.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 I:|:| I:
 DB 29 ARHNHGSF 36

RESULT 15
 US-09-201-228A-326
 ; Sequence 326, Application US/09201228A
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffois, Remy
 ; APPLICANT: Hoiseth, Susan K.
 ; APPLICANT: Zagursky, Robert John
 ; APPLICANT: Metcalf, Benjamin J.
 ; APPLICANT: Peek, Joel A.
 ; APPLICANT: Sankaran, Banumathi
 ; APPLICANT: Fletcher, Leah Diane
 ; TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
 ; TITLE OF INVENTION: AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN
 ; TITLE OF INVENTION: PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF
 ; FILE REFERENCE: 9710-0004-999
 ; CURRENT APPLICATION NUMBER: US/09/201,228A
 ; CURRENT FILING DATE: 1998-11-30
 ; PRIOR APPLICATION NUMBER: US 60/107,077
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: FR 97-16034
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: FR 97-15041
 ; PRIOR FILING DATE: 1997-11-28
 ; NUMBER OF SEQ ID NOS: 5981
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 326
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: *Chlamydia trachomatis*

US-09-201-228A-326

Query Match 56.9%; Score 33; DB 5; Length 290;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10
 ||| :||
Db 40 HNRHYAY 47

Search completed: March 28, 2001, 06:57:03
Job time: 1552 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:36 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep:*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	14	US-09-016-061-62
2	58	100.0	10	17	US-09-339-922A-62
3	54	93.1	10	14	US-09-016-061-40
4	54	93.1	10	17	US-09-339-922A-40
5	54	93.1	117	1	PCT-US98-25828-54
6	54	93.1	117	1	PCT-US98-25828-56
7	54	93.1	117	11	US-08-790-540-2
8	54	93.1	117	11	US-08-790-540A-6
9	54	93.1	117	11	US-08-790-540A-2
10	54	93.1	117	11	US-08-790-540A-6
11	54	93.1	117	11	US-08-791-391-2

12	54	93.1	117	11	US-08-791-391-6
13	54	93.1	117	11	US-08-791-391A-2
14	54	93.1	117	11	US-08-791-391A-6
15	54	93.1	117	13	US-08-986-016-54
16	54	93.1	117	13	US-08-986-016-56
17	54	93.1	117	14	US-09-016-061-2
18	54	93.1	117	14	US-09-016-061-6
19	54	93.1	117	17	US-09-339-922A-2
20	54	93.1	117	17	US-09-339-922A-6
21	54	93.1	118	1	PCT-US98-25828-50
22	54	93.1	118	1	PCT-US98-25828-51
23	54	93.1	118	1	PCT-US98-25828-52
24	54	93.1	118	1	PCT-US98-25828-53
25	54	93.1	118	13	US-08-986-016-50
26	54	93.1	118	13	US-08-986-016-51
27	54	93.1	118	13	US-08-986-016-52
28	54	93.1	119	13	US-08-986-016-53
29	54	93.1	130	1	PCT-US98-25828-44
30	54	93.1	130	13	US-08-986-016-44
31	49	84.5	10	14	US-09-016-061-60
32	49	84.5	10	17	US-09-339-922A-60
33	48	82.8	10	14	US-09-016-061-64
34	48	82.8	10	14	US-09-016-061-66
35	48	82.8	10	17	US-09-339-922A-64
36	48	82.8	10	17	US-09-339-922A-66
37	47	81.0	10	14	US-09-016-061-68
38	47	81.0	10	14	US-09-016-061-70
39	47	81.0	10	14	US-09-016-061-72
40	47	81.0	10	14	US-09-016-061-74
41	47	81.0	10	14	US-09-016-061-76
42	47	81.0	10	14	US-09-016-061-78
43	47	81.0	10	14	US-09-016-061-80
44	47	81.0	10	17	US-09-339-922A-68
45	47	81.0	10	17	US-09-339-922A-80

ALIGNMENTS

RESULT 1
US-09-016-061-62
; Sequence 62, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-62

Query Match      100.0%; Score 58; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 1 ARHNYGSYAY 10

RESULT 2
US-09-339-922A-62
; Sequence 62, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-62

Query Match      100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 1 ARHNYGSYAY 10

RESULT 3
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-40

Query Match      93.1%; Score 54; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0025;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 1 ARHNYGSYAY 10

RESULT 4
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-339-922A-40

Query Match      93.1%; Score 54; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0025;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 1 ARHNYGSYAY 10

RESULT 5
PCT-US98-25828-54
; Sequence 54, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 54
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-54

Query Match 93.1%; Score 54; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106
|||||:|

RESULT 6
PCT-US98-25828-56
; Sequence 56, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-56

Query Match 93.1%; Score 54; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106
|||||:|

RESULT 7
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-2

Query Match 93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106
|||||:|

RESULT 8
US-08-790-540-6
; Sequence 6, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-6

Query Match 93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106
|||||:|

RESULT 9
US-08-790-540A-2
; Sequence 2, Application US/08790540A

GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106

RESULT 10
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106

RESULT 11
US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match 93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
Db 97 ARHNYGSFAY 106

RESULT 12

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US-08-791-391-6
; Sequence 6, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; REFERENCE/DOCKET NUMBER: 31,815
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-6

Query Match          93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches          9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSYAY 10
Db      97 ARHNYGSFAY 106
|||||:|

RESULT 13
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; REFERENCE/DOCKET NUMBER: 31,815
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-6

Query Match          93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches          9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSYAY 10
Db      97 ARHNYGSFAY 106
|||||:|

RESULT 14
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; REFERENCE/DOCKET NUMBER: 31,815
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match          93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches          9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSYAY 10
Db      97 ARHNYGSFAY 106
|||||:|

RESULT 15
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; REFERENCE/DOCKET NUMBER: 31,815
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match          93.1%; Score 54; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches          9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARHNYGSYAY 10
Db      97 ARHNYGSFAY 106
|||||:|
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Db 97 ARHNYGSFAY 106

RESULT 15
US-08-986-016-54
; Sequence 54, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsri 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-54

Query Match 93.1%; Score 54; DB 13; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
|||||||
Db 97 ARHNYGSFAY 106

Search completed: March 28, 2001, 06:55:36
Job time: 1480 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:03 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNGSVAY 10

Scoring table: BLOSUM62
Gapex 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New: *
1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	60.3	512	5	US-09-107-433-5122
2	35	60.3	2184	5	US-09-417-485B-6
3	34	58.6	68	6	US-60-270-153-156
4	34	58.6	156	5	US-09-201-228A-666
5	34	58.6	237	5	US-09-488-725A-3528
6	34	58.6	719	5	US-09-488-725A-2108
7	34	58.6	1152	5	US-09-739-243-6
8	34	58.6	1157	5	US-09-471-177-5
9	34	58.6	1273	5	US-09-763-670-9
10	33	56.9	94	5	US-09-557-917-14
11	33	56.9	94	5	US-09-557-917-45
12	33	56.9	94	5	US-09-557-917-78
13	33	56.9	94	5	US-09-557-917-77
14	33	56.9	94	5	US-09-557-917-84
15	33	56.9	94	5	US-09-557-917-90
16	33	56.9	94	5	US-09-557-917-101
17	33	56.9	246	5	US-09-595-329A-635
18	33	56.9	248	5	US-09-595-329A-634
19	33	56.9	275	5	US-09-595-329A-633
20	32	55.2	15	5	US-09-756-983-11
21	32	55.2	50	5	US-09-673-809-51
22	32	55.2	89	5	US-09-673-809-2
23	32	55.2	94	5	US-09-766-378-37
24	32	55.2	94	5	US-09-692-933-180
25	32	55.2	94	5	US-09-557-917-12
26	32	55.2	94	5	US-09-557-917-13
27	32	55.2	94	5	US-09-557-917-15

28	32	55.2	94	5	US-09-557-917-16	Sequence 16, Appl
29	32	55.2	94	5	US-09-557-917-17	Sequence 17, Appl
30	32	55.2	94	5	US-09-557-917-18	Sequence 18, Appl
31	32	55.2	94	5	US-09-557-917-19	Sequence 19, Appl
32	32	55.2	94	5	US-09-557-917-20	Sequence 20, Appl
33	32	55.2	94	5	US-09-557-917-21	Sequence 21, Appl
34	32	55.2	94	5	US-09-557-917-22	Sequence 22, Appl
35	32	55.2	94	5	US-09-557-917-23	Sequence 23, Appl
36	32	55.2	94	5	US-09-557-917-24	Sequence 24, Appl
37	32	55.2	94	5	US-09-557-917-25	Sequence 25, Appl
38	32	55.2	94	5	US-09-557-917-26	Sequence 26, Appl
39	32	55.2	94	5	US-09-557-917-27	Sequence 27, Appl
40	32	55.2	94	5	US-09-557-917-28	Sequence 28, Appl
41	32	55.2	94	5	US-09-557-917-29	Sequence 29, Appl
42	32	55.2	94	5	US-09-557-917-30	Sequence 30, Appl
43	32	55.2	94	5	US-09-557-917-31	Sequence 31, Appl
44	32	55.2	94	5	US-09-557-917-32	Sequence 32, Appl
45	32	55.2	94	5	US-09-557-917-33	Sequence 33, Appl
					US-09-557-917-111	Sequence 111, App

ALIGNMENTS

RESULT 1
US-09-107-433-5122
; Sequence 5122, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...512
; SEQUENCE DESCRIPTION: SEQ ID NO: 5122:
US-09-107-433-5122

Query Match 60.3%; Score 35; DB 5; Length 512;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGSYAY 10
 |||||
 Db 422 NYGSYY 428

RESULT 2

US-09-417-485B-6
 ; Sequence 6, Application US/09417485B
 ; GENERAL INFORMATION:
 ; APPLICANT: Long, David M.
 ; APPLICANT: Metz, Anneke M.
 ; APPLICANT: Love, Ruschelle A.
 ; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
 ; FILE REFERENCE: 47714-5009-US
 ; CURRENT APPLICATION NUMBER: US/09/417,485B
 ; CURRENT FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 2184
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (330)..(335)
 ; OTHER INFORMATION: Xaa at position 330 = Leu or Ile; Xaa at position 335 =
 ; OTHER INFORMATION: Asp or Gly.
 US-09-417-485B-6

Query Match 60.3%; Score 35; DB 5; Length 2184;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNYGSYAY 10
 |||||
 Db 188 HSYGKLY 195

RESULT 3

US-60-270-153-156
 ; Sequence 156, Application US/60270153
 ; GENERAL INFORMATION:
 ; APPLICANT: JORK NOLLING
 ; TITLE OF INVENTION: NUCLEIC ACID MODIFYING ENZYMES DERIVED FROM THERMOPHILIC
 ; FILE REFERENCE: 031796-035
 ; CURRENT APPLICATION NUMBER: US/60/270,153
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 240
 ; SEQ ID NO 156
 ; LENGTH: 68
 ; TYPE: PRT
 ; ORGANISM: methanogenic phage
 US-60-270-153-156

Query Match 58.6%; Score 34; DB 6; Length 68;
 Best Local Similarity 66.7%; Pred. No. 3.1;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSYAY 10
 |||||
 Db 22 RHNYGFYIY 30

RESULT 4

US-09-488-725A-3528

US-09-201-228A-666
 ; Sequence 666, Application US/09201228A
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffais, Remy
 ; APPLICANT: Hoiseth, Susan K.
 ; APPLICANT: Zagursky, Robert John
 ; APPLICANT: Metcalf, Benjamin J.
 ; APPLICANT: Peek, Joel A.
 ; APPLICANT: Sankaran, Banumathi
 ; APPLICANT: Fletcher, Leah Diane
 ; TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
 ; TITLE OF INVENTION: AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN
 ; TITLE OF INVENTION: PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF
 ; FILE REFERENCE: 9710-0004-999
 ; CURRENT APPLICATION NUMBER: US/09/201,228A
 ; CURRENT FILING DATE: 1998-11-30
 ; PRIOR APPLICATION NUMBER: US 60/107,077
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: FR 97-16034
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: FR 97-15041
 ; PRIOR FILING DATE: 1997-11-28
 ; NUMBER OF SEQ ID NOS: 5981
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 666
 ; LENGTH: 156
 ; TYPE: PRT
 ; ORGANISM: Chlamydia trachomatis
 US-09-201-228A-666

Query Match 58.6%; Score 34; DB 5; Length 156;
 Best Local Similarity 60.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
 |||||
 Db 109 AKHRYVYFAY 118

RESULT 5
 US-09-488-725A-3528
 ; Sequence 3528, Application US/09488725A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq Inc
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
 ; FILE REFERENCE: 784FLPCT
 ; CURRENT APPLICATION NUMBER: US/09/488,725A
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US/09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: US09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: US09/620,312
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: US09/653,450
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US09/662,191
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: US09/693,036
 ; PRIOR FILING DATE: 2000-10-19
 ; PRIOR APPLICATION NUMBER: US09/727,344
 ; PRIOR FILING DATE: 2000-11-29
 ; NUMBER OF SEQ ID NOS: 7144
 ; SOFTWARE: pt_FL_genes_b Versions 1.0
 ; SEQ ID NO 3528
 ; LENGTH: 238
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-488-725A-3528

Query Match 58.6%; Score 34; DB 5; Length 237;
Best Local Similarity 44.4%; Pred. No. 13;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 177 KHNHGAYQF 185

RESULT 6
US-09-488-725A-2108
; Sequence 2108, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2108
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2108

Query Match 58.6%; Score 34; DB 5; Length 719;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
Db 311 HSYNSYTY 318

RESULT 7
US-09-739-243-6
; Sequence 6, Application US/09739243
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/09/739,243
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6

; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-739-243-6

Query Match 58.6%; Score 34; DB 5; Length 1152;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 768 ARENYPTYIY 777

RESULT 8
US-09-471-177-5
; Sequence 5, Application US/094711177
; GENERAL INFORMATION:
; APPLICANT: LAMBERT, BART
; APPLICANT: JANSSENS, STEFAN
; APPLICANT: VAN AUDENHOVE, KATRIEN
; APPLICANT: PEFFEROEN, MARNIX
; APPLICANT: VAN RIE, JEROEN
; APPLICANT: VAN AARSSEN, ROEL
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/471,177
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,809
; FILING DATE: 02-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-135P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-471-177-5

Query Match 58.6%; Score 34; DB 5; Length 1157;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 774 ARENYPTYIY 783

RESULT 9
US-09-763-670-9
; Sequence 9, Application US/09763670
; GENERAL INFORMATION:
; APPLICANT: KUVSHINOV, VIKTOR
; APPLICANT: KANERVA, ANNE
; APPLICANT: KOIVU, KIMMO
; APPLICANT: PEHU, EIJA
; TITLE OF INVENTION: MODIFIED SYNTHETIC DNA SEQUENCES FOR IMPROVED
; FILE REFERENCE: INSECTICIDAL CONTROL
; CURRENT APPLICATION NUMBER: BRN-001
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US/09/763.670
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/FI99/00698
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: FI 981809
; PRIOR FILING DATE: 1998-08-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1273
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-763-670-9

Query Match 58.6%; Score 34; DB 5; Length 1273;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSVAY 10
||| :||
Db 894 ARENYTYIY 903

RESULT 10
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
||||| :
Db 80 RHNYGVF 86

RESULT 11
US-09-557-917-45

; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
||||| :
Db 80 RHNYGVF 86

RESULT 12
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSY 8
||||| :
Db 80 RHNYGVF 86

RESULT 13
US-09-557-917-77
; Sequence 77, Application US/09557917

GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
QY 2 RHNYGSY 8
DB 80 RHNYGVF 86

RESULT 14
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
QY 2 RHNYGSY 8
DB 80 RHNYGVF 86

RESULT 15
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:

APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 56.9%; Score 33; DB 5; Length 94;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
QY 2 RHNYGSY 8
DB 80 RHNYGVF 86

Search completed: March 28, 2001, 06:57:03
Job time: 1552 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:55:36 ; Search time 801.32 Seconds
(without alignments)
1.818 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNGSPDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
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21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	14	US-09-016-061-64
2	59	100.0	10	17	US-09-339-922A-64
3	51	86.4	10	14	US-09-016-061-40
4	51	86.4	10	17	US-09-339-922A-40
5	51	86.4	117	1	PCT-US98-25828-54
6	51	86.4	117	1	PCT-US98-25828-56
7	51	86.4	117	11	US-08-790-540-2
8	51	86.4	117	11	US-08-790-540-6
9	51	86.4	117	11	US-08-790-540A-2
10	51	86.4	117	11	US-08-790-540A-6
11	51	86.4	117	11	US-08-791-391-2

12	86.4	117	11	US-08-791-391-6	Sequence 6, Appl	
13	86.4	117	11	US-08-791-391A-2	Sequence 2, Appl	
14	86.4	117	11	US-08-791-391A-6	Sequence 6, Appl	
15	86.4	117	13	US-08-986-016-54	Sequence 54, Appl	
16	86.4	117	13	US-08-986-016-56	Sequence 56, Appl	
17	86.4	117	14	US-09-016-061-2	Sequence 2, Appl	
18	86.4	117	14	US-09-016-061-6	Sequence 6, Appl	
19	86.4	117	17	US-09-339-922A-2	Sequence 2, Appl	
20	86.4	117	17	US-09-339-922A-6	Sequence 6, Appl	
21	86.4	118	1	PCT-US98-25828-50	Sequence 50, Appl	
22	86.4	118	1	PCT-US98-25828-52	Sequence 52, Appl	
23	86.4	118	1	PCT-US98-25828-51	Sequence 51, Appl	
24	86.4	118	1	PCT-US98-25828-53	Sequence 53, Appl	
25	86.4	118	13	US-08-986-016-50	Sequence 50, Appl	
26	86.4	118	13	US-08-986-016-51	Sequence 51, Appl	
27	86.4	118	13	US-08-986-016-52	Sequence 52, Appl	
28	86.4	119	13	US-08-986-016-53	Sequence 53, Appl	
29	86.4	130	1	PCT-US98-25828-44	Sequence 44, Appl	
30	86.4	130	13	US-08-986-016-44	Sequence 44, Appl	
31	86.4	10	14	US-09-016-061-66	Sequence 66, Appl	
32	86.4	10	17	US-09-339-922A-66	Sequence 66, Appl	
33	81.4	10	14	US-09-016-061-62	Sequence 62, Appl	
34	81.4	10	17	US-09-339-922A-62	Sequence 62, Appl	
35	46	81.4	10	14	US-09-016-061-60	Sequence 60, Appl
36	46	81.4	10	14	US-09-016-061-68	Sequence 68, Appl
37	46	81.4	10	14	US-09-016-061-70	Sequence 70, Appl
38	46	81.4	10	14	US-09-016-061-72	Sequence 72, Appl
39	46	81.4	10	14	US-09-016-061-74	Sequence 74, Appl
40	46	81.4	10	14	US-09-016-061-76	Sequence 76, Appl
41	46	81.4	10	14	US-09-016-061-78	Sequence 78, Appl
42	46	81.4	10	14	US-09-016-061-80	Sequence 80, Appl
43	46	81.4	10	14	US-09-016-061-98	Sequence 98, Appl
44	46	81.4	10	14	US-09-016-061-100	Sequence 100, App
45	46	81.4	10	17	US-09-339-922A-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-016-061-64
Sequence 64, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-64

Query Match      100.0%; Score 59; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 1 ARHNYGSFDY 10

RESULT 2
US-09-339-922A-64
; Sequence 64, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-64

Query Match      100.0%; Score 59; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 1 ARHNYGSFDY 10

RESULT 3
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-64

Query Match      100.0%; Score 59; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 1 ARHNYGSFDY 10

RESULT 2
US-09-339-922A-64
; Sequence 64, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-64

Query Match      100.0%; Score 59; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 1 ARHNYGSFDY 10

RESULT 3
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-40

Query Match      86.4%; Score 51; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. NO. 0.0083;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 1 ARHNYGSFAY 10

RESULT 4
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match      86.4%; Score 51; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. NO. 0.0083;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
Db 1 ARHNYGSFAY 10

RESULT 5
PCT-US98-25828-54
; Sequence 54, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 54
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-54

Query Match 86.4%; Score 51; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db 97 ARHNYGSFAY 106
|||||||

RESULT 6
PCT-US98-25828-56
; Sequence 56, Application PC/TUS9825828A
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: HUMANIZATION OF MURINE ANTIBODY
; FILE REFERENCE: TSRI 598.0
; CURRENT APPLICATION NUMBER: PCT/US98/25828A
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 08/986,016
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine hybridoma LM609
PCT-US98-25828-56

Query Match 86.4%; Score 51; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db 97 ARHNYGSFAY 106
|||||||

RESULT 7
US-08-790-540-2
; Sequence 2, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-2

Query Match 86.4%; Score 51; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db 97 ARHNYGSFAY 106
|||||||

RESULT 8
US-08-790-540-6
; Sequence 6, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-540-6

Query Match 86.4%; Score 51; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db 97 ARHNYGSFAY 106
|||||||

RESULT 9
US-08-790-540A-2
; Sequence 2, Application US/08790540A

GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; APPLICATION NUMBER: US/08/790,540A
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-2

Query Match 86.4%; Score 51; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
|||||||
Db 97 ARHNYGSFAY 106

RESULT 10
US-08-790-540A-6
; Sequence 6, Application US/08790540A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-540A-6

Query Match 86.4%; Score 51; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
|||||||
Db 97 ARHNYGSFAY 106

RESULT 11
US-08-791-391-2
; Sequence 2, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-2

Query Match 86.4%; Score 51; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
|||||||
Db 97 ARHNYGSFAY 106

RESULT 12

US-08-791-391-6
; Sequence 6, Application US/08791391
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391-6

Query Match 86.4%; Score 51; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
| | | | | | | |
DB 97 ARHNYGSFAY 106

RESULT 13
US-08-791-391A-2
; Sequence 2, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-2

Query Match 86.4%; Score 51; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
| | | | | | | |
DB 97 ARHNYGSFAY 106

RESULT 14
US-08-791-391A-6
; Sequence 6, Application US/08791391A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791.391A
; FILING DATE: 30-JAN-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1482
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-391A-6

Query Match 86.4%; Score 51; DB 11; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
| | | | | | | |

Db 97 ARHNYGSFAY 106

RESULT 15
US-08-986-016-54
; Sequence 54, Application US/08986016A
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; TITLE OF INVENTION: Humanization of Murine Antibody
; FILE REFERENCE: Tsri 598.0
; CURRENT APPLICATION NUMBER: US/08/986,016A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
US-08-986-016-54

Query Match 86.4%; Score 51; DB 13; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
| | | | | | | |
Db 97 ARHNYGSFAY 106

Search completed: March 28, 2001, 06:55:36
Job time: 1480 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 06:57:03 ; Search time 79.56 Seconds
(without alignments)
1.656 Million cell updates/sec

Title: US-09-016-061-64

Perfect score: 59

Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA_New.*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	71.2	351	5	US-09-489-039A-13059
2	38	64.4	94	5	US-09-557-917-14
3	38	64.4	94	5	US-09-557-917-45
4	38	64.4	94	5	US-09-557-917-48
5	38	64.4	94	5	US-09-557-917-77
6	38	64.4	94	5	US-09-557-917-84
7	38	64.4	94	5	US-09-557-917-90
8	38	64.4	94	5	US-09-557-917-101
9	37	62.7	378	5	US-09-489-039A-13960
10	36	61.0	228	5	US-09-201-228A-403
11	36	61.0	292	5	US-09-489-039A-12107
12	35	59.3	17	5	US-09-543-004-76
13	35	59.3	17	5	US-09-543-004-77
14	35	59.3	124	5	US-09-543-004-47
15	35	59.3	124	5	US-09-543-004-48
16	35	59.3	124	5	US-09-543-004-49
17	35	59.3	124	5	US-09-543-004-50
18	35	59.3	124	5	US-09-543-004-51
19	35	59.3	124	5	US-09-543-004-52
20	35	59.3	124	5	US-09-543-004-53
21	35	59.3	124	5	US-09-543-004-54
22	35	59.3	124	5	US-09-543-004-55
23	35	59.3	124	5	US-09-543-004-56
24	35	59.3	124	5	US-09-543-004-57
25	35	59.3	124	5	US-09-543-004-58
26	35	59.3	124	5	US-09-543-004-59
27	35	59.3	124	5	US-09-543-004-60

28	35	59.3	124	5	US-09-543-004-61	Sequence 61, Appl
29	35	59.3	124	5	US-09-543-004-62	Sequence 62, Appl
30	35	59.3	124	5	US-09-543-004-63	Sequence 63, Appl
31	35	59.3	124	5	US-09-543-004-64	Sequence 64, Appl
32	35	59.3	124	5	US-09-543-004-65	Sequence 65, Appl
33	35	59.3	124	5	US-09-543-004-66	Sequence 66, Appl
34	35	59.3	124	5	US-09-543-004-67	Sequence 67, Appl
35	35	59.3	329	5	US-09-489-039A-14206	Sequence 14206, A
36	34	57.6	94	5	US-09-557-917-39	Sequence 39, Appl
37	34	57.6	94	5	US-09-557-917-59	Sequence 59, Appl
38	34	57.6	94	5	US-09-557-917-63	Sequence 63, Appl
39	34	57.6	288	6	US-60-259-128-4587	Sequence 4587, Ap
40	33	55.9	94	5	US-09-557-917-55	Sequence 55, Appl
41	33	55.9	94	5	US-09-557-917-62	Sequence 62, Appl
42	33	55.9	94	5	US-09-557-917-87	Sequence 87, Appl
43	33	55.9	94	5	US-09-557-917-108	Sequence 108, App
44	33	55.9	196	5	US-09-741-669-368	Sequence 368, App
45	33	55.9	246	5	US-09-595-329A-635	Sequence 635, App

ALIGNMENTS

RESULT 1
US-09-489-039A-13059
; Sequence 13059, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13059
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13059

Query Match 71.2%; Score 42; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
| | | | | | | |
DB 106 NYGSFDY 112

RESULT 2
US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14

; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 RHNYGSED 9
Db 80 RHNYGVFE 87

RESULT 3

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yokoi
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 RHNYGSED 9
Db 80 RHNYGVFE 87

RESULT 4

US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yokoi
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94

; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 RHNYGSED 9
Db 80 RHNYGVFE 87

RESULT 5

US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yokoi
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 RHNYGSED 9
Db 80 RHNYGVFE 87

RESULT 6

US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yokoi
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT

;
US-09-557-917-84

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 80 RHNYGVFE 87

RESULT 7

US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557.917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 80 RHNYGVFE 87

RESULT 8

US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557.917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE

US-09-557-917-101

Query Match 64.4%; Score 38; DB 5; Length 94;
Best Local Similarity 75.0%; Pred. No. 0.95;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 80 RHNYGVFE 87

RESULT 9

US-09-489-039A-13960
; Sequence 13960, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13960
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13960

Query Match 62.7%; Score 37; DB 5; Length 378;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
| | | | |
Db 110 DYGSFDY 116

RESULT 10

US-09-201-228A-403
; Sequence 403, Application US/09201228A
; GENERAL INFORMATION:
; APPLICANT: Griffais, Remy
; APPLICANT: Hoiseth, Susan K.
; APPLICANT: Zagursky, Robert John
; APPLICANT: Metcalf, Benjamin J.
; APPLICANT: Peek, Joel A.
; APPLICANT: Sankaran, Banumathi
; APPLICANT: Fletcher, Leah Diane
; TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
; TITLE OF INVENTION: AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN
; TITLE OF INVENTION: PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF
; FILE REFERENCE: 9710-0004-999
; CURRENT APPLICATION NUMBER: US/09/201,228A
; CURRENT FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/107,077
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: FR 97-16034
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: FR 97-15041
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 5981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 403
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-201-228A-403

```
Query Match          61.0%; Score 36; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YGSFDY 10
    |||||
Db 98 YGSFDY 103

RESULT 11
US-09-489-039A-12107
; Sequence 12107, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12107
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12107

Query Match          61.0%; Score 36; DB 5; Length 292;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YGSFDY 10
    |||||
Db 41 YGSFDY 46

RESULT 12
US-09-543-004-76
; Sequence 76, Application US/09543004
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 76
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-76

Query Match          59.3%; Score 35; DB 5; Length 17;
Best Local Similarity 85.7%; Pred. No. 0.57;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 NYGSFDY 10
    |||||
Db 5 NYGSVDY 11

RESULT 13
US-09-543-004-77
; Sequence 77, Application US/09543004
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 77
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-77

Query Match          59.3%; Score 35; DB 5; Length 17;
Best Local Similarity 85.7%; Pred. No. 0.57;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 NYGSFDY 10
    |||||
Db 5 NYGSVDY 11

RESULT 14
US-09-543-004-47
; Sequence 47, Application US/09543004
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 47
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-47

Query Match          59.3%; Score 35; DB 5; Length 124;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 NYGSFDY 10
    |||||
Db 54 NYGSVDY 60

RESULT 15
US-09-543-004-48
; Sequence 48, Application US/09543004
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 48
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-48
```

FEATURE:
US-09-543-004-48

Query Match 59.3%; Score 35; DB 5; Length 124;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGSFDY 10
 ||||||
Db 54 NYGSVDY 60

Search completed: March 28, 2001, 06:57:03
Job time: 1552 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	54	100.0	10	14	US-09-016-061-68		Sequence 68, Appl
2	54	100.0	10	17	US-09-339-922A-68		Sequence 68, Appl
3	51	94.4	10	14	US-09-016-061-70		Sequence 70, Appl
4	51	94.4	10	14	US-09-016-061-80		Sequence 80, Appl
5	51	94.4	10	17	US-09-339-922A-70		Sequence 70, Appl
6	51	94.4	10	17	US-09-339-922A-80		Sequence 80, Appl
7	50	92.6	10	14	US-09-016-061-40		Sequence 40, Appl
8	50	92.6	10	14	US-09-016-061-72		Sequence 72, Appl
9	50	92.6	10	14	US-09-016-061-74		Sequence 74, Appl
10	50	92.6	10	14	US-09-016-061-76		Sequence 76, Appl
11	50	92.6	10	14	US-09-016-061-78		Sequence 78, Appl

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-68

Query Match 100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSPAS 10
DB 1 ARHNYGSPAS 10

RESULT 2

US-09-339-922A-68

Sequence 68, Application US/09339922A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
complementarity determining region (CDR)
US-09-339-922A-68

Query Match 100.0%; Score 54; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSPAS 10
DB 1 ARHNYGSPAS 10

RESULT 3

US-09-016-061-70

Sequence 70, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-70

Query Match 94.4%; Score 51; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0022;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSPAS 10
DB 1 ARHNYGSPAT 10

RESULT 4

US-09-016-061-80

Sequence 80, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-80

Query Match 94.4%; Score 51; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0022;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
| | | | | | | | | |
DB 1 ARHNYGSFAA 10

RESULT 5

US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-70

Query Match 94.4%; Score 51; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0022;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
| | | | | | | | | |
DB 1 ARHNYGSFAT 10

RESULT 6

US-09-339-922A-80
; Sequence 80, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-80

Query Match 94.4%; Score 51; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0022;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
| | | | | | | | | |
DB 1 ARHNYGSFAA 10

RESULT 7

US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-40

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
DB 1 ARHNYGSFA 9

RESULT 8

US-09-016-061-72
; Sequence 72, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-09-016-061-72

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/016,061
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
RESULT 9
US-09-016-061-74
; SEQUENCE 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-74
Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
RESULT 10
US-09-016-061-76
; SEQUENCE 76, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-76

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
RESULT 11
US-09-016-061-78
; SEQUENCE 78, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/016.061
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-78

Query Match 92.6%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 12
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13

US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 14

US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 15

US-09-339-922A-76
; Sequence 76, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-76

Query Match 92.6%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:20
Job time: 1331 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:13 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New: *
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2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pap: *
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pap: *
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pap: *
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pap: *
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	72.2	94	5	US-09-557-917-14
2	39	72.2	94	5	US-09-557-917-45
3	39	72.2	94	5	US-09-557-917-48
4	39	72.2	94	5	US-09-557-917-77
5	39	72.2	94	5	US-09-557-917-84
6	39	72.2	94	5	US-09-557-917-90
7	39	72.2	94	5	US-09-557-917-101
8	35	64.8	94	5	US-09-557-917-39
9	35	64.8	94	5	US-09-557-917-59
10	35	64.8	94	5	US-09-557-917-63
11	34	63.0	94	5	US-09-557-917-55
12	34	63.0	94	5	US-09-557-917-62
13	34	63.0	94	5	US-09-557-917-87
14	34	63.0	94	5	US-09-557-917-108
15	34	63.0	246	5	US-09-595-329A-635
16	34	63.0	248	5	US-09-595-329A-634
17	34	63.0	275	5	US-09-595-329A-633
18	34	63.0	288	6	US-60-259-128-4587
19	33	61.1	94	5	US-09-557-917-19
20	33	61.1	94	5	US-09-557-917-30
21	33	61.1	94	5	US-09-557-917-83
22	33	61.1	94	5	US-09-557-917-85
23	33	61.1	94	5	US-09-557-917-91
24	33	61.1	94	5	US-09-557-917-93
25	33	61.1	94	5	US-09-557-917-106
26	33	61.1	94	5	US-09-557-917-109
27	33	61.1	479	5	US-09-489-039A-13978

28	32	59.3	15	5	US-09-756-983-11	Sequence 11, Appl
29	32	59.3	80	5	US-09-673-809-51	Sequence 51, Appl
30	32	59.3	89	5	US-09-673-809-2	Sequence 2, Appl
31	32	59.3	94	5	US-09-766-378-37	Sequence 37, Appl
32	32	59.3	94	5	US-09-692-933-180	Sequence 180, Appl
33	32	59.3	94	5	US-09-557-917-12	Sequence 12, Appl
34	32	59.3	94	5	US-09-557-917-13	Sequence 13, Appl
35	32	59.3	94	5	US-09-557-917-15	Sequence 15, Appl
36	32	59.3	94	5	US-09-557-917-16	Sequence 16, Appl
37	32	59.3	94	5	US-09-557-917-17	Sequence 17, Appl
38	32	59.3	94	5	US-09-557-917-18	Sequence 18, Appl
39	32	59.3	94	5	US-09-557-917-20	Sequence 20, Appl
40	32	59.3	94	5	US-09-557-917-21	Sequence 21, Appl
41	32	59.3	94	5	US-09-557-917-22	Sequence 22, Appl
42	32	59.3	94	5	US-09-557-917-24	Sequence 24, Appl
43	32	59.3	94	5	US-09-557-917-25	Sequence 25, Appl
44	32	59.3	94	5	US-09-557-917-26	Sequence 26, Appl
45	32	59.3	94	5	US-09-557-917-111	Sequence 111, Appl

ALIGNMENTS

RESULT 1

US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RHNYGSFAS 10
|||||
Db 80 RHNYGVFES 88

RESULT 2

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-45

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 3
US-09-557-917-48
; Sequence 48, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-48

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 4
US-09-557-917-77
; Sequence 77, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-77

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 5
US-09-557-917-84
; Sequence 84, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-84

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 6
US-09-557-917-90
; Sequence 90, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32; Indels 2; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 72.2%; Score 39; DB 5; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.32; Indels 2; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGVFES 88

RESULT 8
US-09-557-917-39
; Sequence 39, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979

; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-39

Query Match 64.8%; Score 35; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 2; Indels 3; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGGMES 88

RESULT 9
US-09-557-917-59
; Sequence 59, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-59

Query Match 64.8%; Score 35; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 2; Indels 3; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGGMES 88

RESULT 10
US-09-557-917-63
; Sequence 63, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-63

Query Match 64.8%; Score 35; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGMES 88

RESULT 11
US-09-557-917-55
; Sequence 55, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-55

Query Match 63.0%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGMES 88

RESULT 12
US-09-557-917-62
; Sequence 62, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-62

Query Match 63.0%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGMES 88

RESULT 13
US-09-557-917-87
; Sequence 87, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-87

Query Match 63.0%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10
| | | | |
Db 80 RHNYGMES 88

RESULT 14
US-09-557-917-108
; Sequence 108, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; TITLE OF INVENTION: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 108
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-108

Query Match 63.0%; Score 34; DB 5; Length 94;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 RHNYGSFAS 10
Db 80 RHNYGVES 88

RESULT 15
US-09-595-329A-635
; Sequence 635 Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595.329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: ()...()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 63.0%; Score 34; DB 5; Length 246;
Best Local Similarity 66.7%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 RHNYGSFAS 10
Db 131 KHNYGSAPS 139

Search completed: March 28, 2001, 07:22:13
Job time: 1505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:20 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNGSFAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
4: /cgnl_7/ptodata/1/paa/US080_COMB.pep.*
5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
7: /cgnl_7/ptodata/1/paa/US083_COMB.pep.*
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10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
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15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
17: /cgnl_7/ptodata/1/paa/US093_COMB.pep.*
18: /cgnl_7/ptodata/1/paa/US094_COMB.pep.*
19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
22: /cgnl_7/ptodata/1/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	55	100.0	10 14	US-09-016-061-70 Sequence 70, Appl
2	55	100.0	10 17	US-09-339-922A-70 Sequence 70, Appl
3	51	92.7	10 14	US-09-016-061-68 Sequence 68, Appl
4	51	92.7	10 17	US-09-339-922A-68 Sequence 68, Appl
5	50	90.9	10 14	US-09-016-061-40 Sequence 40, Appl
6	50	90.9	10 14	US-09-016-061-72 Sequence 72, Appl
7	50	90.9	10 14	US-09-016-061-74 Sequence 74, Appl
8	50	90.9	10 14	US-09-016-061-76 Sequence 76, Appl
9	50	90.9	10 14	US-09-016-061-78 Sequence 78, Appl
10	50	90.9	10 14	US-09-016-061-80 Sequence 80, Appl
11	50	90.9	10 17	US-09-339-922A-40 Sequence 40, Appl

12	50	90.9	10 17	US-09-339-922A-72	Sequence 72, Appl
13	50	90.9	10 17	US-09-339-922A-74	Sequence 74, Appl
14	50	90.9	10 17	US-09-339-922A-76	Sequence 76, Appl
15	50	90.9	10 17	US-09-339-922A-78	Sequence 78, Appl
16	50	90.9	10 17	US-09-339-922A-80	Sequence 80, Appl
17	50	90.9	117 1	PCT-US98-25828-54	Sequence 54, Appl
18	50	90.9	117 1	PCT-US98-25828-56	Sequence 56, Appl
19	50	90.9	117 11	US-08-790-540-2	Sequence 2, Appl
20	50	90.9	117 11	US-08-790-540-6	Sequence 6, Appl
21	50	90.9	117 11	US-08-790-540A-2	Sequence 2, Appl
22	50	90.9	117 11	US-08-790-540A-6	Sequence 6, Appl
23	50	90.9	117 11	US-08-791-391-2	Sequence 2, Appl
24	50	90.9	117 11	US-08-791-391-6	Sequence 6, Appl
25	50	90.9	117 11	US-08-791-391A-2	Sequence 2, Appl
26	50	90.9	117 11	US-08-791-391A-6	Sequence 6, Appl
27	50	90.9	117 13	US-08-986-016-54	Sequence 54, Appl
28	50	90.9	117 13	US-08-986-016-56	Sequence 56, Appl
29	50	90.9	117 14	US-09-016-061-2	Sequence 2, Appl
30	50	90.9	117 14	US-09-016-061-6	Sequence 6, Appl
31	50	90.9	117 17	US-09-339-922A-2	Sequence 2, Appl
32	50	90.9	117 17	US-09-339-922A-6	Sequence 6, Appl
33	50	90.9	118 1	PCT-US98-25828-50	Sequence 50, Appl
34	50	90.9	118 1	PCT-US98-25828-51	Sequence 51, Appl
35	50	90.9	118 1	PCT-US98-25828-52	Sequence 52, Appl
36	50	90.9	118 1	PCT-US98-25828-53	Sequence 53, Appl
37	50	90.9	118 13	US-08-986-016-50	Sequence 50, Appl
38	50	90.9	118 13	US-08-986-016-51	Sequence 51, Appl
39	50	90.9	118 13	US-08-986-016-52	Sequence 52, Appl
40	50	90.9	119 13	US-08-986-016-53	Sequence 53, Appl
41	50	90.9	130 1	PCT-US98-25828-44	Sequence 44, Appl
42	50	90.9	130 13	US-08-986-016-44	Sequence 44, Appl
43	47	85.5	10 14	US-09-016-061-62	Sequence 62, Appl
44	47	85.5	10 17	US-09-339-922A-62	Sequence 62, Appl
45	46	83.6	10 17	US-09-339-922A-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-016-061-70
; Sequence 70, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-70

Query Match 100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAT 10
Db 1 ARHNYGSFAT 10

RESULT 2

US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-70

Query Match 100.0%; Score 55; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAT 10
Db 1 ARHNYGSFAT 10

RESULT 3

US-09-016-061-68
; Sequence 68, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-68

Query Match 92.7%; Score 51; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0019;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAT 10
Db 1 ARHNYGSFAS 10

RESULT 4

US-09-339-922A-68
; Sequence 68, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-68

Query Match 92.7%; Score 51; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0019;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAT 10
Db 1 ARHNYGSFAS 10

RESULT 5

US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-40

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 6
US-09-016-061-72
Sequence 72, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-72

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 7
US-09-016-061-74
Sequence 74, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-74

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

;
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-80

Query Match 90.9%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 11
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 12
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9
| | | | | | | | | |

RESULT 13
US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 14
US-09-339-922A-76
; Sequence 76, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-76

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

RESULT 15
US-09-339-922A-78
; Sequence 78, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-78

Query Match 90.9%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:20
Job time: 1331 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:22:13 ; Search time 213.09 Seconds
(without alignments)
0.618 Million cell updates/sec

Title: US-09-016-061-70

Perfect score: 55

Sequence: 1 ARHNYGSFAT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101180 seqs, 13177366 residues

Total number of hits satisfying chosen parameters: 101180

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep:*
- 2: /cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep:*
- 3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep:*
- 4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
- 5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep:*
- 6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	65.5	94	5	US-09-557-917-14
2	36	65.5	94	5	US-09-557-917-45
3	36	65.5	94	5	US-09-557-917-48
4	36	65.5	94	5	US-09-557-917-77
5	36	65.5	94	5	US-09-557-917-84
6	36	65.5	94	5	US-09-557-917-90
7	36	65.5	94	5	US-09-557-917-101
8	34	61.8	288	6	US-60-259-128-4587
9	34	61.8	503	5	US-09-099-463A-8
10	33	60.0	246	5	US-09-595-329A-635
11	33	60.0	248	5	US-09-595-329A-634
12	33	60.0	275	5	US-09-595-329A-633
13	33	60.0	467	1	PCT-US00-33549-61
14	33	60.0	479	5	US-09-489-039A-13978
15	32	58.2	15	5	US-09-756-983-11
16	32	58.2	80	5	US-09-673-809-51
17	32	58.2	89	5	US-09-673-809-2
18	32	58.2	94	5	US-09-766-378-37
19	32	58.2	94	5	US-09-692-933-180
20	32	58.2	94	5	US-09-557-917-12
21	32	58.2	94	5	US-09-557-917-13
22	32	58.2	94	5	US-09-557-917-15
23	32	58.2	94	5	US-09-557-917-16
24	32	58.2	94	5	US-09-557-917-17
25	32	58.2	94	5	US-09-557-917-18
26	32	58.2	94	5	US-09-557-917-19
27	32	58.2	94	5	US-09-557-917-20

28	32	58.2	94	5	US-09-557-917-21	Sequence 21, Appl
29	32	58.2	94	5	US-09-557-917-22	Sequence 22, Appl
30	32	58.2	94	5	US-09-557-917-24	Sequence 24, Appl
31	32	58.2	94	5	US-09-557-917-25	Sequence 26, Appl
32	32	58.2	94	5	US-09-557-917-26	Sequence 27, Appl
33	32	58.2	94	5	US-09-557-917-27	Sequence 28, Appl
34	32	58.2	94	5	US-09-557-917-28	Sequence 29, Appl
35	32	58.2	94	5	US-09-557-917-29	Sequence 30, Appl
36	32	58.2	94	5	US-09-557-917-30	Sequence 31, Appl
37	32	58.2	94	5	US-09-557-917-31	Sequence 32, Appl
38	32	58.2	94	5	US-09-557-917-32	Sequence 33, Appl
39	32	58.2	94	5	US-09-557-917-33	Sequence 34, Appl
40	32	58.2	94	5	US-09-557-917-34	Sequence 35, Appl
41	32	58.2	94	5	US-09-557-917-35	Sequence 36, Appl
42	32	58.2	94	5	US-09-557-917-36	Sequence 37, Appl
43	32	58.2	94	5	US-09-557-917-37	Sequence 38, Appl
44	32	58.2	94	5	US-09-557-917-38	Sequence 111, App
45	32	58.2	94	5	US-09-557-917-111	

ALIGNMENTS

RESULT 1

US-09-557-917-14
; Sequence 14, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-14

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db 80 RHNYGVF 86

RESULT 2

US-09-557-917-45
; Sequence 45, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17

; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-45

Query Match 65.5%; Score 36; DB 5; Length 94;
 Best Local Similarity 85.7%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 |||||
 Db 80 RHNYGVF 86

RESULT 3
 US-09-557-917-48
 ; Sequence 48, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 48
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-48

Query Match 65.5%; Score 36; DB 5; Length 94;
 Best Local Similarity 85.7%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 |||||
 Db 80 RHNYGVF 86

RESULT 4
 US-09-557-917-77
 ; Sequence 77, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 77
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-77

Query Match 65.5%; Score 36; DB 5; Length 94;
 Best Local Similarity 85.7%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 |||||
 Db 80 RHNYGVF 86

RESULT 5
 US-09-557-917-84
 ; Sequence 84, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933
 ; PRIOR FILING DATE: 1996-07-19
 ; PRIOR APPLICATION NUMBER: JP 9-77979
 ; PRIOR FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 84
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: BOVINE
 US-09-557-917-84

Query Match 65.5%; Score 36; DB 5; Length 94;
 Best Local Similarity 85.7%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
 |||||
 Db 80 RHNYGVF 86

RESULT 6
 US-09-557-917-90
 ; Sequence 90, Application US/09557917
 ; GENERAL INFORMATION:
 ; APPLICANT: Aida, Yoko
 ; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
 ; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
 ; CURRENT APPLICATION NUMBER: US/09/557,917
 ; CURRENT FILING DATE: 2000-04-21
 ; PRIOR APPLICATION NUMBER: 09/147,550
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: PCT/JP97/02485
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: JP 8-190933

; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-90

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 7
US-09-557-917-101
; Sequence 101, Application US/09557917
; GENERAL INFORMATION:
; APPLICANT: Aida, Yoko
; TITLE OF INVENTION: METHODS FOR JUDGING THE POSSIBILITY OF THE ONSET OF
; FILE REFERENCE: BOVINE LEUKEMIA AND THE RESISTANCE THERETO
; CURRENT APPLICATION NUMBER: US/09/557,917
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/147,550
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02485
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: JP 8-190933
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: JP 9-77979
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 94
; TYPE: PRT
; ORGANISM: BOVINE
US-09-557-917-101

Query Match 65.5%; Score 36; DB 5; Length 94;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 80 RHNYGVF 86

RESULT 8
US-60-259-128-4587
; Sequence 4587, Application US/60259128
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: GRACE1
; CURRENT APPLICATION NUMBER: US/60/259,128
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 5129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4587
; LENGTH: 288

; TYPE: PRT
; ORGANISM: Candida albicans
US-60-259-128-4587

Query Match 61.8%; Score 34; DB 6; Length 288;
Best Local Similarity 83.3%; Pred. No. 9.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 93 HNYGAF 98

RESULT 9
US-09-099-463A-8
; Sequence 8, Application US/09099463A
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)
; and Central Nervous System Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,463A
; FILING DATE: 18-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/050,242
; FILING DATE: 19-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.4420001/JAG/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-099-463A-8

Query Match 61.8%; Score 34; DB 5; Length 503;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
Db 162 RHNYMSAAT 170

RESULT 10
US-09-595-329A-635
; Sequence 635, Application US/09595329A
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 635
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(246)
; OTHER INFORMATION: Ceres Seq. ID no. 1013211
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-635

Query Match 60.0%; Score 33; DB 5; Length 246;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
:|||||
Db 131 KHNYGS 136

RESULT 11
US-09-595-329A-634
; Sequence 634, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 634
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres Seq. ID no. 1013210
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-634

Query Match 60.0%; Score 33; DB 5; Length 248;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
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Db 133 KHNYGS 138

RESULT 12
US-09-595-329A-633
; Sequence 633, Application US/09595329A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai

; APPLICANT: VYACHESLAV, Brover
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-0948P
; CURRENT APPLICATION NUMBER: US/09/595,329A
; CURRENT FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3309
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(275)
; OTHER INFORMATION: Ceres Seq. ID no. 1013209
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-329A-633

Query Match 60.0%; Score 33; DB 5; Length 275;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
:|||||
Db 160 KHNYGS 165

RESULT 13
PCT-US00-33549-61
; Sequence 61, Application PC/TUS0033549
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Human
; TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 018623-016110PC
; CURRENT APPLICATION NUMBER: PCT/US00/33549
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/641,528
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Human papillomavirus type 33
PCT-US00-33549-61

Query Match 60.0%; Score 33; DB 1; Length 467;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFAT 10
:|:|:|:|
Db 378 QHSYSTFAT 386

RESULT 14
US-09-489-039A-13978
; Sequence 13978, Application US/09489039A

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13978
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13978

Query Match 60.0%; Score 33; DB 5; Length 479;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFA 9
Db 85 RHDYRSEA 92

RESULT 15
US-09-756-983-11
; Sequence 11, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-983-11

Query Match 58.2%; Score 32; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 11 RHNYG 15

Search completed: March 28, 2001, 07:22:13
Job time: 1505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 28, 2001, 07:18:20 ; Search time 828.17 Seconds
(without alignments)
1.759 Million cell updates/sec

Title: US-09-016-061-72

Perfect score: 56

Sequence: 1 ARHNGSFAD 10

Scoring table: BLOSUMP2

Gapop 10.0 , Capext 0.5

Searched: 898110 seqs, 145640331 residues

Total number of hits satisfying chosen parameters: 898110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main.*

- 1: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgnl_7/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgnl_7/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgnl_7/ptodata/1/paa/US08_COMB.pep.*
- 5: /cgnl_7/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgnl_7/ptodata/1/paa/US082_COMB.pep.*
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- 8: /cgnl_7/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgnl_7/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgnl_7/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgnl_7/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgnl_7/ptodata/1/paa/US088_COMB.pep.*
- 13: /cgnl_7/ptodata/1/paa/US089_COMB.pep.*
- 14: /cgnl_7/ptodata/1/paa/US090_COMB.pep.*
- 15: /cgnl_7/ptodata/1/paa/US091_COMB.pep.*
- 16: /cgnl_7/ptodata/1/paa/US092_COMB.pep.*
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- 19: /cgnl_7/ptodata/1/paa/US095_COMB.pep.*
- 20: /cgnl_7/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgnl_7/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgnl_7/ptodata/1/paa/US098_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	14	US-09-016-061-72
2	56	100.0	10	17	US-09-339-922A-72
3	52	92.9	10	14	US-09-016-061-74
4	52	92.9	10	17	US-09-339-922A-74
5	50	89.3	10	14	US-09-016-061-40
6	50	89.3	10	14	US-09-016-061-68
7	50	89.3	10	14	US-09-016-061-70
8	50	89.3	10	14	US-09-016-061-76
9	50	89.3	10	14	US-09-016-061-78
10	50	89.3	10	14	US-09-016-061-80
11	50	89.3	10	17	US-09-339-922A-40

12	50	89.3	10	17	US-09-339-922A-68	Sequence 68, Appl
13	50	89.3	10	17	US-09-339-922A-70	Sequence 70, Appl
14	50	89.3	10	17	US-09-339-922A-76	Sequence 76, Appl
15	50	89.3	10	17	US-09-339-922A-78	Sequence 78, Appl
16	50	89.3	10	17	US-09-339-922A-80	Sequence 80, Appl
17	50	89.3	117	1	PCT-US98-25828-54	Sequence 54, Appl
18	50	89.3	117	1	PCT-US98-25828-56	Sequence 56, Appl
19	50	89.3	117	11	US-08-790-540-2	Sequence 2, Appl
20	50	89.3	117	11	US-08-790-540-6	Sequence 6, Appl
21	50	89.3	117	11	US-08-790-540A-2	Sequence 2, Appl
22	50	89.3	117	11	US-08-790-540A-6	Sequence 6, Appl
23	50	89.3	117	11	US-08-791-391-2	Sequence 2, Appl
24	50	89.3	117	11	US-08-791-391-6	Sequence 6, Appl
25	50	89.3	117	11	US-08-791-391A-2	Sequence 2, Appl
26	50	89.3	117	11	US-08-791-391A-6	Sequence 6, Appl
27	50	89.3	117	13	US-08-986-016-54	Sequence 54, Appl
28	50	89.3	117	13	US-08-986-016-56	Sequence 56, Appl
29	50	89.3	117	14	US-09-016-061-2	Sequence 2, Appl
30	50	89.3	117	14	US-09-016-061-6	Sequence 6, Appl
31	50	89.3	117	17	US-09-339-922A-2	Sequence 2, Appl
32	50	89.3	117	17	US-09-339-922A-6	Sequence 6, Appl
33	50	89.3	118	1	PCT-US98-25828-50	Sequence 50, Appl
34	50	89.3	118	1	PCT-US98-25828-51	Sequence 51, Appl
35	50	89.3	118	1	PCT-US98-25828-52	Sequence 52, Appl
36	50	89.3	118	1	PCT-US98-25828-53	Sequence 53, Appl
37	50	89.3	118	13	US-08-986-016-50	Sequence 50, Appl
38	50	89.3	118	13	US-08-986-016-51	Sequence 51, Appl
39	50	89.3	118	13	US-08-986-016-52	Sequence 52, Appl
40	50	89.3	119	13	US-08-986-016-53	Sequence 53, Appl
41	50	89.3	130	1	PCT-US98-25828-44	Sequence 44, Appl
42	50	89.3	130	13	US-08-986-016-44	Sequence 44, Appl
43	47	83.9	10	14	US-09-016-061-62	Sequence 62, Appl
44	47	83.9	10	17	US-09-339-922A-62	Sequence 62, Appl
45	46	82.1	10	17	US-09-339-922A-100	Sequence 100, App

ALIGNMENTS

RESULT 1

US-09-016-061-72

; Sequence 72, Application US/09016061

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; APPLICANT: Glaser, Scott M.

; TITLE OF INVENTION: Anti-Alpha v Beta 3 Recombinant Human

; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,061

; FILING DATE: 30-JAN-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/791,391

; FILING DATE: 30-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IX 2965

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

```
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match      100.0%; Score 56; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
Db 1 ARHNYGSFAD 10

RESULT 2
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match      100.0%; Score 56; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
Db 1 ARHNYGSFAD 10

RESULT 3
US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-72

Query Match      100.0%; Score 56; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
Db 1 ARHNYGSFAD 10

RESULT 2
US-09-339-922A-72
; Sequence 72, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-72

Query Match      100.0%; Score 56; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
Db 1 ARHNYGSFAD 10

RESULT 3
US-09-016-061-74
; Sequence 74, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-74

Query Match      92.9%; Score 52; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
Db 1 ARHNYGSFAD 10

RESULT 4
US-09-339-922A-74
; Sequence 74, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-74

Query Match      92.9%; Score 52; DB 17; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
Db 1 ARHNYGSFAD 10

RESULT 5
US-09-016-061-40
; Sequence 40, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alphav Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-40

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
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Db 1 ARHNYGSFA 9

RESULT 6
US-09-016-061-68
Sequence 68, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-68

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 1 ARHNYGSFA 9

RESULT 7
US-09-016-061-70
Sequence 70, Application US/09016061
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-70

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 1 ARHNYGSFA 9

RESULT 8
US-09-016-061-76
; Sequence 76, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-76

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 9
US-09-016-061-78
; Sequence 78, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-061-78

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 10
US-09-016-061-80
; Sequence 80, Application US/09016061
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
us-09-016-061-80

Query Match 89.3%; Score 50; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 11
US-09-339-922A-40
; Sequence 40, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-339-922A-40

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 12
US-09-339-922A-68
; Sequence 68, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-68

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

Db 1 ARHNYGSFA 9

RESULT 13
US-09-339-922A-70
; Sequence 70, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-70

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 14
US-09-339-922A-76
; Sequence 76, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-76

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 15
US-09-339-922A-78
; Sequence 78, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-78

Query Match 89.3%; Score 50; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNYGSFA 9

Search completed: March 28, 2001, 07:18:20
Job time: 1331 sec